

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttggctctga | gtgctttctt | ttggctgtta | tggcttatga | ccgctacact | gccatttgcc | 180 |
| accctctaag | atacaccaat | ctcatgagcc | ctaaaatttg | tggacttatg | actgcctttt | 240 |
| cctggatect | gggctctacg | gatggaatta | ttgatgttgt | agcaacattt | tcctttcctt | 300 |
| actgtgggtc | tcgggaaata | gcccacttct | tctgtgactt | ccccctccct | actaatcctc | 360 |
| tcatgcagtg | acacatcaat | atttgaaaag | attcttttca | tctgctgtat | agtaatgatt | 420 |
| gttttccctg | ttgcaatcat | cattgcttcc | tatgctcgag | ttatcctggc | tgctattcac | 480 |
| atgggatctg | gagaggggtc | tcgcaaagct | tttactactt | gttcctctca | cctcttggtg | 540 |
| gtgggaatgt | actatggagc | agctttgttc | atgtacatac | ggccacatc  | tgatcgctcc | 600 |
| ccaacacagg | acaagatggt | gtctgtattc | tacaccatcc | tcactccc   |            | 648 |

&lt;210&gt; 802

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g652 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 802

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tttgtggaca | ttgcctgttc | ctcagccaca | gcacccaaga | tgattgaaga | ctttgtttct | 60  |
| gagaaaaaga | ctatttccta | ctggggctgt | ataactcaga | tgtttacctt | ccactttttt | 120 |
| ggttgtgctg | agatttttgt | tttgactgtc | atggcttttg | atcgctatgc | tgctatctgc | 180 |
| caacccctcc | gttacactgt | catcatgagt | gctaatgctt | atactgtgct | ggcatcactg | 240 |
| tcctggttgg | gggccctggg | tcattccttt | gttcagaccc | tcctgacctt | ccagctgccc | 300 |
| ttctgtaatg | ctcaggttat | agaacattac | ttttgtgatg | tccacccagt | cctaaaactt | 360 |
| gcctgtgctg | atacaactct | ggtaaatatg | ttggtggttg | ccaacagtgg | tctcatctcc | 420 |
| ctgggggtgt | tcctcattct | tttggcctcc | tacacagtca | ttctgtttag | tcttcaaaaa | 480 |
| cagtctgcag | agagctgaca | caaagttctc | tctacctgtg | gatctcatct | gactatagta | 540 |
| actttcttct | ttgttcctgt | tatctttatt | tatctccatc | cactactttc | ccattggata | 600 |
| aagctgtgtc | tgtgttctat | accaccatca | ccccca     |            |            | 635 |

&lt;210&gt; 803

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g653 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 803

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| ttgcctgaca | tcggtttcac | ctccacacgg | tccccaagat | gattgtggac | atccagttctc | 60  |
| acagcagagt | catctcctat | gcaggctgcc | tgactcagat | gtctctcttt | gccatttttt  | 120 |
| gaggcaggga | agagagacat | gtccttgagt | gtgatggcct | acgaccagtt | tgtagccatc  | 180 |
| tgtcaccctc | catatcgttc | agccatcttg | aaccctgttt | tctgtggctt | cctagatttg  | 240 |
| ttgtccttgt | ttttttttct | tttttttttt | tctcagttct | ttagactccc | agctgcacaa  | 300 |
| cttgattgcc | ttacaaatga | cctgcttcaa | ggatgtggaa | attcctaatt | tcttctggga  | 360 |
| accttctcaa | ctcccccata | ttgcatgttg | tgacatcttc | accaggaaca | tcaacctgta  | 420 |
| tttccctgct | gccatatttg | gttttcttcc | catctcgggg | acccttttct | cttactctaa  | 480 |
| aattgtttcc | tccattctga | gggtttcctc | gtcaggtggg | aggtataaag | ccctctccac  | 540 |
| ctgtgggtct | cacgtgtcag | ttgtttgctg | agtttatgga | acaggcgttg | gagggtaact  | 600 |
| cagttcggat | gtgtcatttt | cccccagaaa | gggtgcagtg | gcctcagtga | tgtacgcggt  | 660 |
| tgtcaccccc |            |            |            |            |             | 670 |

&lt;210&gt; 804

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g654 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 804

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| ctcctggatc  | tttgttacac  | cacatgtaca | gtcccacaaa | tgctagtaaa  | tttatgcagc | 60  |
| atcaggaaag  | taatcagtta  | tcgtggctgt | gtagcccagc | ttttcatatt  | tctggccttg | 120 |
| ggggctactg  | aatatcttct  | cctggccgtc | atgtcccttg | ataggtttgt  | agctatttgt | 180 |
| cggcctctcc  | attactcagt  | tatcatgcac | cagagactct | gcctccagtt  | ggcagctgca | 240 |
| tccagggtta  | ctgggttttag | taactcagtg | tgggtgtcta | ccctgactct  | ccagctgcca | 300 |
| ctctgtgacc  | cctatgtgat  | agaccacttt | ctctgtgaag | tccctgcact  | gctcaagtta | 360 |
| tcttgtgttg  | agacaacagc  | aaatgaggct | gaactattcc | ttgtcagtga  | gctcttccat | 420 |
| ctaatacccc  | tgacactcat  | ccttatatca | tatgctttta | ttgtccgagc  | agtattgagg | 480 |
| atacagtcctg | ctgaaggctg  | acaaaaagca | tttgggacat | gtgggttccca | tctaattgtg | 540 |
| gtgtctcttt  | ttaatagtac  | agccgtctct | gtgtacctgc | aaccaccttc  | gcccagctcc | 600 |
| aaggaccaag  | gaaagatggt  | ttctctcttc | tatggaatca | ttgcaccc    |            | 648 |

&lt;210&gt; 805

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g655 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 805

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| ttgcctgaca | tcgggtttcac | ctccaccatt | gtccccaaga | tgattgtgga  | catccagctct | 60  |
| cacagcagag | tgatctccta  | tgcaggccgc | ctgactcaga | tgtctctctt  | tgccattttt  | 120 |
| ggaggcatgg | aagacagaca  | tgctcctgag | tgtgatggcc | tatgaccggg  | tcgtagccat  | 180 |
| ctgtcaccct | ctatatcatt  | cagccatcat | gaatccgtgt | ttctgtggct  | tcctactttt  | 240 |
| gttgtctttt | ttttttctca  | gtcttttaga | cgcccagctg | cacaacttga  | ttgccttaca  | 300 |
| aatgacctgc | ttcaaggatg  | tggaaattcc | taatttcttc | tgtgaccctt  | ctcaactccc  | 360 |
| ccatcttgca | tgttgtgaca  | ccttcaccaa | taacataatc | atgtattttc  | ctgctgccat  | 420 |
| atthtggttt | cttcccatct  | cggggaccct | tttctcttac | gataaaaattg | tttcctccat  | 480 |
| tctgagggtt | tcacatcag   | gtgggaagta | taaagccttc | tccacctatg  | ggctctcacct | 540 |
| gtcagatggt | tcctgatttt  | atggaacagg | cggtggaggg | tacctcagtt  | cagatgtgtc  | 600 |
| atcttccccg | agaaagactg  | cagtggcctc | agtgatgtac | acagtgggtca | cccc        | 655 |

&lt;210&gt; 806

&lt;211&gt; 662

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g656 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 806

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| tttcttgaca | tcgggtttcac | ctccaccaca  | gtccccaaga | tgattgtgga | catccagctct | 60  |
| cacagcagag | tcattctcta  | tgcaggctgc  | cagactcaga | tgtctctctt | tgccattttt  | 120 |
| ggagacacgg | aagagagaca  | tgttcctgag  | tgtggtggcc | tatgaccggg | ttgtagccat  | 180 |
| ctgtcaccct | ctatatcggt  | cagccatctt  | aaaccctgt  | ttctgtggct | tcctagattc  | 240 |
| gttgtccttg | gttttttttt  | ttttctcagt  | cttttagact | cccagctgca | caacttgatt  | 300 |
| gccttacaaa | tgacctgctt  | caaggatgtg  | gaaattccta | atthtctctg | ggaaccttct  | 360 |
| caactccccc | atcttgcatg  | ttgtgacatc  | ttcaccagga | acatcaacct | gtatttccct  | 420 |
| gctgccatat | ttgggtttct  | tcccatctcg  | gggacgcttt | tctcttgcta | taaaattggt  | 480 |
| tccttcattc | tgagggtttc  | atcatcaggt  | gggaagtata | aaccttctcc | gcctgtgggt  | 540 |
| ctcatctgtc | agttgtttac  | tgatttttatg | gaacaggctt | tggagggtac | ctcagttcag  | 600 |
| atgtgtcatc | ttccccgaga  | aagactgcag  | tggcctcagt | gatgtacgca | gtggtcaccc  | 660 |
| cc         |             |             |            |            |             | 662 |

&lt;210&gt; 807

&lt;211&gt; 647

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g657 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 807

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| gtgctggatg | tggatgtat   | cactgtcact  | gttcctgcaa  | tgttgggtcg | tctcttgtec | 60  |
| cacaagtcca | caatttccta  | tgacgcctgc  | ctctcccagc  | tctctctctt | ccaccttctg | 120 |
| gctgggatgg | actgcttcct  | gctgaccgcc  | atggcctatg  | accgactcct | ggccatctgc | 180 |
| cagccccca  | cctacagcac  | ccgcatgagt  | cagacagtcc  | agaggatgtt | ggtggctgcg | 240 |
| tcttgggctt | gtgccttcac  | caacgcactg  | acccacactg  | tggccatgtc | cacgctcaac | 300 |
| ttctgtggcc | caaagtgggt  | caatcacttc  | tactgtgacc  | tcccacagct | cttcagctc  | 360 |
| tcctgtctta | gcacccaact  | caatgagctg  | ctgctctttg  | tagcagcagc | cttcattggt | 420 |
| gtggcaccct | tggcttctcat | cagtgtgccc  | tatgcccattg | tggtagctgc | tgtgctgcaa | 480 |
| atcgctccgc | tgagggcaga  | aagaaggcct  | tctccacatg  | tggctcccac | ctcactgtgg | 540 |
| tgggcatctt | ctatgggaca  | ggtgtcttca  | gctacatgag  | gctgggttca | gtggaatctt | 600 |
| cagacaagga | taagggggtt  | gggggttttca | tgactgtgat  | caacccc    |            | 647 |

&lt;210&gt; 808

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g658 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 808

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| tttgtggaca | tagcctgttc | ctcagccaca | gcacccaaga  | tgattgaaga | ctttgtttct  | 60  |
| gagaaaaaga | ctatttccta | ctggggctgt | ataactcaga  | tgtttacctt | ccactttttt  | 120 |
| ggttgtgctg | acattttttg | tttgactgtc | atggcttttg  | atcgctgtgc | tgctatctgc  | 180 |
| caacccctcc | gttacactgt | catcatgagt | gctaattgctt | atactgtgct | ggcatcactg  | 240 |
| tcctgggttg | gggcccctgg | tcatttcctt | gttcagaccc  | tcctgacctt | ccagctgccc  | 300 |
| ttctgtaatg | ctcaggttat | agaccattac | ttttgtgatg  | tccacccagt | cctaaaaactt | 360 |
| gcctgtgctg | atacaactct | ggtaaatatg | ttgggtggtg  | ccaacagtgg | tctcatctcc  | 420 |
| ctgggggtgt | tcctcattct | tttggcctcc | tacacagtca  | ttctgtttag | tcttcaaaaa  | 480 |
| cagtctgcag | agagctgaca | caaagtcttc | tctacctgtg  | gatctcatct | gactatagta  | 540 |
| actttcttct | ttgttcctgt | tatctttatt | tatctccatc  | cactactttc | ccattggata  | 600 |
| aagctgtgtc | tgtgttctat | accaccatca | cccca       |            |             | 635 |

&lt;210&gt; 809

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g659 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 809

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| ttctctgacc | tctgcttctc | ttccgtgacc  | attcccaagt | tgttacagaa  | catgcagaac | 60  |
| caggacccat | ccatccccta | tgcggaactgc | ctgacccaaa | tgtacttctt  | cctgttattt | 120 |
| ggagacctgg | agagcttctc | ccttgtggcc  | atggcctatg | accgctatgt  | ggccatctgc | 180 |
| ttccccctgc | actacaccgc | catcatgagc  | cccatgctct | gtctcgccct  | ggtggcgctg | 240 |
| tcctgggtgc | tgaccacctt | ccatgccatg  | ttacacactt | tactcatggc  | caggttgtgt | 300 |
| ttttgtgcag | acaatgtgat | ccccactttt  | ttctgtgata | tgtctgctct  | gctgaagctg | 360 |
| gccttctctg | acactcgagt | taatgaatgg  | gtgatattta | tcattgggagg | gctcattctt | 420 |
| gtcatcccat | tcctactcat | ccttgggtcc  | tatgcaagag | ttgtctcctc  | catcctcaag | 480 |
| gtcccttctt | ctaagggtat | ctgcaaggcc  | ttctctactt | gtggctccca  | cctgtctgtg | 540 |
| gtgtcactgt | tctatggaac | cgttattggt  | ctctacttat | gctcatcagc  | taatagttct | 600 |
| actctaaagg | acactgtcat | ggctatgatg  | tacactgtgg | tgaccccc    |            | 648 |

&lt;210&gt; 810

&lt;211&gt; 438

&lt;212&gt; DNA

<213> Unknown (H38g660 nucleotide)

<220>

<223> Synthetic construct

<400> 810

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| actttgcaga | atatcacctc | cacttccatc | atthttcctgc | tcactgggtgt | tcctgggctg  | 60  |
| gaagccttcc | acacctggat | ctccattccc | ttctgtctcc  | tcctctgtaac | tgctctcttg  | 120 |
| ggaaacagcc | tgatcctctt | cgctaccatc | actcagccca  | gcctccacga  | accaatgtac  | 180 |
| tatttctctc | ccatgctgtc | cgccactgac | ctcggcctgt  | ccatatccac  | tctgggtcacc | 240 |
| atgctgagta | tattctgggt | caatgtgagg | gaaatcagct  | ttaatgcctg  | cttgtcccac  | 300 |
| atgttcttta | ttaaattctt | cactgtcatg | gaatcctcag  | tgctgttggc  | catggctttt  | 360 |
| gacgttttgg | tgccgtctct | atccccttag | tatgccatga  | tttaactgac  | tcagatagct  | 420 |
| aaaatgagtg | cagtgtat   |            |             |             |             | 438 |

<210> 811

<211> 1002

<212> DNA

<213> Unknown (H38g661 nucleotide)

<220>

<223> Synthetic construct

<400> 811

|            |            |             |            |             |             |      |
|------------|------------|-------------|------------|-------------|-------------|------|
| gcagggtgtg | aaaacgataa | tacaagttct  | ttcgaaggct | tcactcctggt | gggcttctct  | 60   |
| gacgtcccc  | acctagagct | gacgtctctt  | gtggttgtcc | tcactcttta  | tctgctgact  | 120  |
| cttcttggca | acatgaccat | tgtcttgctt  | tcagctctgg | attcccggct  | gcacacacca  | 180  |
| atgtatttct | ttttggcaaa | cctctcattc  | ctggacatgt | gtttcaccac  | aggttccatc  | 240  |
| cctcagatgc | tctacaacct | ttgggggtcca | gataagacca | tcagctatgt  | gggttgtgccc | 300  |
| atccagctgt | actttgtcct | ggccctggga  | ggggtggagt | gtgtcctcct  | ggctgtcatg  | 360  |
| gcataagacc | gctatgctgc | agtctgcaaa  | cccctgcact | acaccatcat  | catgcaccca  | 420  |
| cgtctctgtg | gacagctggc | ttcagtgcca  | tggctgagtg | gctttggcaa  | ttctctcata  | 480  |
| atggcacccc | agacattgat | gctacccgcg  | tgtgggcaca | gacgagttga  | ccactttctc  | 540  |
| tgtgagatgc | cagcactaat | tggtatggcc  | tgtgtagaca | ccatgatgct  | tgaggcactg  | 600  |
| gcttttgccc | tggcaatctt | tatcatcctg  | gcaccactca | tcctcattct  | catttcttat  | 660  |
| ggttacgttg | gaggaacagt | gcttaggatt  | aagtcagctg | ctggggcgaaa | gaaagccttc  | 720  |
| aacacttgca | gctcgcactc | aattgttgtc  | tctctcttct | atggtacaat  | catatacatg  | 780  |
| tacctccagc | cagcaaatac | ttattcccag  | gaccagggca | agtttcttac  | ccttttctac  | 840  |
| acaattgtca | ctcccagtg  | taaccccctg  | atctatacac | taagaaacaa  | agatgttaaa  | 900  |
| gaggccatga | agaaggtgct | aggggaaggg  | agtgcagaaa | tatagtaagg  | ggtgattaaa  | 960  |
| ctttgggatt | gtattttgac | ccatcttcta  | tatatgttgt | ta          |             | 1002 |

<210> 812

<211> 827

<212> DNA

<213> Unknown (H38g662 nucleotide)

<220>

<223> Synthetic construct

<400> 812

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| ctctacctca | tcaagcatga  | ccacagtctt  | catgagccca  | tgtactactt  | cctcaccatg  | 60  |
| ctggcaggca | cagacctcat  | ggtgacattg  | accacgatgc  | ctactgtaat  | gggcataccta | 120 |
| tgggtgaatc | acagggaaga  | ttagcagtg   | gggctgcttc  | ctacaggctt  | actttattca  | 180 |
| ctccctttct | gttggtggaat | caggttccct  | cctggcaatg  | gcatatgac   | gtctcattgc  | 240 |
| catccgcaat | cctttgagat  | atgctctcca  | tttccaccaa  | tactagagtc  | atagcgttag  | 300 |
| gagtgggatt | gttcctaagg  | ggtttgggtat | ccatcctgcc  | tgtaattttg  | cgtctttttc  | 360 |
| catttccata | tggcaaatct  | catgttatca  | cacgttgctt  | tctgcctcca  | ccaagaaatc  | 420 |
| atgagactgg | cttggtgctga | cataacttcc  | aataaaacttt | accctgtaat  | tttgatctct  | 480 |
| ttaacaatct | ccctaaactc  | tctgatcacc  | ccctcctcct  | atatacctaat | ccttaataact | 540 |
| gtcataggca | ttgcctctg   | tgaaaaaaaaa | ccaaagccct  | caataacctgt | atctcccaca  | 600 |



|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| taagttgtgt  | ccttatctcc | tatgttacgg | tgatggggtt | gacattcatt | tacaaatttg | 660 |
| ggaagaatgt  | gccaaagggt | gtccacatta | tcataagtta | catctacttc | ctctttcccc | 720 |
| ctttaatgaa  | ccctgtcatc | tacagcatca | aaaccaagca | aatacaatat | ggcattatcc | 780 |
| gcctttttatc | taaacatagg | tttagtaggt | aaactcggat | ctggaaa    |            | 827 |

&lt;210&gt; 813

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g663 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 813

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| ttggccgaca  | tcggtttcac | ctccaacacg | gtccccaaga  | tgattgtgga  | catccaatct | 60  |
| cacagcagag  | tcattctcta | tgagggtgc  | ctgactcaga  | tgtctctctt  | tgctgttttt | 120 |
| ggaggcatgg  | aagaaagaca | tgctcctgag | tgtaggggcc  | tatgaccggg  | ttgtagccat | 180 |
| ctgtcacccct | ctatatgtgt | cagccatctt | taaccctgtg  | ttctgtgggt  | tcctagattt | 240 |
| gttgtctttt  | tttttttttt | ttctcagtct | ttcagactcc  | cagctgcaca  | acttgattgc | 300 |
| cttacaaatg  | acctgcttca | aggatgtgga | aattccta    | ttcttctggg  | aaccttctca | 360 |
| actctcccat  | cttgcattgt | gtgacacctt | caccagggaac | atcagtattt  | ccctgctgcc | 420 |
| atatttggtt  | ttcttcccat | ctcggggacc | cttttctctt  | acgataaaat  | tgttttctcc | 480 |
| attctgaggg  | tttcatcatc | aggtgggaag | cataaggcct  | tctccaccag  | ggggctctac | 540 |
| ctgtcagttg  | tttctgtatt | ttatggaaca | ggcattggag  | gtacacctag  | ttcagatgtg | 600 |
| tcattcttccc | cgagaaaggc | tgtagtggtc | tcagtgtatg  | acacgggtggc | catcccc    | 657 |

&lt;210&gt; 814

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g664 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 814

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| ttgcctgaca  | tcggtttccc  | ctccccacg   | gtccccaaga | tggttgtgga  | catccaatct  | 60  |
| cacagcagag  | tcattctcta  | tgagggtgc   | ctgactcaga | tgtctctctt  | tgccattttt  | 120 |
| ggaggcatgg  | aagagacaca  | tgctcctgaa  | tgtagtggtc | tatgtccggg  | ttgtagccat  | 180 |
| ctgtcacccct | ctatatcatt  | cagccatcat  | gaaccctgtg | ttctgtgggt  | tcttactttt  | 240 |
| gttgtctttt  | ttttttctcg  | gtctttttaga | cgcccagctg | cacaacatga  | ttgccttaca  | 300 |
| aatgacctgc  | atcaaggatg  | tggaattccc  | taatttcttc | tgtagaccct  | ctcaactccc  | 360 |
| acaccttgcg  | tggttgtgaca | ctttcaccaa  | taacatagtc | atgtatttcc  | ttgctgccat  | 420 |
| atttggtttt  | cttccatctt  | caggatcat   | tttctcttac | tataaaattg  | tttctctccat | 480 |
| gctgagtgtt  | tcattcatcag | gtgggaagta  | taaagccttc | tccatctgtg  | gggtctccct  | 540 |
| gtcagttgtt  | tgcttatttt  | atggaaaagt  | cgttgggggg | tacctgagtt  | cagatgtgtc  | 600 |
| atcttccccc  | agaaagggtg  | cagtggcctc  | aatgatgtac | acgggtgatca | cccc        | 655 |

&lt;210&gt; 815

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g665 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 815

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctagtggact | tttgttactc | ttcagctgtc | actcccacag | tcattgctgg | gctcgttata | 60  |
| ggagacaagg | tcattcttta | caatgcatgt | gctgctcaaa | tggtcttttt | tgagcccttt | 120 |
| gccactgtgg | aaaatttcc  | cttggcctcg | atggcctatg | accgccatga | tgagtggtgc | 180 |
| aaacccttac | attacaccac | caccatgaca | acaagtgtgt | gtgcatgtct | ggctataatc | 240 |
| tggtatgtct | gtgggtttct | gaatgcctcc | atacacattg | gggaaacatt | gtctctcttt | 300 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctgtatgtcc | aatgaagtc  | attgcttttt | ctgtgatgtt | ccaccagtca | tggctctgtc | 360 |
| ttgctgtgat | agacatgtga | atgggctagt | tctcatttat | gtagccagtt | tcaatatctt | 420 |
| ttctgccatc | ctagttatct | tgatctccta | cctattcata | tttatcacca | tcctaaggac | 480 |
| gcactcggct | tcaggatacc | agaaggcttt | gtccacctgt | gcctcccacc | tcactgcagt | 540 |
| catcatcttc | tatgggacta | ttatctccat | gtacttacag | cccagctctg | gtcactccat | 600 |
| ggacacagac | aaactggcat | ctgtgtccta | tactatgatc | atcccc     |            | 646 |

&lt;210&gt; 816

&lt;211&gt; 649

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g666 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 816

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| ttgcctgaca | tcggttttcac | ctccaccatg | gtccccaaga  | tgattgtgga | atccaatctc | 60  |
| acagcagagt | catctcctac  | gcaggctgcc | tgactcagat  | gtctctcttt | gccatttttg | 120 |
| gaggcatgga | agagagacat  | gtccttgagt | gtgatggcct  | atgaccgggt | tgtagccatc | 180 |
| tgccaccctc | tatatcatte  | agccatcatg | aaccctgtgt  | tctgtggcct | cctagttttg | 240 |
| ctgtcttttt | tttctttctt  | tttctcagct | gcacaacttg  | attgccttaa | aaatgacctg | 300 |
| cttcaaggat | gtggaaaattc | ctaatttctt | ctgtgacctt  | tctcaactcc | cccatcttgc | 360 |
| atgttgtgac | accttcacca  | ataagataat | catgtatttc  | cctgctgcca | tatttggttt | 420 |
| tcttcccatc | tcagggaccc  | ttttctctta | ctctaaaatt  | gtttctctca | ttctgagggt | 480 |
| ttcatcatca | ggtgggaagt  | ataaagcctt | ctccacctgt  | gggtctcacc | tgtcagttgt | 540 |
| ttgtctgagt | tatggaacag  | gcgttggagg | ttacctcagt  | tcagatgatg | tgcatcttcc | 600 |
| ccccagaaag | ggtgcagtgg  | cctcagtgat | gtacacgggtg | gtcaccccc  |            | 649 |

&lt;210&gt; 817

&lt;211&gt; 651

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g667 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 817

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| atcattgata  | tttcgtatgc | ttccaacaaa  | gtccccaaga  | tgctgacaaa | ccttggtctg  | 60  |
| aacaagagaa  | aaacaatctc | ctttgtccca  | tgacacatgc  | agaccttttt | atacatggct  | 120 |
| tttgtctaca  | ctgagtgtct | catcttggtg  | atgatgtcct  | acgatcggta | catggctatc  | 180 |
| tgccaccctc  | tgcaatatte | tgatcatcatg | agatggggag  | tgtgcacagt | cctggctgtc  | 240 |
| acttcttggg  | catgtgggtc | ccttctggcc  | ctgggtccatg | tggttctcat | cctgaggctg  | 300 |
| cccttctgtg  | ggcccatatg | aatcaaccac  | ttcttctgtg  | aaatcctgtc | tgctcctcaag | 360 |
| ttggcctgtg  | ctgacacctg | gctcaaccag  | gtgggtcatct | ttgctgcttc | agtgttcctc  | 420 |
| ctgggtggggc | cgctctgcct | ggtgctggtc  | tctactcgc   | gcatectggc | ggccatcttg  | 480 |
| gggatccagt  | ctggggaggg | ccgcagaaaag | gccttctcca  | cctgctcctc | ccacctttgc  | 540 |
| atggtggggac | tcttcttttg | cagcgccatt  | gtcatgtaca  | tggtcccca  | gtcccggcac  | 600 |
| cctgaggagc  | agcagaaggt | cctttccctg  | ttttacagcc  | ttttcaacc  | g           | 651 |

&lt;210&gt; 818

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g668 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 818

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ctagtggact | tttgttactc | ttcagctgtc | actccacacag | tcatagctgg | gtctggtata | 60  |
| ggagacgagg | tcattcttta | cagtgcattg | gctgctcaaa  | tggtcttttt | tgcagccttt | 120 |
| gccactgtgg | aaaatttctt | cttggcctca | atggcctatg  | accgctatga | tgcagtgtgc | 180 |

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| aaacccctac | attacaccac  | caccatgaca  | acaagtgtgt | gtgcatgtct | ggctataatc | 240 |
| tggtatgtct | gtgggtttctt | gaatgcctcc  | atacacattg | gggaaacatt | gtctctcttt | 300 |
| ctgaatgtcc | aatgaagtcc  | attgcatttt  | ctgtgatgtt | ccaccagtca | tggtctgtgc | 360 |
| ttgctgtgat | agacatgtga  | atgagctagt  | tctcatttat | gtagccagtt | tcaatatctt | 420 |
| ttctgccatc | ctagtaatcc  | tgggtctccta | cctattcata | tttatcacca | tcctagagat | 480 |
| gcactcagct | tcaggatacc  | agaaggcttt  | gtccaactgt | gcctcccacc | tcactgcagt | 540 |
| catcatcttc | tatgggacta  | ttatcttcat  | gtacttacag | cccagctctg | gtcactccat | 600 |
| ggacacagac | aaactggcat  | ctgtgtttcta | tactatgatc | atcccc     |            | 646 |

&lt;210&gt; 819

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g669 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 819

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| atggctgctg | agaattcctc  | cttcgtgaca  | cagttttatcc | tgcgaggctt | aactgaccaa | 60  |
| ccgggagtc  | agatccccct  | cttcttctctg | tttctaggct  | tctacgtggt | cactgtggtg | 120 |
| gggaacctgg | gcttgataac  | cctgataagg  | ctcaactctc  | acttgacac  | ccctatgtac | 180 |
| ttcttctct  | ataacttgct  | cttcatagat  | ttctgctatt  | ccagtgttat | cactcccaaa | 240 |
| atgctgatga | gctttgtctt  | aaagaagaac  | agcatctcct  | acgcagggtg | tatgactcag | 300 |
| ctcttctct  | ttcttttctt  | tgttgtctct  | gagtccttca  | tcctgtcagc | aatggcgat  | 360 |
| gaccgctatg | tggccatctg  | taaccactg   | ttgtacatgg  | tcaccatgtc | tccccagtg  | 420 |
| tgttttctcc | ttttgttggg  | tgtctatggg  | atgggggttg  | ctggggccat | ggccacaca  | 480 |
| gcgtgcatga | tgggtgtgac  | cttctgtgcc  | aataaccttg  | tcaaccacta | catgtgtgac | 540 |
| atccttcccc | ttcttgagtg  | tgcttgacc   | agcacctatg  | tgaatgagct | tgtagtgttt | 600 |
| gttgttgtgg | gcattgatat  | tgggtgtgcc  | acagtcacca  | tcttcatttc | ctatgctctc | 660 |
| attctctcca | gcattctcca  | cattgatctc  | acggaggggca | ggtccaaagc | cttcagcacc | 720 |
| tgcagctccc | acataattgc  | agtttctctg  | ttctttgggt  | caggagcatt | catgtacctc | 780 |
| aaaccttttt | ctctttttagc | tatgaaccag  | ggcaagggtg  | cttccctatt | ctataccact | 840 |
| gtggtgcccc | tgtctaaccc  | attaatttat  | agcctgagga  | ataaggacgt | caaagttgct | 900 |
| ctaaagaaaa | tcttgaacaa  | aatgcatttc  | tcc         |            |            | 933 |

&lt;210&gt; 820

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g670 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 820

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| atgactctga | gaaacagctc | ctcagtgact | gagttttatcc | ttgtgggatt  | atcagaacag | 60  |
| ccagagctcc | agctccctct | tttcttctta | ttcttagggga | tctatgtgtt  | cactgtggtg | 120 |
| ggcaacttgg | gcttgatcac | cttaattggg | ataaatccta  | gccttcacac  | ccccatgtac | 180 |
| tttttctct  | tcaacttgct | ctttatagat | ctctgttatt  | cctgtgtgtt  | tacccccaaa | 240 |
| atgctgaatg | actttgtttc | agaaagtatc | atctcttatg  | tgggatgtat  | gactcagcta | 300 |
| tttttctct  | gtttctttgt | caattctgag | tgtatgtgt   | tgggtatcaat | ggcctatgat | 360 |
| cgtatgtgg  | ccatctgcaa | ccccctgctc | tacatgggtc  | ccatgtcccc  | aagggtctgc | 420 |
| tttctgctga | tgtttgggtc | ctatgtggta | gggtttgctg  | gggccatggc  | ccacactgga | 480 |
| agcatgctgc | gactgacctt | ctgtgattcc | aacgtcattg  | accattatct  | gtgtgacgtt | 540 |
| ctccccctct | tgcagctctc | ctgcaccagc | acccatgtca  | gtgagctggg  | atttttcatt | 600 |
| gttgttggag | taatcaccat | gctatccagc | ataagcatcg  | tcatctctta  | cgctttgata | 660 |
| ctctccaaca | tcctctgtat | tccttctgca | gagggcagat  | caaagcctt   | tagcacatgg | 720 |
| ggctcccaca | taattgctgt | tgtctgtttt | tttgggtcag  | ggacattcac  | ctacttaaca | 780 |
| acatcttttc | ctggctctat | gaacctaggc | agatttgcc   | cagtctttta  | caccaatgtg | 840 |
| gttcccatgc | ttaacccttc | gatctacagt | ttgaggaata  | aggatgataa  | acttgccctg | 900 |
| ggcaaaaccc | tgaagagagt | gctcttc    |             |             |            | 927 |

<210> 821  
 <211> 887  
 <212> DNA  
 <213> Unknown (H38g671 nucleotide)

<220>  
 <223> Synthetic construct

<400> 821  
 atgaaatgaa tggcagtgga aaataactct tcggtgactg aattttatcct tgtgagatta 60  
 acaaactccc gctgccccag tgttttatct ttaatgtggt ccctgtgggg agaatttgaa 120  
 cataatttta tgtccctaaa ttctcacctt cataccccca cacacttttt cctcttcacg 180  
 ctatccttca ttgatgtctg ctattcattt gtctgtacca caaaaattcc aatgggcttt 240  
 atctcagaga ggaacatcat ctcccttttg ggatggccaa cgtagctata tttcttttgc 300  
 atctttgtca aagaacctaa aaatggggtc attgtgggaa taatgttctc agccaagatg 360  
 cttgtagccg agagataatg gactagtcgt tgatgtgaaa ctagaaaatg cacatggccc 420  
 tagaaaggtc tgatttttaga atgggataaa caggatctgc tacaagaaa catttaatca 480  
 tattcttgta ttacagcgat tatttccaga gatagtggag ctgcagagct ttgggacaag 540  
 gttccttagc gaagcaagac acactctcta gaattgcaca tgtactttta aaagtctgtt 600  
 acatattata atatgttttt atatttgga acagaaaaaa ataagttatt tatatcacia 660  
 atcatagaaa atggatcttt acaaaatctt catgttttgt gggttactca caagaaaaat 720  
 tttctccgct catttctact tctcaaatgg ttcaaggaaa aatgctcctt aaaggatata 780  
 tctgattctg gagaatgagc ttacctatgt gtgcaatttt tatctttgtc agaagatact 840  
 actaccttct gaaaaagttg aaaacactgc tttataagaa cagctat 887

<210> 822  
 <211> 939  
 <212> DNA  
 <213> Unknown (H38g672 nucleotide)

<220>  
 <223> Synthetic construct

<400> 822  
 atgctggcta gaaacaactc cttagtgact gaatttatct ttgctggatt aacagatcgt 60  
 ccagagttcc ggcaaccctt ctttttctct tttctagtgg tctacattgt caccatggta 120  
 ggcaaccttg gcttgatcat tcttttcggg ctaaattctc acctccacac accaatgtac 180  
 tatttctct tcaatctctc cttcattgat ctctgttact cctctgtttt cactcccaaa 240  
 atgctaataga actttgtatc aaaaaagaat attatctcct atgttgggtg catgactcag 300  
 ctgtttttct ttctcttttt tgtcatctct gaatgctaca tgttgacctc aatggcatat 360  
 gatcgctatg tggccatctg taatccattg ctgtataagg tcaccatgtc ccatcaggtc 420  
 tgttctatgc tcaacttttg tgcttacata atgggattgg ctggagccac ggcccacacc 480  
 ggggtgcatg ttagactcac ctctgcaggt gctaatatca tcaaccatta ctgtgtgac 540  
 atactcccc tctccagct ttctgcacc agcacctatg tcaacgaggt ggttgttctc 600  
 attgttggtg gtattaatat catggtaccc agttgtacca tctcatttc ttatgttttc 660  
 attgtcacta gcattcttca tatcaaatcc actcaaggaa gatcaaaagc cttcagtact 720  
 tgtagctctc atgtcattgc tctgtctctg ttttttgggt cagcggcatt catgtatatt 780  
 aaatattctt ctggatctat ggagcaggga aaagtttctt ctgttttcta cactaatgtg 840  
 gtgcccagtc tcaatcctct catctacagt ttgaggaaca aggatgtcaa agttgactg 900  
 aggaaagctc tgattaaaat tcagagaaga aatatattc 939

<210> 823  
 <211> 1071  
 <212> DNA  
 <213> Unknown (H38g673 nucleotide)

<220>  
 <223> Synthetic construct

<400> 823  
 atgaattggg taaataagag tgtccacacag gagttcatct tgttagtttt ctcagatcaa 60

```

ccatggctag agattccacc ctttgtgatg tttctgtttt cctatatctt gacaatcttt 120
ggcaatctga caataattct tgtgtcacat gtggatttca aactccacac ccctatgtac 180
ttttttctta gcaatctctc actcctggac ctttgctata ccacaagtac agttccacaa 240
atgctggtaa acatatgcaa caccaggaaa gtaatcagtt atgggtggctg tgtggcccag 300
cttttcattt tcctggcctt ggggtccaca gaatgtcttc tcctggcctg catgtgcttt 360
gataggtttg tagctatttg tgggcctctc cattactcaa ttatcatgca ccagaggctc 420
tgcttccagt tggcagctgc atcctggatt agtggcttta gcaattcagt attacagtc 480
acctggacac ttaagatgcc actgtgtggt cacaaagaag tggatcactt cttctgtgaa 540
gtccctgctc tgcctcaagt gtctgtggt gacacaacag caaatgaggc tgaactattc 600
ttcatcagtg tgctattcct tctaataccc gtgacactca tccttatatc gtatgctttt 660
attgtccaag cagtgttgag aatccagctc gctgaaggctc aacgaaaggc atttgggaca 720
tgtggctccc atctaattgt ggtgtcactt ttttatggta cagctatctc catgtacctg 780
caaccacctt caccagctc caaagaccgg ggaaagatgg tttctctctt ctgtggaatc 840
attgcacca tgctgaatcc ccttatatat acacttagga acaaagaggt aaaggaagcc 900
tttaaaaggt tgggtgcaaa gagtcttctt aatcaagaaa taagaaatat gcaaatgata 960
agcttttgcta aagacacagt gcttacttac cttactaact tctccgcaag ttgtcctatt 1020
tttgtcatta ctatagaaaa ctattgtaat ctccctcaaa gaaaatttcc t 1071

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&lt;210&gt; 824

&lt;211&gt; 991

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g674 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 824

```

atggctcctg gaaatggctt tttcatgact aaaatcattt tgctggagtt aacagatcag 60
ccagatctcc aactccctct gttcttctg tttctagtgt atggctcactg cgttgggaaa 120
tttggcttgg taactctcgt tgtgctcaat tcacaccttc ataccccat gtacttttctc 180
ctctttaact tgccttcat agatctctgt tattcttctg tgtttacacc ccaaagtctg 240
atgaacttca taacacagaa ggatattatc tcccacatgg ggtgcatgtc ccagcttttc 300
ttttttcttt attttttttt ggtatttctg aatgctatgt gctcacctca atggcctatg 360
atcagcatgt caccatgatc accatgtagc catctgtaac ccacttttgt ataattatgc 420
catgtcccc aaagtgtact ctcaccttat gcttggttta tacttgctag ctttttctag 480
tgccatggcc cacactggat gcatgctgag actgaccttc tgtgatgcaa acaccatcca 540
tccctatttg tgtgacatcc tccctctgct ccagctctct tgcaccggca cctacatcaa 600
tgagctgggtg gtttccactg cagcagtcac tattttccac tgtcaccata tttatctctt 660
gtgggttgag ctctacatc atcctccaca tcaactccaa ggagggcagg tccaaagcct 720
tgaacacctg cagttccaac ctaattgctg tttctcttag tttggatcgt gtgcatttat 780
gtgtctcaaa ccatcttctg ctgggtccat ggatgaggga aagatttctt ctgtctttta 840
caccaataca gtcctcttga tgaacccctt aatctacagt ttgatgaata aaatgttcaa 900
ctttctctga gaaaaaac ctagtaggaa aaaattttga ctagaaatag tatcttctg 960
tgcatgtatt ttaggacag ggagcttctg t 991

```

&lt;210&gt; 825

&lt;211&gt; 997

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g675 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 825

```

atggctcctg gaaatggctc tttgatgaat gaattcattc tgggtggggtt aacagactag 60
ccagatcttt aactccctct gttcttcatg tttcttgtaa tgtatgttgt cactgtgata 120
agaaactttg tcttggtaat tctaactatg cgaaattcac gtcttcacac tcccaagtac 180
tttttcttt cttaaattgtt cttcacagac ctctgttatt cttctgtgtt tatactccaa 240
cttccgagga agtgtatttc agaggagaat gttatctcct acatggtttg catgatctag 300
cttttctttt tcttttctg tttttttttt tttttaattt atttctgaat gttatatgct 360
gacgtcaatg gcctatgatt gctgtgtggc catctgttac ccacttctt atcacattgc 420

```

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| catgtccctt | aaagtgtgtt | tcagccttat  | gcttggttcc | tacttcctat  | ccttttctgg  | 480 |
| ggccatggcc | cacactggat | gcattgctgag | gctgacctgt | gatgcaaaaca | ccatcaatca  | 540 |
| ttacttccgt | gacatccctc | ctgtgttcca  | gctctcctgc | accagcacct  | acatcaatga  | 600 |
| actggtggtt | ttcattgtgg | caggcatcaa  | taccattgtg | cccactgtca  | cogtctttat  | 660 |
| ctcttatggt | gacatccctc | ccaggatcct  | ccacatcagt | tccaatgagg  | gaagggtccaa | 720 |
| agccttcagc | acttgcagtt | cccacataat  | tgctgtttct | ctgttctttg  | gattaagtgc  | 780 |
| atztatgtat | ctcaaaccat | cttctgctgg  | gtctatggat | gagggaaaat  | tctcttctgt  | 840 |
| tttttatatg | aacgggcttc | ccatgatgag  | ctccttaatc | tacagcttaa  | ggaggaaaga  | 900 |
| tgtaaatttt | gccatgggaa | aatctctgag  | taggagaatg | tttttgccat  | aaacaacatt  | 960 |
| tctctgtgta | tgtagttaca | ggatggggat  | tctctgt    |             |             | 997 |

&lt;210&gt; 826

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g676 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 826

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| atggacagtc  | taaaccaaac | aagagtgact  | gaatttgtct | tcttgggact | caactgataac | 60  |
| cgggtgctgg  | aaatgctgtt | tttcatggca  | ttctcagcca | tttatatgct | aacgctttca  | 120 |
| gggaacattc  | tcatcatcat | tgccacagtc  | tttactccaa | gtctccatac | ccccatgtat  | 180 |
| ttcttctga   | gcaatctgtc | ctttattgac  | atctgccact | catctgtcac | tgtgcctaag  | 240 |
| atgttggagg  | gtttgctttt | agaaagaaaag | accatttctt | ttgacaactg | catcacacag  | 300 |
| ctcttcttcc  | tacatctctt | tgctgtgcc   | gagatcttcc | tgctgatcat | tgtggcgtat  | 360 |
| gatcgttacg  | tggctatctg | cactccactc  | cactacccca | atgtgatgaa | catgagagtc  | 420 |
| tgtatacagc  | ttgtctttgc | tctctgggtg  | gggggtactg | ttcactcact | agggcagacc  | 480 |
| ttcttgacta  | ttcgtctacc | ttactgtggc  | cccaacatta | ttgacagcta | cttctgtgat  | 540 |
| gtgcctcttg  | ttatcaagct | ggcctgcaca  | gatacatacc | tcacaggaat | actgattgtg  | 600 |
| accaatagtg  | gaaccatctc | cctctcctgt  | ttcttggcgc | tggtcacctc | ctatatggtc  | 660 |
| atcctgggtt  | ctcttcgaaa | acactcagct  | gaagggcgcc | agaaagccct | gtctacctgc  | 720 |
| tcggccctct  | tcatgggtgg | tgcctctctc  | tttgggccc  | gtatcttcat | ctatactcgg  | 780 |
| ccagacacca  | gcttctccat | tgacaagggtg | gtgtctgtct | tctacacagt | ggtcacccct  | 840 |
| ttgctgaatc  | ccttcattta | caccttgagg  | aatgaggagg | taaaaagtgc | catgaagcag  | 900 |
| ctcaggcgaga | gacaagtttt | tttcacgaaa  | tcatataca  |            |             | 939 |

&lt;210&gt; 827

&lt;211&gt; 992

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g677 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 827

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| atggctcctg | gaaatatttc | tactgtggct  | gaattaattc  | tggtgggggtt | aaaagaccag | 60  |
| acagatctcc | aaccgcccct | gttcttccctg | tttctagtaa  | tggtgtgtgt  | tgctgggtag | 120 |
| gggaatttgg | gcttggtaac | tctgattgtg  | ttcagttcac  | actttcatgc  | acccatgtac | 180 |
| ttttttcttt | ttagtttagc | ttttatagac  | cacttttatt  | cttctgtgtt  | tattccaaaa | 240 |
| atgctgatga | acttcataac | agagaagaat  | attatttctt  | atgcgggttg  | catgtcagct | 300 |
| ttttttcttt | tttttttttt | tttttttttt  | ttatttctga  | atgctatgtt  | ttgacgtcaa | 360 |
| tggtctctga | tcactagtgg | ccatggccat  | ctgttaaccg  | cttctgtata  | acattgccat | 420 |
| gtcccctaaa | gtgtgttcca | gccatattgt  | tggttccctac | ttctggccct  | tttctggggc | 480 |
| catggcccat | accaggtgca | tgctgaaact  | gacctcctgt  | gaggcaaaaca | ccatcaacca | 540 |
| ctacttctgt | gacacccttc | atctgctcca  | gctctcttgc  | accagcacct  | acgtcagtga | 600 |
| gttgatgggt | ttcattgcag | caggcatcat  | tttcaactgt  | cccagtatca  | ccatctttat | 660 |
| ctcttatttt | tttacctctc | cattatecta  | tcagcttcac  | tgagggctgg  | tcaaaatttt | 720 |
| tcagcacctg | cagtttccac | aaaattgcc   | tttctctgtt  | ctttggatta  | ggtgcacat  | 780 |
| tgtgtcttaa | attatctcca | actgggacta  | taaatgaagg  | taaaatatct  | tctgtcttcc | 840 |
| acattgatgt | agttcccatg | ataaactcct  | caatttacag  | cttaagaaac  | aatgatgtta | 900 |

aacttgccctg gagaaaaatc ctaagttgga gaaaatttcc atttgaaact atctctctcc 960  
atgcatatag ttacaggaca aggagattct gt 992

<210> 828

<211> 966

<212> DNA

<213> Unknown (H38g678 nucleotide)

<220>

<223> Synthetic construct

<400> 828

|  |     |
|--|-----|
| atgagtgtcg tagaagccaa taacatttct gggcctgtga gtgaatttat cctcctgggc  | 60  |
| ttcccctgcc tgctgcaggg agaccaagat cctcctcttt gtggtcttct cctcatctta  | 120 |
| ccttctgacc ctcatgggta acacatccat catctgcgct gtgtgggtcaa gccagaaact | 180 |
| ccacacacct atgtacatcc tcttggtctaa tttctcttcc ctggagatct gctgcattag | 240 |
| ttctgatgtc ccaaaatggt ggccaatctc atctcccata tcaagagcat ctccatgtct  | 300 |
| ggctgcctgc tccagttctt ctacttctcc atgtgtgctg cagaaggcta ctttctgtct  | 360 |
| gtgatgtcct ttgatcgggt ccttaccatc tgtcgacctt tgcattatcc cacagtcatg  | 420 |
| actcaccacc tgtgtgtctg attagtggcc ttctgcaggg caggtgggtt tctatccata  | 480 |
| ctgatgcctg cagtgcctat gtcccagagt cctttctgtg gccctaacat cactgaccat  | 540 |
| tttttctgta acctgggacc attgctggca ctgtcctgtg ccccgattcc caaaactact  | 600 |
| ctgacttggtg ctacagtaag ctctctcatc atcttcatca ccttctctta cattcttggg | 660 |
| tcccatatct tagttttgct agctgttctg tgggtcccag ctggctcagg caggaacaaa  | 720 |
| gctttctcta catgtgcttc ccatttcttg gttgtttctt tcttctatgg ctcatgcatg  | 780 |
| gtgatgtatg tgagtccagg ctccaggagc cgccctggga cacagaaatt tgtgacattg  | 840 |
| ttttactgca cagcaacccc attctttaat cccctgacct acagtctctg gaacaaagat  | 900 |
| atgacagatg cccttaaaaa agtgctggga gtgccatcaa aagaaatata ttggaacaca  | 960 |
| ctgaaa   | 966 |

<210> 829

<211> 1003

<212> DNA

<213> Unknown (H38g679 nucleotide)

<220>

<223> Synthetic construct

<400> 829

|  |      |
|--|------|
| atggaagagg ccctcctact caatcaaact tctttagtga catattttcg gcttagaggt  | 60   |
| ttatctgtaa atcataaggc acggatagct atgttttcca tgttccctcat tttttatgtc | 120  |
| ctgacactga ttgggaatgt tctcattgtc ataactatta tctatgacca ccggctccat  | 180  |
| actcccactg atttcttctc cagcaacctg tcttttattg atgtctgcca ctccactgtc  | 240  |
| actgtcccca agatgctgag agacgtgtgg tcagaggaaa agctcatctc ttttgatgcc  | 300  |
| tgtgtgaccc agatgttctt cctgcacctc tttgcctgca cagagatctt cctcctcacc  | 360  |
| gtcatggcct atgatcggta tgtggccatc tgtaaacccc tgcagtacat gatagtgtg   | 420  |
| aactggaagg tatgtgtgct gctggctgtg gccctctgga caggagggac catccactcc  | 480  |
| atagccctca cctcccttac catcaagctg ccctactgtg gtcctgatga gattgacaac  | 540  |
| ttcttctgtg atgtacctca ggtgatcaag ctggcctgca ttgacacacc cagctccttg  | 600  |
| agatcctcat tgtctccaac agtggattga tctccgtggg ctgttttgtg gtcctggtgg  | 660  |
| tgtcctacgc agtcactctg gtgagtctga ggcagcagat ctccaagggc aagtggaagg  | 720  |
| ccctgtccac ctgtgcagcc catctcactg tagttacact gttcctggga cactgcactc  | 780  |
| tcatctattc ccgcccaccc accagcctcc cagaggacaa ggcagtatct gtgtttttca  | 840  |
| ctgcagtcac cccctgtctg aacccatta tctataccct taggaatgaa gaaatgaaga   | 900  |
| gtgccttaaa caagttagtg gggagaaaag agagaaaaga agaaaaatga aaatgtctac  | 960  |
| gtccttagga tacgtggtgc tccaaattaa agaagcgcct tgc                    | 1003 |

<210> 830

<211> 478

<212> DNA

<213> Unknown (H38g680 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 830

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| acgggggactg | gatgatggct | gtgtcatgcc | atgatecctaa | ctccccctcac | ttccagttac  | 60  |
| cttactgtgg  | cctaacaagg | tgggctatac | ttctgtgata  | tcctgcagtg  | tacctctagc  | 120 |
| ctgtaaggac  | acatccttag | cccagagggt | agggttttaca | aatgttggtc  | ttttgtctct  | 180 |
| catttgcttt  | tttctcatcc | ttgtttccta | tacttgcatt  | gggatttcca  | tatcaaaaaat | 240 |
| ccgctcagca  | gagggcaggc | agcgggcctt | ctccacctgc  | agcgctcacc  | tcaactgcaat | 300 |
| cctttgtgct  | tatgggccag | tcategttat | ctatctacaa  | cccaatccca  | gtgccttgct  | 360 |
| tggttccata  | attcagatat | tgaataatct | ggtaacccca  | atgttgaatc  | cactaatcta  | 420 |
| tagccttagg  | aataaggatg | taaaatcaga | tcagccctga  | ggaatgtatt  | tcccaaga    | 478 |

&lt;210&gt; 831

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g681 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 831

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttactatttt | taatgttctt | tattacttcc | ttgggtcata | aattccatct | gatatcattt | 60  |
| cccttcagtc | aacaaaccac | ctaacaaaaa | tactttataa | tttttgaagt | atgactctgc | 120 |
| tgataacata | cactcacagc | attaatttat | tgttaaatgt | ccttggtcta | gggtatagac | 180 |
| ctattttagt | ggtataccct | ttagtcccag | agtattgttc | ttatttctag | ggcggtgtcc | 240 |
| ttctgggttt | tcattagaaa | gcctaagttt | ttaccgaacc | tctttcactt | ggcagcactt | 300 |
| gcatttataa | ttctattgcc | ctagttgagg | gtaactgcta | aaatcttttc | tctcagccat | 360 |
| ctggctgctg | ttttctactt | actttcttag | agtcttgtct |            |            | 400 |

&lt;210&gt; 832

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g682 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 832

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| atggctactt  | caaaccattc  | ttcaggggct  | gagtttatac | tggcagggtt | gacacaacgc  | 60  |
| ccagaacttc  | aactgccact  | cttctctctg  | ttccttggaa | tatatgtggt | cacagtgggtg | 120 |
| gggaacctgg  | gcatgatctt  | cttaattgct  | ctcagttctc | aactttaccc | tccagtgtat  | 180 |
| tattttctca  | gtcatttgtc  | tttcattgat  | ctctgtact  | cctctgtcat | tacccttaag  | 240 |
| atgctggtga  | actttgttcc  | agaggagaac  | attatctctt | ttctggaatg | cattactcaa  | 300 |
| ctttatttct  | tccttatttt  | tgtaatgca   | gaaggctacc | ttctgacagc | catggaatat  | 360 |
| gaccgttatg  | ttgctatctg  | tcgcccactg  | ctttacaata | ttgtcatgtc | ccacagggtc  | 420 |
| tgttccataa  | tgatggctgt  | ggtatactca  | ctgggttttc | tgtggggcac | agtccatact  | 480 |
| acccgcatgt  | cagtgttgct  | attctgtagg  | tctcatacgg | tcagtcatta | tttttgtgat  | 540 |
| attctccccct | tattgactct  | gtcttgctcc  | agcaccaca  | tcaatgagat | tctgctgttc  | 600 |
| attattggag  | gagttaatac  | cttagcaact  | acactggcgg | tccttatctc | ttatgctttc  | 660 |
| attttctcta  | gtatccttgg  | tattcattcc  | actgaggggc | aatccaaagc | ctttggcact  | 720 |
| tgtagctccc  | atctcttggc  | tgtgggcate  | ttttttgggt | ctataacatt | catgtatttc  | 780 |
| aagccccctt  | ccagcactac  | tatggaaaaa  | gagaagggtg | cttctgtgtt | ctacatcaca  | 840 |
| ataatcccca  | tgtctgaatcc | tctaattctat | agcctgagga | acaaggatgt | gaaaaatgca  | 900 |
| ctgaagaaga  | tgactagggg  | aaggcagtc   | tcc        |            |             | 933 |

&lt;210&gt; 833

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g683 nucleotide)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 833

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| atggtgatcc | tgtcctggga | aaaccaaacg  | atgagagtgg | aattcgtgct | tcaaggattc  | 60  |
| tcttccatca | gacagttaaa | tattttcctc  | tttatgataa | ttttagtttt | ctacatctta  | 120 |
| actgtttctg | gaaacatcct | cattgtcctt  | ctagttttag | tcagacatca | tctccacacc  | 180 |
| cctatgtact | tcctcctggg | gaacttgccc  | tgtctggaga | tctggtatac | ctctaaccac  | 240 |
| atccccaaaa | tgttgctgat | tatcatagct  | gaatagaaga | ctatctctgt | ggctggctgg  | 300 |
| ctggcacaa  | tctacttctt | cggatccctg  | gctgccacgg | agtgcctctt | gctcaactgtg | 360 |
| atgtcctatg | atcgtacct  | agccatctgc  | cagcctcttt | gctaccgtgt | cctcatgact  | 420 |
| ggcccccttt | gcatcaggct | agctgctggc  | tcttggttct | gctgcttctt | ccttacagca  | 480 |
| atcaccatgg | tcttgctatg | tagactaacc  | ttctgtggac | cctatgaaac | tgatcacttc  | 540 |
| ttttgtgact | tcacccctct | gggttcattc  | tcctgcatgg | atacctcagt | gactgagacc  | 600 |
| attgcctttg | ccacctcttc | tgcagtaact  | ctgacccat  | ttctctctat | tgtagcctcc  | 660 |
| tactcctgcy | tcctttctgc | tatcctaaga  | atccccatct | gcacaggcca | gaaaaaggcc  | 720 |
| ttctccacct | gctcttccca | cctcaactgtg | gtcatagtgt | tttatgggac | actgattgcc  | 780 |
| acataccttg | tgccctcagc | caactcatcc  | caactcttgt | gcaaagggtc | ctctctgctc  | 840 |
| tacatcatcc | tgacacccat | gtttaacccc  | atcatttata | gcctgagaaa | tagagacatc  | 900 |
| catgaagctc | tgaagaagtg | cttgaggaag  | aagtcagggt | tttgcctt   |             | 948 |

&lt;210&gt; 834

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g684 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 834

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ccagtgagga  | ccttggagac | tactaatatc | actggatttg | tgaatgagtt | catcctcttg | 60  |
| ggcttcccc   | gccgtggga  | gatccagatc | ctcctttttg | tggtcttctc | tctcatctac | 120 |
| cttctgaccc  | tcctaggtaa | cacatccatc | atctgtgctg | tgtggtcaag | ccagaaactc | 180 |
| cacacaccta  | tgtacatcct | actggccaat | ttctccttcc | tggagatctg | ctgtgtcagt | 240 |
| tctgacgtgc  | ccataatggc | agccaatctc | atctcccaga | cacagagcat | ctcctgtgct | 300 |
| ggctgcctgc  | tccggttcta | cttcttctcc | atgtgtgctg | cagagtgcct | atttctgtca | 360 |
| gtgatgtctt  | ttgatagggt | tcctgccatt | tgtagacctt | tgactatcc  | caccttaatg | 420 |
| acccatcacg  | tttgtgtca  | ttttgtgat  | cttctgctgg | gtgggtggct | gtctctgggt | 480 |
| attgacctct  | ttgacactaa | tatctcaggt | gctcttttgt | ggtccaaaca | ctatcgacca | 540 |
| ttttttctgt  | gatctggcac | ctttgctggc | actgtcttgt | gctccaatac | ctggaattac | 600 |
| tctgacttgt  | ggtatcatta | gcgctctcat | catctttctt | accttcttgt | atataccttg | 660 |
| gacttatttc  | tgtgttctaa | gcacagtgtc | acaggtgcct | tcaggcttag | gaaggcataa | 720 |
| ggctttctca  | acttgtggct | gtcaccttgc | tgtagtgtct | ctcttctatg | gttctcttat | 780 |
| gggtgatgtat | gttagccag  | gttctgggga | ctatcatggg | ataaagaaat | ttgcgacctt | 840 |
| gttctatact  | ttgtcaactc | cattctttta | tcctctgata | tacagtttcc | ggaacaagga | 900 |
| tatgaaagag  | gcactaaaga | aatttctgag | gaatcgccac | actgtc     |            | 946 |

&lt;210&gt; 835

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g685 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 835

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cttatagcta | caggaaactg | gacaagaata | agtaagttaa | tctcatgag  | cttctcttcc | 60  |
| ctgcctactg | aaatacagtc | attactcttt | ctgacatttc | taaccatcta | cctggtcacc | 120 |
| ctgatgggaa | actgcctcat | cattctgggt | accctagctg | acccatgct  | acacagcccc | 180 |
| atgtacttct | tcctcagaaa | cttatctttc | ctggagattg | gcttcaacct | agtcattgcy | 240 |

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| cccaacatgc | tgtggaccct | gcttgcccag  | gacacaacca  | tctccttcct  | tggctgtgce  | 300 |
| acttagatgt | atttcgtctt | cttctttggg  | gtggctgaat  | gcctcctcct  | ggctaccatg  | 360 |
| gcatatgacc | gctatgtggc | catctgcagt  | ccttgcacta  | cccagtcac   | atgaacccaa  | 420 |
| ggactcttgc | caaactgggt | gctacctcct  | ggttcccagg  | ctttcctgta  | gctactgtgc  | 480 |
| agaccacatg | gctcttcagt | tttccattct  | gtggcaccaa  | caagggtgaac | cacttcttct  | 540 |
| gtgacagccc | acctgtgctg | aggctgggtct | gtgcagacac  | agcactcttt  | gagatctacg  | 600 |
| ccatcgctcg | aaccattctg | gtggtcatga  | tcccctgctt  | gctgatcttg  | tgttcctata  | 660 |
| ctcacattgc | tgctgccatc | ctcaagatcc  | catcagctaa  | aggggaagaat | aaagcctttt  | 720 |
| ctacatgttc | ctcacacctc | cttggtgtct  | ctctttttcta | tatatcatta  | agcctcacct  | 780 |
| acttcgggce | taaatacaat | aattcacctg  | agggcaagaa  | gctgctatca  | ttgtcctaca  | 840 |
| ctgttatgac | tcccattgtg | aaccccatta  | tctacagcct  | gagaaataac  | gagggtgaaga | 900 |
| atgccctcag | caggacgggc | tctaaggccc  | tagccctcag  | aaactg      |             | 946 |

&lt;210&gt; 836

&lt;211&gt; 973

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g686 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 836

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atggctgtgg | aaaatgactc | ttcagtgaca | agagtttatt  | cttttgggat | taacagacca | 60  |
| gcctgagatc | taattgcccc | tgtttttctt | gttcttgggtg | aactatatga | ccaccatggt | 120 |
| gggcaacttg | agtttaatta | atctaatttg | cctgaattca  | caccttcaca | ctcccatgta | 180 |
| ttttttctct | ttcaatctgt | ccttcattga | tctctgttat  | tcatttgtct | ttacccccaa | 240 |
| aatgctgatg | agctttatct | cagagaggaa | catcatctcc  | tttccaggat | gcgtaactca | 300 |
| gctctttttc | ttctgctttt | ttgtccactc | tgagtgtctat | gtgctgacag | ccatggccta | 360 |
| tgatcgctat | gtggccatct | gcaaaccctt | tctgtacatg  | gtcaccacgt | cccctcagat | 420 |
| ctgttctcta | ctgatgcttg | gttcatatgt | gatgggggtt  | gctggggcca | tggtccacac | 480 |
| agagtgtatg | atgaagctca | tcttttgtga | ctccaacgtc  | atcaaccatt | acatgtgtga | 540 |
| catcttccca | ctgctccagc | tctcctgcag | cagcacctag  | gccaatgagc | tggtgatgtc | 600 |
| tgttattgta | ggcacagttg | ttatagtatc | aagcctcatt  | atcttaattc | cttatgcttt | 660 |
| gattcttttc | aatatccttc | acatgtcctc | agccgagggt  | tggttcaaag | ccatcggtac | 720 |
| ctgtggctcc | cacataataa | ctgttggcct | attctatgaa  | tttgggctga | tcactcatgt | 780 |
| taagttatca | tctgattggg | atatgggtca | ggggaagttt  | ctctcagtg  | tttacacgaa | 840 |
| tgaggtagcc | atgctgaacc | ccctcattta | tagcctcagg  | aacaaggatg | tcaaacttgc | 900 |
| tctaaaggaa | accctaaata | aaattacaaa | ctgagtagag  | ccaatggtgc | tgcttagacc | 960 |
| cctctccaat | tgc        |            |             |            |            | 973 |

&lt;210&gt; 837

&lt;211&gt; 992

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g687 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 837

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| atgagataga | taaatacagac | acaagtgata  | gaattcctcc | ttctgggact | ctctgatggg  | 60  |
| ccacacaccg | agcagctgct  | atttatcgta  | ttattgggtg | tctacctggt | cactgtgctt  | 120 |
| ggaaatctgc | ttctaacttc  | ccttggtcat  | gttgactccc | aacttcacac | acccatgtat  | 180 |
| ttttttctct | gcaacttgct  | tctggctgac  | ctctatttct | ctaccaacat | acttcctcag  | 240 |
| gcactagtcc | acctgctttc  | cataaacaac  | ctcattgcat | tcacactttc | tctaactcaa  | 300 |
| cttctctttt | tctctatttt  | tgggtgaccc  | agtgcgccct | tattgcagtg | atgtcctata  | 360 |
| atccctatgt | tgcaatctgc  | aatcctctgc  | attaccctaa | catcatgacc | tggaaagtgt  | 420 |
| gtgtccagct | ggcaacagga  | tcatggacca  | gtggcattct | ggtgtctgtg | gtagacacca  | 480 |
| ccttcacact | gaggctaccc  | taccgaggca  | gtaacagcat | tgctcatttc | ttttgtgagg  | 540 |
| ccctgcact  | attgatctta  | gcattccacag | acacccatgc | atcagagatg | gccattttatc | 600 |
| ttacgggggt | tgtgattctc  | ctcatacctg  | tttttctgat | tctggtatcc | tatggccgta  | 660 |
| tcatagtaac | tgtggtcaag  | atgaagtcaa  | ctgtggggag | tctcaaggca | ttttctacct  | 720 |

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| gtggctccca | cctcatggtg | gtcatacttt  | taaattggatc | agcaatactc | acttgcata  | 780 |
| cacccaagtc | ttccaaacag | cagtaaaaaat | cggtgtctgt  | tttctatgca | atagtaactc | 840 |
| ccatgcttaa | ttccctcatc | tatagcctga  | gaaacaagga  | tgtgaaggca | gctctgagga | 900 |
| aagtagccac | aaggaatttc | ccatgaaggc  | ttggaatctc  | acactgacag | tgagctcaga | 960 |
| gaaccttttg | gcttcctact | tcaaagactt  | gc          |            |            | 992 |

&lt;210&gt; 838

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g688 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 838

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| atggaaaaaa | gcaataatag  | cactttgttt  | attctcttgg | ggttttccca | aaataagaac  | 60  |
| attgaagtcc | tctgctttgt  | attatattttg | ttttgctaca | ttgctatttg | gatgggaaac  | 120 |
| ttactcataa | tgattttctat | cacgtgcacc  | cagctcattc | accaacccat | gtattttcttc | 180 |
| ctcaattacc | tctcactctc  | cgacctttgc  | tacacatcca | cagtgaaccc | caaattaatg  | 240 |
| gttgacttac | tggcagaaag  | aaagaccatt  | tcctataata | actgtatgat | acaactcttt  | 300 |
| accacccatt | tttttggagg  | catagagatc  | ttcattctca | cagggatggc | ctatgaccgc  | 360 |
| tatgtggcca | tttgcaagcc  | cctgcactac  | accattatta | tgagcaggca | aaagtgtaac  | 420 |
| acaatcatca | tagtttggtg  | tactggggga  | tttatacatt | ctgccagtca | gtttctcttc  | 480 |
| accatctctg | taccattttg  | tggcccaaat  | gatatagatc | actactctcg | cgatgtgtat  | 540 |
| cctttgctg  |             |             |            |            |             | 549 |

&lt;210&gt; 839

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g689 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 839

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| ttgcctgaca | tcggtttcac  | ctccaccacg  | gtccccaaga  | tgagcgtgga | catccagtct | 60  |
| cacagcagag | tcattctccta | tgcaggctgc  | ctgactcaga  | tgtctctctt | tgccattttt | 120 |
| ggaggcatgg | aagagagaca  | tgctcctgag  | gtgatggcct  | atgacctggt | tgtagccatc | 180 |
| tgtcaccttc | tatatcgttc  | agccatcttg  | aaccctgttg  | tccgtggctt | cctagatttg | 240 |
| ttgtctttgt | tgttggtttt  | tttttttttc  | tctcagctct  | ttagactccc | agctgcacaa | 300 |
| cttgattgcc | ttacaaatga  | cctgcttcaa  | ggatgtggaa  | attccgaatt | tcttctggga | 360 |
| accttctcaa | ctcccccatc  | ttgcatgttg  | tgacaccttc  | accaggaaca | acaacatgta | 420 |
| tttccctgct | gccgtatttg  | gttttcttcc  | catctcgggg  | acccttttct | cttactgtaa | 480 |
| aattgtttcc | tccattctga  | gggtttcctc  | atcaggtggg  | aagtacaaac | cttctccacc | 540 |
| tgtgggtctc | acctgtcagt  | tgtttgctga  | ttttatggag  | caggcgttgg | agggtacctt | 600 |
| ggttcagatg | tgatcatctt  | cccagagaaag | gggtgcagtgg | cctcagtgac | gtacgtacac | 660 |
| ggtggtcacc |             |             |             |            |            | 670 |

&lt;210&gt; 840

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g690 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 840

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggacgtca | ggctcatctg | caccaccgta | cccaagatgg | ccttcaacta | cttgtctggc | 60  |
| agcaagtcca | tttctatggc | tggctgtgcc | acacaaattt | tcttctgtgt | atcactgctt | 120 |
| ggctctgaat | gctttctgtt | ggctgttatg | tcttatgact | gctacattgc | catttgccac | 180 |
| cctctaagat | acaccaatct | catgagaccc | aaaatttgta | gacttatgac | tgccttctcc | 240 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tggatcctgg | gctctacaga | tggaatcatt | tatgctgtag | ccacattttc | cttctcctac | 300 |
| tgtgggtctc | gggaaatagc | ccacttcttc | tgtgagttac | cttccctact | aatcctctca | 360 |
| tgcaatgaca | cgtcaatatt | tgaaaagggt | attttcattt | gctctatagt | aatgcttggt | 420 |
| ttccctgttg | caatcatcat | tgcttcctat | gctggagtta | ttctggctgt | cattcacatg | 480 |
| ggatctggag | agggtcgtcg | caaagctttc | acgacctgtt | cctctcacct | catggtggtg | 540 |
| ggaatgttct | atggagcagg | tttgttcatg | tacatacagc | ccacatctga | tcgctcccca | 600 |
| acgcaggaca | agctgggtgc | tgtattctac | accatcctca | ctccc      |            | 645 |

&lt;210&gt; 841

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g691 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 841

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| aatctcctcc | ccgtgtggac  | ccctggaagc  | agggtgtccct | tcattgatcac | aaattttctgt | 60  |
| ctccgagaag | caaggcatgt  | cctttcccaa  | gaaacttttc  | cagaatcaca  | aacttttcct  | 120 |
| actctttgca | gggatgaatg  | tattttctgca | gactgtgatg  | gcctatgacc  | actttgtggc  | 180 |
| catctgtcac | cccctgcact  | acagggtcat  | catgaatcct  | gggatctttg  | gactgtgggt  | 240 |
| tctggtgtcc | tggagcatga  | gtgccctgaa  | ttcctcactg  | caaagcagaa  | tgtgttgcag  | 300 |
| ctgtccttct | gcacaaaactt | ggaaatcccc  | ccattttttt  | ctgtgaactt  | aatcagttga  | 360 |
| tcctgcttgc | ctgtttctaac |             |             |             |             | 380 |

&lt;210&gt; 842

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g692 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 842

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| tttgttgatt | tctgttattc | caccacgatt | acacccaaac | tgctggagaa | cttggtttgtg | 60  |
| gaagatagaa | ctatctcctt | cacaggatgc | atcatgcagt | tattctttgt | ctgcatattt  | 120 |
| gtagtaacag | aaacattcat | gctggcagtg | atggcctatg | accgatatgt | ggcgggtgtg  | 180 |
| aaccctcttc | tctacacagt | tgcaatgtac | cagaggcttt | gctccttggt | agtggctacg  | 240 |
| tcatactgtt | gggggatagt | ctgttccctg | acacttacct | agtttctact | ggaattatcc  | 300 |
| ttcagaggaa | ataatatcat | taataacttt | gtctgtgagc | acgctgccgt | cgttgctgtg  | 360 |
| tcttggtctg | acccctgtgt | gagccaggag | atcactttag | tttctgccac | attcaatgaa  | 420 |
| ataagcggcc | tggtgatcat | tctcactccc | tatgctttca | tttttatcac | tgtcatgaag  | 480 |
| acgccttcca | ctggggggcg | caagaaagcg | ttctccacgt | ctgcctccca | cttgacggcc  | 540 |
| attaccattt | tccatgggac | tatccttttc | ctctactgtg | ttcctaacte | caaaagtctg  | 600 |
| tggctcatgg | tcaagggtgg | ctctgtcctt | tacacagtgg | tcattccc   |             | 648 |

&lt;210&gt; 843

&lt;211&gt; 643

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g693 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 843

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| ttgccagaca | ttggttttcac | cttggccacg | gtccccaaga  | tgattgtaga | catgcaatca | 60  |
| catagcagaa | tcattctccca | tgcaggctgt | ctgacacaga  | tacctttctt | tgctcttttt | 120 |
| gtatgtatag | atgacatgct  | cctgactgtg | atggcctatg  | actgatttgt | ggccatctgt | 180 |
| caccccttgc | actacccagt  | catcatgaat | cctcacctct  | gtgtcttctt | agtgttgatg | 240 |
| tcttttctct | tagcctgttg  | gattcctagc | tgcaacaactg | gattgttaca | attcacctgc | 300 |
| ttcaagaatg | tggaaatctc  | taattttttc | tgtgactgat  | ctcaacttct | caaccttgcc | 360 |

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| tggtctgact  | gtcatcagta | acatatccat | acgttttagat | agtactatat | ttgggtttct | 420 |
| tcccatattca | gggatccctt | tgtcttacta | taaaattgtg  | ccctccattc | taagaattcc | 480 |
| attgtcagat  | gggaagtata | aagccttctc | cacctgcggc  | tctcacctgg | caattgtttg | 540 |
| cttattttat  | ggaacaggca | ttggcatgta | cctgacttca  | gctgtgtcac | cagccccag  | 600 |
| gaatggtgtg  | gtggcatcag | tggtgtacgc | tatggtcacc  | ccc        |            | 643 |

&lt;210&gt; 844

&lt;211&gt; 652

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g694 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 844

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| ttgcctgaca | tcggtttcac  | ccccaccacg | gtccccaaga | tgattgtgga | catccagtct  | 60  |
| cacagcagag | tcattctatgc | aggctgcctg | actgtgatgt | ctctctttgc | catttttgga  | 120 |
| ggcatggaag | agacacatgc  | tcctgaatgt | gatggcctat | gtccggtttg | tagccatctg  | 180 |
| tcaccctcta | tatcattcag  | ccatcatgaa | cccggtgttc | tgtggcttct | tacttttgtt  | 240 |
| gtcttttttt | tttctcggtc  | ttttagacgc | ccagctgcac | aacatgattg | ccttaciaaat | 300 |
| gacctgcttc | aaggatgtgg  | aaattcctaa | tttcttctgt | gacctttctc | aactccccca  | 360 |
| tcttgcatgt | tgtgacacct  | tcaccaataa | cataatcatg | tattttcctg | ctgccatatt  | 420 |
| tggttttctt | cccatctcgg  | ggaccctttt | ctcttactat | gaaattgttt | cctccattct  | 480 |
| gagggtttca | tcataagggtg | ggaagtataa | ggccttcgcc | acctgtgggt | ctcacctgtc  | 540 |
| agtcgtttgc | tgattttatg  | gaacaggcgt | tggagggtac | ctcagttcag | atgtgtcatc  | 600 |
| ttccccgaga | aagactgcag  | tggcctcagt | gatgtacgca | gtggtcacc  | cc          | 652 |

&lt;210&gt; 845

&lt;211&gt; 692

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g695 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 845

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ttgcctgaca  | tcggtttcac | ctccaccaca | gtcgccaaga | tgattgtgga | catccagtct | 60  |
| cacagcagag  | tcattctcta | tgcaggctgc | ctgactcaga | tgtctctctt | tgccattttt | 120 |
| ggaggcatgg  | aagagagaca | tgctcctgag | tgtgatggcc | tatgaccggt | ttgtagccat | 180 |
| ctgtcaccct  | ctatatcgtt | cagccatctt | gagcccggtg | ttctgtgcct | tcctagattt | 240 |
| gttggtctttg | ttttgttttg | ttttgttttg | ttttgttttg | ttttgttttg | ctcagtcttt | 300 |
| tagactccca  | gctgcacaac | ttgattgcct | tacaaatgac | ctgcttcaaa | gatgtggaaa | 360 |
| ttcctaattt  | cctctgggaa | ccttctcaac | tcccccatct | tgcattgtgt | gacaccttca | 420 |
| ccaggaacat  | caacatgtat | ttccctgctg | ctgtatttgg | ttttcttccc | atctcgggga | 480 |
| ccttttctct  | tacaatggag | taaaattgtt | tcctccactc | tgagggtttc | atcatcaggt | 540 |
| gggaagtata  | aaccttctcc | acctgtgggt | ctcacctgtc | agttgtttgc | tgattttgtg | 600 |
| gaacaggcgt  | tggagggtac | ctcggttcag | atgtgtcatc | ttccccgaga | aagagtgcag | 660 |
| tggcctcagt  | gatgtacacg | gtggtcacc  | cc         |            |            | 692 |

&lt;210&gt; 846

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g696 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 846

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgctggcta | gaaacaactc | cttagtgact | gaatttatcc | ttgctggatt | aacagatcgt | 60  |
| ccagagttcc | ggcaaccctt | ctttttcctg | ttcctagtga | tctacattgt | caccatggta | 120 |
| ggcaaccttg | gcttgatcac | tcttttcggt | ctaaattctc | acctccacac | accaatgtac | 180 |

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| tatttcctct | tcaatctctc | cttcattgat | ctctgttact | cctctgtttt | cactcccaaa  | 240 |
| atgctaata  | acttttgtc  | aaaaaagaat | attatctcca | atgttggtg  | catgactcgg  | 300 |
| ctgtttttct | ttctctttt  | cgatcatctc | gaatgttaca | tgttgacctc | aatggcatat  | 360 |
| gategctatg | tggccatctg | taatccattg | ctgtataagg | tcaccatgtc | ccatcagggtc | 420 |
| tgttctatgc | tcacttttgc | tgtttacata | atgggattgg | ctggagccac | ggcccacacc  | 480 |
| gggtgcatgc | ttagactcac | cttctgcagt | gctaatatca | tcaaccatta | cttgtgtgac  | 540 |
| atactcccc  | tcctccagct | ttcctgcacc | agcacctatg | tcaacgaggt | ggttgttctc  | 600 |
| attgttgtgg | gtactaatat | cacggtaccc | agttgtacca | tcctcatttc | ttatgttttc  | 660 |
| attgtcacta | gcattcttca | tatcaaatcc | actcaaggaa | gatcaaaagc | cttcagtact  | 720 |
| tgtagctctc | atgtcattgc | tctgtctctg | ttttttgggt | cagcggcatt | catgtatatt  | 780 |
| aaatattctt | ctggatctat | ggagcagggg | aaagtttctt | ctgttttcta | cactaatgtg  | 840 |
| gtgcccattg | tcaatcccc  | catctacagt | ttgaggaaca | aggatgtcaa | agttgcactg  | 900 |
| aggaaagctc | tgattaaaa  | tcagaggaga | aatatattc  |            |             | 939 |

&lt;210&gt; 847

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g697 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 847

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| atgaccatgg  | aaaattattc | tatggcagct | cagtttgtct  | tagatgggtt | aacacagcaa | 60  |
| gcagagctcc  | agctgcccct | cttcctcctg | ttcctgggaa  | tctatgtggt | cacagtagtg | 120 |
| ggcaacctgg  | gcatgattct | cctgattgca | gtcagccctc  | tacttcacac | ccccatgtac | 180 |
| tatttcctca  | gcagcttgct | cttcgtcgat | ttctgtctat  | cctctgtcat | tactcccaaa | 240 |
| atgctgggtga | acttcctagg | aaagaagaat | acaatccttt  | actctgagtg | catggtccag | 300 |
| ctctttttct  | ttgtgggtct | tgtgggtggc | gaggggttacc | tcctgactgc | catggcatat | 360 |
| gategctatg  | ttgccatctg | tagcccactg | ctttataatg  | cgatcatgtc | ctcatgggtc | 420 |
| tgtcactgc   | tagtgcggc  | tgccttcttc | ttgggctttc  | tctctgcctt | gactcatata | 480 |
| agtgccatga  | tgaactgtc  | cttttgcaaa | tcccacatta  | tcaaccatta | cttctgtgat | 540 |
| gttcttcccc  | tcctcaatct | ctcctgctcc | aacacacacc  | tcaatgagct | tctacttttt | 600 |
| atcattgcgg  | ggtttaaac  | cttgggtgcc | accctagctg  | ttgctgtctc | ctatgccttc | 660 |
| atcctctaca  | gcatecttca | catccgctcc | tcagagggcc  | ggtccaaagc | ttttggaaca | 720 |
| tgcagctctc  | atctcatggc | tgtgggtgac | ttctttgggt  | ccattacctt | catgtatttc | 780 |
| aagccccctt  | caagtaactc | cctggaccag | gagaaggtgt  | cctctgtatt | ctacaccacg | 840 |
| gtgatcccca  | tgctgaaccc | tttaatatat | agtctgagga  | ataaggatgt | gaagaaagca | 900 |
| ttaaggaagg  | tcttagtagg | aaaa       |             |            |            | 924 |

&lt;210&gt; 848

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g698 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 848

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atggcacctg | gaaatggctc | tttcgtgact  | gaattcattc | tggcgggatt | aacacatcag | 60  |
| ccagatctcc | agtcctctct | gttcttccctg | tttctagtaa | tctatgtggt | cactctgttg | 120 |
| ggaaaacttg | gcttggtaac | tctaattggg  | ctgaactcac | accttcatac | ccccatgtac | 180 |
| ttcttccctc | ttaacttgct | cttcatagat  | ctctgttatt | cttctgtgtt | tacacccaaa | 240 |
| atgctaata  | actttatttc | agagaagaat  | attatctcct | tcaaggggtg | catgacccaa | 300 |
| cttttctttt | tctgtttttt | ttggtcattt  | ctgaatgtta | tgtgctgacg | tcaatggcgt | 360 |
| atgatcgctg | tggccatctg | taaccactt   | ctgtatcaca | ttgccatgtc | tcctacagtg | 420 |
| tgtccagacc | ttatgttttg | ttcctatttg  | atggcctttt | ctggtgccat | ggcccacact | 480 |
| ggatgcattg | tgagactgac | tttctgtgat  | gcgaacacca | tcgatcacta | cttctgtgac | 540 |
| atcctccctc | tgtccagct  | ctcctgcacc  | agcacctaca | tcaatgagct | ggtgggtttc | 600 |
| actgtgggtg | gcatacaac  | cattgtgccc  | actgttacca | tctttatctc | ttatggtttc | 660 |
| atcctctcca | gcatectcca | tatcagttcc  | aaggagggca | ggtccaaagc | tttcagcact | 720 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tgcagttccc | atataattgc | tgtttctctg | ttctttggat | caggtgcatt | tatgtatctc | 780 |
| aacctatctt | ctgctgggtc | catggataag | agaaaattat | cttctgtctt | ttatacaaat | 840 |
| gtggttccca | tgttgaacct | cttaatctac | agcctgagga | acaaagatgt | taaatttgcc | 900 |
| ctaagaaaag | ccctgagtag | taggaaactt | tgataagtaa | tagtatgtgt | ctgtgtgtat | 960 |
| agtcacaaga | cagggatatt | ctgt       |            |            |            | 984 |

&lt;210&gt; 849

&lt;211&gt; 940

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g699 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 849

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| atgaaaccag  | ggaatgagac  | acaaatttca | caattccttc  | tcctgggact  | ttcagaggaa | 60  |
| ccagaattgc  | agcccttcc   | ctttgggcta | tttctgtcca  | tgtacctggt  | caccgtgctc | 120 |
| gggaacctgc  | tcatactct   | ggccacaatc | tcagactccc  | acctccacac  | ccccatgtac | 180 |
| ttcttccctc  | ccaacctgtc  | ctttgcagac | atctgttttg  | tgtctaccac  | tgtcccaaag | 240 |
| atgctgggtga | acatccagac  | acagagcaga | gtcatcacct  | atgcagactg  | catcacccag | 300 |
| atgtgctttt  | ttatactctt  | tgtagtgttg | gacagcttac  | tcctgactgt  | gatggcctat | 360 |
| gaccgggttg  | tggccatctg  | tcacccctcg | cactacacag  | tcattatgaa  | ctcctggctc | 420 |
| tgtggactgc  | tgggttctggt | gtcctggatc | gtgagcatcc  | tatatctctt  | gttacaaagc | 480 |
| ataatggcat  | tgcagctgtc  | cttctgtaca | gaattgaaaa  | tccttcattt  | tttctgtgaa | 540 |
| cttaatcagg  | tcattccact  | tgctgttccc | gacactttta  | ttaatgacat  | gatgatgaat | 600 |
| tttacaagtg  | tgtgtctggg  | tgggggatgc | ctcgtctggaa | tattttactt  | actttaagat | 660 |
| actttgttgc  | atatgttcga  | tctcatcagc | tcaggggatg  | aataaagcac  | tttccacctg | 720 |
| tgcattctac  | ctctcagttg  | tctccttatt | ttattgtaca  | ggcgtaggtg  | tgtaccttag | 780 |
| ttctgtgtga  | accataact   | cactctcaaa | tgctgcagcc  | tcgggtgatgt | acactgtggt | 840 |
| cacctccatg  | ctgaacctct  | tcattctacg | cctgaggaat  | aaagacataa  | acagagctct | 900 |
| gaatcgattc  | ttcagagagc  | agaaacagga | gggccatttt  |             |            | 940 |

&lt;210&gt; 850

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g700 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 850

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| cacacagagc | cacggaatct  | cacaggtgtc | tgagaattcc | tcctcctggg  | actctcagag  | 60  |
| gatccagaac | tgcagtcggg  | cctcgctttg | ctgtccctgt | ccctgtccct  | gaatctgggc  | 120 |
| acggtgctga | ggaacctgct  | cagcatcctg | gctgtcagct | ctgactcccc  | cctccacacc  | 180 |
| cccattgact | tcttctcttc  | caacctgtgc | tgggtctgac | tcgggtctac  | ctcggccacg  | 240 |
| gttcccaagg | tgattctgga  | tatgcagtcg | catagcagag | tcattctctca | tgtgggctgc  | 300 |
| ctgacacaga | tgtctttctt  | ggctcctttt | gcatgtatag | aaggcatgct  | cctgactgtg  | 360 |
| atggcctatg | gctgctttgt  | agccatctgt | cgccctctgc | actaccagct  | catagtgaat  | 420 |
| cctcacctct | gtgtcttctt  | cgttttgggt | tcctttttcc | ttaacctgtt  | ggattcccag  | 480 |
| ctgcacagtt | ggatttgtgt  | acaattcacc | atcatcaaga | atgtggaaat  | ctctaatttt  | 540 |
| ttctgtgacc | cctctcagct  | tctcaacctt | gctgttctcg | acagcgtcat  | caatagcata  | 600 |
| ttcatatatt | tcgatatgtac | tatgtttggt | ttcttcccca | tttcagggat  | ccttttctct  | 660 |
| tactataaaa | ttgtcccttc  | cattctaaag | atgtcatcgt | cagatgggaa  | gtataaagcc  | 720 |
| ttctccacct | atggctctca  | cctaggaggt | gtttgtctgt | tttatggaac  | agtcattggc  | 780 |
| atgtacctgg | cttcagccgt  | gtcaccaccc | cccaggaatg | gtgtgggtggc | atcagtgtatg | 840 |
| taggctgtgg | tcacccccat  | gctgaacctt | ttcatctaca | gcctgagaaa  | cagggacata  | 900 |
| caaagtgcc  | tgcggagggt  | gcgcagcaga | acagtcgaat | ctcatgatct  | gttccatcct  | 960 |
| ttttcttgtg | t           |            |            |             |             | 971 |

&lt;210&gt; 851

&lt;211&gt; 1014

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g701 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 851

```

cccattgagc agggaaatta caccagggtg aaggaatctc ttttttcaag gactgaccca      60
gtcccaagag ctgagcttgg tcttatttct tttcttattt tttgtgtact cagcaactgt      120
gctgggtaac ctctcatca tggctgtggt gacctgtgag tctcgccttc acacccccac      180
gtacttctcg ctctgcaatc tctctgtgtt ggttatctgc ttctcctcca tcactgtctcg      240
gaaggtgcta atagaccttt caagcagaaa gaccatctcc ttcaatggtt gcatgacaca      300
gatgtttttc ttccacctcc tcggtgggac agacgttttt tctctctttg tgatggcggt      360
tgaccaatac atggccatct tcaagccctt gcactgtgtg accatcgtga gtaggggaca      420
gtgtctccct acatcgtgag tagggggcgt gagtgaggcg caggcctcat catggcttcc      480
tgggtggggg gtttgtccac tccattgtgc aggtatttct gttgtctcca ctcccttctg      540
tggaacatcat atgattgatg gtttctactg tgatgtcccc caggctctca aacttgccctg      600
caccacacac tttgtctctg aggtcttaat gatttccaat aatggcttga tctctatgct      660
gtggttcata tttctcctca tatcttacac ggtcatcttg atgatgttga ggtctcacac      720
tgaggaaggc aggaggaaaag ccacgcgcac ctgcacctcc cacatcactg tggtgacct      780
gcatttcgtg ccctgcacat atgtgcatgc ccagccttca ctgccctccc cagggacaga      840
gctgtctcca tcacctttac agtcattatt cctgtcctga accccatgat ctacacctg      900
aggaaccagg agatgaagtc agccttgagg aggcggaaga aaagaccttc tggaaaggga      960
tagatgctac gaagtccaga ttggaaaatc agaactgaaa agtatttctt cata      1014

```

&lt;210&gt; 852

&lt;211&gt; 1004

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g702 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 852

```

tctaataacc cgcagaattt aacagatgtc tctttattcc tcctcctaga agctcagagg      60
atccagaaca gcagcctgtc ctgctgggc tgttctgtgc catgtgcctg gtcacgggtgc      120
tggggaacct gtcacatcct ctggccgtca gccctgactc ccacctccac acccccatgt      180
acctcttctc ctccaacctg tccttgccctg acatcgggtt cacctccagc atgggtcccca      240
agatgattgt ggacatctaa tctcacagca gactcatctc ctaggcaggc tgcctgactc      300
ccatgtctct ctttgccatt tttggaggca tgggaagagag acatgctcct gagtgtgatc      360
cctatgaccc gtttgtagcc atctgtcacc ctctatatca ttcagccatc atgaaccgt      420
gtttctgtgg ctttctagtt ttgttgtctt ttttttctca gtctctttta gacgccagg      480
tgcacaactt gattgcctta caaatgacct gcttcaagga tgtggaaatt cctaatttct      540
tctgggaacc ttctcaactc ccccatcttg catgttgcca caccttcacc aataacataa      600
tcatgtattc ccctgctgcc atatttggtt ttcttcccat ctcggggacc cttttctctt      660
actataagat tgtttcctcc attctgaggg ttcatcctc aggtgggaag tataaggcgt      720
gtccacactg tgggtctcac ctgtcagttg tttgctgatt ttatggaaca ggcttttggg      780
ggtacctcag ttcagatgtg tcatcttccc cgggaaaggc tgcagtggcc tcagtgtatg      840
acacggtggt ccccccatg ccgaacctt tcatctacag cctgagaaac agggatatta      900
aaagcgtcct gcggcgcccg cacggcagca cagtctaag tcaatatctc cttatctgtt      960
ccatgccttt tgtagtgtgg gttaaaaaag gcagcaaggc caaa      1004

```

&lt;210&gt; 853

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g703 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 853



```

atgaaaaact gtaccagggt aaaagaattt attttccttg gcctaaccce gaatggggac      60
acaagattgg tcctatttct ttctactctc ttgggtgtaca tgacgactct gctgggaaac      120
ctcctcatca tggtcactgt cacctgtgaa tcttgccctc acatgcccat gtattttttg      180
ctccataatt tatctattgc cgatatctgc ttctactcca tcacagagcc caagggtctg      240
gtggaccttc tgtctgagag aaagaccatc tccttcaatg gttgcttcac tcagatgttt      300
ctcttccacc ttattggagg ggtggatgca tttctctat cagtgatggc attggatcaa      360
tatgtggcca tttccaagtc cctgcactat gcgaccatca tgagtagaga ccgttgcat      420
gggctcacag tggctgcctg gttggggggc tttgtccact ccattgtgca gattaccctg      480
ttgtctccac tccctttctg tggaccaaatt gttcttgaca ctttctactg tgatgttccc      540
caggttctca aactcgccca tacagacatt ttcatacttg agctgttgat gattttccaa      600
aatggactgc tcaccacact gtgggtttttc ctgctcctgg tgcctacat ggtcatatta      660
tcattactca agtctcagggc aggatagggc aggaggaaag tcactctccac ctgcacctcc      720
cacatcactg tggtgacctt gcattttgtg ccctgcactc atgtctatgc ccggcctttc      780
actgccctcc ccacggataa ggccatctct gtcaccttca ctgtcatctc ccctctgctc      840
aacccttgat ctacactctg agaaaccatg agatgaagtc aacctatgaag agactgaaga      900
ctctgacctt ctgataggaa atagaccagt gcttccctcc ttctc      945

```

&lt;210&gt; 854

&lt;211&gt; 962

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g704 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 854

```

cacacagagc caccgaatct cacagggtgc tgaaaagtgc tcctgggact ctctctgaga      60
ggatccagaa ctgcagccca tcctcgctgg gctgtccctg tccatgtatc tggtcacggc      120
gctgaggaac gtgctcatca tcctggctgt cagctctgac tcccacctcc acacccccat      180
gtacttcttc ctctccagcc tgtgctgggc tgacatcggc ttcacctcgg ccactgttcc      240
caagatgact gtggacatgc agtcgcatag cagagtcac tcttatgtga gctgcctgac      300
acagatatct ttcttggtcc tttttgcatg tatggaagac atgctcctgt gatggcctat      360
gacagagttg tggccatctg tcacccctcg cactatccag tcatcatgaa tcctcacctt      420
cgtgtcttct tagttttgct gtcctttttc cttagcttgt tggattccca gctgcacagt      480
tggattgtgt tacaattcac cttattcaag aatgtggaaa actctagttt tgtctgtgac      540
ccctctcaac ttctcaacct tgctgttctt gacagcgtca tcaatagcat attcatatat      600
ttcgatagta ctatggttgg ttttcttccc atttcaggga tcctttttat ttactataaa      660
attgtccctt ccattctaag gatgtcatca tcagatggga agtataaagc cttctccacc      720
tatggctctc aactggcagc tctttgctga ttttatggaa caggcattgg catgtacctg      780
acttcagctg tggcactacc ccccaggaat ggtgtcgtgg catcagtgat gtaggctgtg      840
gtcaccccca tgcgtaactt tttcatctac agcctgagaa acaggggacat acaaagtgcc      900
ctgaggaggc tgcgcagcag aacagtcgaa tctcatgatc tgttccatcc tttttcttgt      960
gt

```

&lt;210&gt; 855

&lt;211&gt; 952

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g705 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 855

```

aagcagcagg aaaatgggac ctgtctgggtg acagaattcc tgatgatggg attctccaac      60
ctcccacacc tgaggaaacac actcttcacc ctgttcttcc ttacctacct ggtcaccttc      120
ggtggcaacy tcaccatcat caccatcacc catgcggata ggccccgcca cactcccatg      180
taccacttcc tgggtggtgt gtcctctctg gagacctgct atacacgctg gtcaccatcc      240
ccagcatgct ggctcatctg ctgatggaga ccaggccatc tccatccctg gctgtcaggc      300
tcagatgttt ttcttctctg gtcctgggatg cagccactgc ttcttcttta cctgatggg      360
ttatgaccgc tatgtggcca tctgccacc cctgcgctac tctatgggtc tgagaccac      420
cgtttgcttc tgctggggag cctgggtttt ctgctctggg ttctcgggtg ccttgatcga      480

```

|  |     |
|--|-----|
| gaccagcatg atctttctcat cgcctttttg cggcggagac cacgtggagc acttcttctg   | 540 |
| tgacatcgcc cgggtgctga agctcagctg cgccaagagt gccagcaagg cgctgggcat    | 600 |
| ctttttcctg agcgtcctg tgggtgctgat gtccttcgtc ccgatacctt tctcctatgc    | 660 |
| cttcatcgtg gctgccatcg tgaggatttc cttggcagcc ggccggcgca aggccttctc    | 720 |
| cacctgtgtg gcccacgtca ccgtggctgt agtacatttt gactgcgcct ccatcatcta    | 780 |
| cttgcgctccg gagtccgggg ccaaccccgga ccaggaccgc ttgggtggctg tgttctacac | 840 |
| ggtggtgatg ccactgctga accctgtggt gtgcactctg tggacaagg aggtgagagt     | 900 |
| ggctctgagg aggaccctgg cgtggagccg tggggttttt aaataagaat ct            | 952 |

&lt;210&gt; 856

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g706 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (339)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 856

|  |     |
|--|-----|
| ctgctggacc acttcatctg tgagctgccg gcgttgctca agctggcctg cggaggcgac  | 60  |
| ggagacacta ccgagaacca gatgttcgcc gccgcgtgg tcacccctgct gctgccgttt  | 120 |
| gccgtcatcc tggcctccta cgggtgccgtg gcccgagctg tctgttgcat gcggttcagc | 180 |
| ggaggccgga gggagggcg tgggcacgtg ttgggtccca cctgacagcc gtctgcctgt   | 240 |
| tctacggctc ggccatctac acctacctgc agcccgcgca gcgctacaac cagcacgggn  | 300 |
| ncagnttcgt atcgctcttc tacacccgtg gtcacaccc                         | 339 |

&lt;210&gt; 857

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g707 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 857

|   |     |
|---|-----|
| atggatcaga gaaattacac cagagtgaag gaatttacct tcctgggaat tactcagtec | 60  |
| cgagaactga gccaggctct atttaccttc ctgtttttgg tgtacatgac aactctaagt | 120 |
| ggaaacttcc tcacatggtg tacagttacc tgtgaatctc accttcatac gcccatgtac | 180 |
| ttcctgctcc gcaacctgtc tattcttgac atctgctttt cctccatcac agctcctaag | 240 |
| gtcctgatag atcttctatc agagacaaaa accatctcct tcagtggctg tgtcactcaa | 300 |
| atgttcttct tccaccttct ggggggagca gacgtttttt ctctctctgt gatggcggtt | 360 |
| gaccgtata tagccatctc caagcccctg cactatatga ccatcatgag tagggggcga  | 420 |
| tgcacaggcc tcacgtggg cttcctgggt ggggggcttg tccactccat agcgcagatt  | 480 |
| tctctattgc tccactccc tgtctgtgga cccaatgttc ttgacacttt ctactgcgat  | 540 |
| gtcccccagg tcctcaaaact tgctgcact gacaccttca ctctggagct cctgatgatt | 600 |
| tcaaataatg ggtagtcag ttggtttgta ttcttcttct tcctcatatc ttacacggtc  | 660 |
| atcttgatga tgctgaggtc tcacactggg gaaggcagga ggaaagccat ctccacctgc | 720 |
| acctcccaca tcacctgggt gacctgcat ttctgtccct gcacttatgt ctatgcccg   | 780 |
| cccttctactg cctccccac agacactgcc atctctgtca ccttcaactgt catctccct | 840 |
| ttgctcaatc ctataattta cacgtgagg aatcaggaaa tgaagttggc catgaggaaa  | 900 |
| ctgaagagac ggctaggaca atcagaaagg attttaatt                        | 939 |

&lt;210&gt; 858

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g708 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 858

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| gtagccatat  | gtaatccctt  | gctttatcca  | gtgatgatgt | ccaacaaact  | cagcgctcag  | 60  |
| ttgctaagta  | tttcatatgt  | aattgggttc  | ctgcaccttc | tggttcatgt  | gagtttacta  | 120 |
| ttgcgactaa  | ctttctgcag  | gtttaacata  | atacattatt | tctactgtga  | aattttacaa  | 180 |
| ctgttcaaaa  | tttcatgcaa  | tgggtccatct | attaacgcac | taataatatt  | tatttttgggt | 240 |
| gctttttatc  | aaatacccac  | tttaatgact  | atcataatct | cttataactcg | tgtgctcttt  | 300 |
| gatattctga  | aaaaaaaagtc | tgaaaagggc  | agaagcaaag | ccttctccac  | atgcggcgcc  | 360 |
| catctgcttt  | ctgtctcatt  | gtactacgga  | actctgatct | tcatgtatgt  | gcgtcctgca  | 420 |
| tctggccttag | ctgaagacca  | agacaaaagt  | tattctctgt | tttacacgat  | tataattccc  | 480 |
| ctgcta      |             |             |            |             |             | 486 |

&lt;210&gt; 859

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g709 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 859

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| atgtactact  | tcctctgcc  | cctggccttg | gtagacgcgg | gcttcactac | tagcgtgggtg | 60  |
| ccgccgctgc  | tggccaacct | gcgcggacca | gcgctctggc | tgccgcgcag | ccactgcacg  | 120 |
| gcccagctgt  | gcgcacgcgt | ggctctgggt | tcggccgaat | gcgtcctcct | ggcgggtgatg | 180 |
| gctctggacc  | gcgcggccgc | agtgtgccgc | ccgctgcgct | atgcgggggt | cgtctccccg  | 240 |
| cgcctatgtc  | gcacgctggc | cagcgcctcc | tggctaagcg | gcctcaccaa | ctcggttgcg  | 300 |
| caaaccgcgc  | tcctggctga | gcggccgctg | tgccgcgccc | gcctgctgga | ccacttcac   | 360 |
| tgtgagctgc  | cggcgcttgc | caagctggcc | tgccgaggcg | acggagacac | taccgagaac  | 420 |
| cagatgttcg  | ccgcccgctg | ggtcatcctg | ctgctgccgt | ttgccgtcat | cctggcctcc  | 480 |
| tacgggtgccg | tggcccgagc | tgtctgttgc | atgcggttca | gcggaggccg | gaggaggcg   | 540 |
| gtgggcacgt  | gtgggtccca | cctgacagcc | gtctgcctgt | tctacggctc | ggccatctac  | 600 |
| acctacctgc  | agcccgcgca | gcgctacaac | caggcacggg | gcaagttcgt | atcgctcttc  | 660 |
| tacaccgtgg  | tcacacctgc | tctcaaccgc | ctcatctaca | ccctcaggaa | taagaaagt   | 720 |
| aagggggcag  | cgaggaggct | gctgcggagt | ctggggagag | gccaggctgg | gcag        | 774 |

&lt;210&gt; 860

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g710 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 860

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| atgcagagag | ccaatcactc  | cacagtgacc  | caattcattc | tcgtcggtct | ctctgtcttc  | 60  |
| ccccacctcc | agctgatgct  | cttctgtctg  | ttctgtctga | tgtacctgtt | cacgtgtctg  | 120 |
| ggcaacctgc | tcacatggc   | caccgtctgg  | agcgagcgca | gcctccacac | gcccattgtac | 180 |
| ctcttctgt  | gcgcctctc   | cgtctccgag  | atcctctaca | ccgtggccat | catcccgcgc  | 240 |
| atgctggccg | acctgctgtc  | caccacgcgc  | tccatcgctc | tcttggcctg | tgccagtcag  | 300 |
| atgttcttct | ccttcagctt  | cggttcacac  | cactccttcc | tgtcacctgc | catgggttac  | 360 |
| gaccgctacg | tggccatctg  | ccacccccctg | cgctacaacg | tgtcatgag  | cccgcggggc  | 420 |
| tgcgcctgcc | tgggtgggtg  | ctcctggggt  | gggtggcttg | tcatggggat | ggtggtgacc  | 480 |
| tcggccattt | tcacacctgc  | cttctgtgga  | cacaaggaga | tccaccattt | tgtttgccat  | 540 |
| gtgccacctc | tgttgaagtt  | ggcctgtgga  | gacgatgtgc | tgggtggtgg | caaaggcgtg  | 600 |
| ggcttggtgt | gtatcacggc  | cctgctgggc  | tgttttctcc | tcacctcctc | ctcctatgcc  | 660 |
| ttcatcgtgg | ccgccatctt  | gaagatccct  | tctgctgaag | gtcggaaaca | ggccttctcc  | 720 |
| acctgtgcct | ctcacctcac  | tgtggtgggc  | gtgcactatg | gctttgcctc | cgctcatttac | 780 |
| ctgaagccca | aaagtcccca  | gtctctggaa  | ggagacacct | tgatgggcat | cacctacacg  | 840 |
| gtcctcacac | ccttctctcag | ccccatcctc  | ttcagcctca | ggaacaagga | gctgaaggctc | 900 |
| gccatgaaga | agaccttctt  | cagtaaactc  | taccagaaaa | aaaatgta   |             | 948 |

<210> 861  
 <211> 674  
 <212> DNA  
 <213> Unknown (H38g711 nucleotide)

<220>  
 <223> Synthetic construct

<400> 861  
 ttgcctgaca tcgggtttcac ctccaccacg gtccccaaga tgattgtgga catceagtct 60  
 cacagcagag tcctctccta tgcgggctgc ctgatcagat gtctctcttt gccacttttg 120  
 gaagcatgga agagaggcat gtccttgagt gtgatggcat atgaccgggt ttagccatc 180  
 tgtcaccctc tatatcggtc agccatcttg aaccctgtat tctgtggctt cctagatttg 240  
 ttgtctttgt tttttttgt ttgtttgttt tgtttttctc agtcttctag actcccagct 300  
 gcacaacttg attgccttac aaatgacctg ctccaaggat gtggaaattc ctaatttctt 360  
 ctgggaacct tctcarctcc cccatcttgc atgttgtgac accttcacca ggaacatcaa 420  
 catgtatttc cctgctgccc tatttgggtt tcttcccatc tcagggaacct tttctcttac 480  
 tgtaaaattc tttcctccat tctgagggtt tcatcatcag gtgggaagta taaaccttct 540  
 ccacctgtgg gtctcacctg tcagttgttt gctgatttta tgggaacaggc gttggagggt 600  
 acctcggttc agatgtgtca tcttccccga gaaagrgtgc agtggcctca gtgatgtaca 660  
 yggtggtcac cccc 674

<210> 862  
 <211> 653  
 <212> DNA  
 <213> Unknown (H38g712 nucleotide)

<220>  
 <223> Synthetic construct

<400> 862  
 ttgcctgaca tcgggtttcac ctccaccatg gtccccaaga tgattgtgga atccaatctc 60  
 acagcagagt catctcctat gcaggccgcc tgactcagat gtctctcttt gccatttttg 120  
 gaggcagga agagagacat gtccttgagt gtgatggcct atgaccgggt ttagccatc 180  
 tgtcaccctc tatgtcattc agccatcacg aaccctgtgt tctgtggctt tctagttttg 240  
 ttgtcttttt tttttctcag tccttttagac gccagctgc acaacttgat tgccttaca 300  
 aggacctgct tcaaggatgt ggaaattcct aatttcttct gtgaccttc tcaattcccc 360  
 gtcttgcatg ttgtggcacc ttcaccaata acataatcat gtatttccct gctgccatat 420  
 ttggttttct tcccatctcg gggaccttt tctcttacga taaaattgtt tctccattc 480  
 tgagggtttc atcatcaggt gggaagcata aggccttctc caccaggggg tctcacctgt 540  
 cagttgtttg ctgattttat ggaacaggcg ttggagagta cctcggttca gatgtgtcat 600  
 cttccccgag aaagggtgca gtggcctcag tgatgtacac ggtggtcacc ccc 653

<210> 863  
 <211> 648  
 <212> DNA  
 <213> Unknown (H38g713 nucleotide)

<220>  
 <223> Synthetic construct

<400> 863  
 ctgggtggact ttggatactc ctcagctgtc actcccaagg tcatggctgg gttccttata 60  
 gaagacaagg tcatctctta caatgcagt gtgctcaaa tgtatatctt ttagctttt 120  
 gccactgtgg aaaattacct cttggcctca atggcctatg accgctatgc agcagtgtgc 180  
 aaacccttac attacaccac aaccatgaca acaactgtgt gtgctcgtct ggccataggc 240  
 tcctacctct gtggtttctt gaatgcctcc atccacactg gggacacatt tagtctctct 300  
 ttctgtaagt ccaatgaagt ccatcacttt ttctgtgata ttccagcagt catggttctc 360  
 tcttgctctg atagacatat tagcgagctt gttcttattt atgtgtgtgag cttcaatate 420  
 tttatagctc tcttggttat cttgatatcc tacacattca ttttatcac catcctaaag 480

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgcactcag | cttcagtata | ccagaagcct | ttgtccacct | gtgcctctca | tttcattgca | 540 |
| gtcggcatct | tctatgggac | tattatcttc | atgtacttac | aaccagctc  | cagtcactcc | 600 |
| atggacacag | acaaaatggc | acctgtgttc | tatacaatgg | tcatcccc   |            | 648 |

&lt;210&gt; 864

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g714 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 864

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| attgttgaca | tatcctatgc | ttccaactat | gtccccaaga | tgctgacgaa | tcttatgaac  | 60  |
| caggaaagca | ccatctcctt | ttttccatgc | ataatgcaga | cattcttgta | tttggtttt   | 120 |
| gtcacgtag  | agtgtctgat | tttggtggtg | atgtcctatg | atcgctatgc | ggacatctgc  | 180 |
| caccccttac | gttacaatat | cctcatgagc | tggagagtgt | gcactgtcct | ggctgtggct  | 240 |
| tcctgggtgt | tcagcttctc | cctggctctg | gtccctttag | ttctcctcct | gaggctgccc  | 300 |
| ttctgcgggc | ctcatgaaat | caaccacttc | tgtgaaatcc | tgtctgtcct | caagttggcc  | 360 |
| tgtgctgaca | cctggctcaa | ccaggtgggc | atctttgcag | cctgcgtgtt | catcctgggtg | 420 |
| gggccactct | gcctgggtgt | ggtctcctac | ttgcgcaccc | tggccgccat | cttgaggatc  | 480 |
| cagtctgggg | agggccgcag | aaaggccttc | tccacctgct | cctcccacct | ttgcgtgggtg | 540 |
| ggactcttct | ttggcagcgc | cattgtcacg | tacatggccc | ccaagtcccc | ccatcctgag  | 600 |
| gagcagcaga | aagttctttc | cctgttttac | agccttttca | atcca      |             | 645 |

&lt;210&gt; 865

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g715 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 865

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtggccatct | gtaaaccctt | tcattatgtg | gtcatcatga | acaacagggt | gtgtacctta | 60  |
| ttagttctct | gctgttggtg | ggctggcttg | atgatcattg | ttccaccact | tagcttaggc | 120 |
| ctccagctcg | aattctgtga | ctccaatgcc | attgatcatt | ttagctgtga | tgcaggctct | 180 |
| ctcctaaaga | tctcatgtct | agatacatgg | gtaatagaac | agatgggtat | acttatggct | 240 |
| gtatttgcac | tcattatcac | cccagtttgt | gtgattctgt | cctacttgta | catagtcaga | 300 |
| acaattctga | agttcccttc | tgttcagcaa | aggaaaaagg | ccttttctac | ctgttcatcc | 360 |
| cacatgattg | tggtttccat | tgccatagga | agctgcatct | tcacttatat | caagccctct | 420 |
| gcaaaagatg | aggtggccat | aaataaagga | gtttcagttc | ttactacttc | tgtcgcaccc | 480 |
| ttgttg     |            |            |            |            |            | 486 |

&lt;210&gt; 866

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g716 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(670)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 866

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttgcctgaca | tcggtttcac | ctccaccacg | gtccccaaga | tgattgtgga | catccagtct | 60  |
| cacagcagag | tcactctcta | tgcaggctgc | ctgactcaga | tgtctctctt | tgccattttt | 120 |
| ggaggcatgg | aagagagaca | tgctcctgag | cgtgatggcc | tacgaccagt | ttgtagccat | 180 |
| ctgtcaccct | ccatctcggt | cagccatctt | gaacccgtgt | ttctgtggct | tccaagattt | 240 |

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| gttgctccttg | tntttttttt | tttttttttt | tttttctca   | ggctttttaga | ctcccagctg | 300 |
| cataacttga  | ttgccttaca | aatgacctgc | ttcaaggatg  | tggaaatttc  | taatgtcttc | 360 |
| tgggaacctt  | ctcaactctc | ccatcttgca | tgttggtgaca | ccttcaccag  | gaacatcagt | 420 |
| atttccttgc  | tgccatattt | ggttttcttc | ccatcttggg  | gacctttttc  | tcttactgta | 480 |
| aaattgtttc  | ctccattctg | agggtttcat | catcagggtg  | gaagtataaa  | ccttctccac | 540 |
| ctgtgggtct  | cacctgtcag | ttgtttgctg | attttatgga  | acagggtgtg  | gagggtacct | 600 |
| cagttcagat  | gtgtcatctt | ccctgagaaa | ggctgcagtg  | gcctcagtg   | tgtacaagat | 660 |
| ggtcaccccc  |            |            |             |             |            | 670 |

&lt;210&gt; 867

&lt;211&gt; 654

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g717 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 867

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| ttggctgaca  | tcggtttcac | ctccaacacg  | gtccccaaga | tgattgtgga | catccaatct | 60  |
| cacagcagag  | tcatctccta | tgcaggctgc  | ctgactcaga | tgtctctctt | tgtgtttttt | 120 |
| ggaggcatgg  | aagaaagaca | tgtctctgag  | tgtgagggcc | tatgaccggt | ttgtagccat | 180 |
| ctgtcacccct | ctatattatt | cagccatcat  | gaacccatgt | ttctgtggct | tcctagtttt | 240 |
| gtgttttttt  | tttttctcag | tcttttagac  | tcccagctgc | acaatttgat | tgctttacaa | 300 |
| atgacctgca  | tcaaggatgt | ggaaattcct  | aatttcttct | gtgaccttct | tcaactcccc | 360 |
| catcttgcac  | gttgtgacac | cttcaccatt  | aacatagtca | tgtatttccc | tgccgccata | 420 |
| tttggttttc  | ttcccatctc | ggggaccctt  | ttctcttact | ctaaaattgt | ttcctccatt | 480 |
| ctgaggggtt  | catcatcagg | tgggaagtat  | aaagccttct | ccacctgtgg | gtctcacctg | 540 |
| tcagttggtt  | gctgagttta | tgggaacaggc | gttgagggtt | acctcagttc | agatgtgtca | 600 |
| tcttccctga  | gaaaggctgc | agtggcctca  | gtgatgtaca | cggtggtcac | cccc       | 654 |

&lt;210&gt; 868

&lt;211&gt; 882

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g718 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 868

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| ttgattttct  | tcttaatcta  | tccgcttctc  | ctgggtgggt | atgaccagat | cctgggtgggt | 60  |
| gtgatggcag  | aggccagcct  | tcacaagcct  | gtgtacttct | tcctgataaa | cctctcagcc  | 120 |
| ctagacatcc  | tctccactac  | agtcaactgtc | cccaagacgc | tgcccctggt | cttgcttggg  | 180 |
| gaccaacttc  | tcagcttccc  | tgccctgttc  | ctacagatgt | acctgttcca | cagcttctcc  | 240 |
| tgtctcagaag | ccttcacatc  | gggtggctcat | gcctatgacc | gctatgtagc | tatctgccac  | 300 |
| ccactgcaat  | accctgttct  | catgaaccca  | cagaccaatg | ctgtcttggc | aaccggtgcc  | 360 |
| tggtctactg  | ccctcctcct  | gcccattcca  | gcagtagtac | agacctccca | gatggcattt  | 420 |
| gacagcattg  | ctgacatcta  | ccactgtctc  | tgtgatcatc | tggctgtggg | ccaggcctcc  | 480 |
| tgtctctgata | ccacccccag  | accttcatgg  | gtttctgcat | cgccatgggt | gtgtccttcc  | 540 |
| tcccccttct  | cctgggtgctt | ctctcctatg  | cccacatctt | gacctcgggt | cttcgcatta  | 600 |
| actcccaaga  | aggacgtccc  | aaagccttct  | ccacctgcag | ctcccatctc | ccggtagtgg  | 660 |
| gcacctacta  | ctcatccatt  | gccatagcct  | atgtggccta | cagcgctgac | ctgcccctcg  | 720 |
| acttccacgt  | catgggcaat  | gttgtacatg  | tcttcttctt | cctcttcttc | ttcttcttcc  | 780 |
| tcttctctct  | cttctctctc  | ctcttctgtt  | tcttcttctt | cttcttctcc | ttctcttctc  | 840 |
| tcttctctct  | cttctctctc  | tccttcttct  | tcttcttctt | tt         |             | 882 |

&lt;210&gt; 869

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g719 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 869

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| atggagatgg  | aaaactgcac | cagggtaaaa | gaatttattt | tccttggcct  | gacccagaat  | 60  |
| cggaagtg    | gcttagtctt | atttcttttc | ctactcttgg | tgtatgtgac  | aactttgctg  | 120 |
| ggaaacctcc  | tcatcatggt | cactgttacc | tgtgaatctc | gccttcacac  | gcccattgat  | 180 |
| tttttgctcc  | ataatttatc | tattgccgat | atctgcttct | cttccatcac  | agtgcccaag  | 240 |
| gttctgggtg  | accttctgtc | tgaaagaaag | accatctcct | tcaatcattg  | cttcactcag  | 300 |
| atgtttctat  | tccaccttat | tggaggggtg | gatgtatttt | ctctttcggg  | gatggcattg  | 360 |
| gatcgatatg  | tggccatctc | caagcccctg | cactatgcga | ctatcatgag  | tagagaccaa  | 420 |
| tgcattgggc  | tcacagtggc | tgcctgggtg | gggggctttg | tccactccat  | cgtgcagatt  | 480 |
| tcctgttg    | tccactccc  | tttctgcgga | cccaatgttc | ttgacacttt  | ctactgtgat  | 540 |
| gtccaccggg  | tctcaaact  | ggcccataca | gacattttca | tacttgaact  | actaatgatt  | 600 |
| tccaacaatg  | gactgtctac | cacactgtgg | tttttcctgc | tcctgggtgc  | ctacatagtc  | 660 |
| atattatcat  | tacccaagtc | tcaggcagga | gagggcagga | ggaaagccat  | ctccacctgc  | 720 |
| acctcccaca  | tactgtgggt | gacctgcat  | ttctgtgccc | tgcattctatg | tctatgcccg  | 780 |
| gcccttcaact | gccctccc   | tgataaggc  | catctctgtc | accttcaactg | tcattctcccc | 840 |
| tctgtctaac  | cccttgatct | acactctgag | gaaccatgag | atgaagtcag  | ccatgaggag  | 900 |
| actgaagaga  | agacttgtgc | cttctgatag | aaaa       |             |             | 934 |

&lt;210&gt; 870

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g720 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 870

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| acaatgcagc | aaaataacag  | tgtgcctgaa  | ttcatactgt  | taggattaac  | acaggatccc  | 60  |
| ttgaggcaga | aaatagtgtt  | tgtaactctt  | tttaattttct | atatgggaac  | tgtgggtggg  | 120 |
| aatatgctca | ttattgtgac  | catcaagtcc  | agccggacac  | taggaagccc  | catgtacttc  | 180 |
| tttctatttt | atttgtcctt  | tgcagattct  | tgtttttcaa  | cttccacagc  | ccctagatta  | 240 |
| attgtggatg | ctctctctga  | aaagaaaatt  | ataacctaca  | atgagtgcac  | gacacaagtc  | 300 |
| tttgactac  | atttatttgg  | ctgcatggag  | atctttgtcc  | tcattctcat  | ggctgttgat  | 360 |
| cgctatgtgg | ccatctgtaa  | gcccttgcgt  | tacccaacca  | tcattgagcca | gcaggctctgc | 420 |
| atcatcctga | ttgttcttgc  | ctggataggg  | tctttaatac  | actctacagc  | tcagattatc  | 480 |
| ctggccttaa | gattgccttt  | ctgtggaccc  | tatttgattg  | atcattattg  | ctgtgatttg  | 540 |
| cagcccttgt | tgaaacttgc  | ctgcatggac  | acttacatga  | tcaacctgct  | gttgggtgct  | 600 |
| aacagtgggg | caatttgcctc | aagtagtttc  | atgattttga  | taatttcata  | tattgtcatc  | 660 |
| ttgcattcac | tgagaaacca  | cagtgcacaa  | gggaagaaaa  | aggctctctc  | cgcttgcacg  | 720 |
| tctcacataa | ttgtagtcac  | cttattcttt  | ggcccatgta  | tattcatata  | tacacgcccc  | 780 |
| ccgaccactt | tccccatgga  | caagatgggtg | gcagtatttt  | atactatttg  | aacacccttt  | 840 |
| ctcaatccac | tcattctacac | atctgaggaa  | tgcagaagtg  | aaaaatgcca  | tgagaaag    | 898 |

&lt;210&gt; 871

&lt;211&gt; 943

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g721 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 871

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| atggagttgg  | gaaatgtcac  | cagagtaaaa | gaatttatat | ttctgggact | tactcaatcc | 60  |
| caagaccaga  | gtttgggtctt | gtttcttttt | ttatgtcttg | tgtacatgac | gactctgctg | 120 |
| ggaaacctcc  | tcatcatggt  | caccgtgacc | tgtgagtctc | gccttcacac | ccccatgtac | 180 |
| ttctgtctcc  | gcaatctagc  | catccttgac | atctgcttct | cctccacaac | tgctcctaaa | 240 |
| gtcttgctgg  | accttctgtc  | aaagaaaaag | accatatact | atacaagctg | catgacacag | 300 |
| atatttctct  | tccacctcct  | tggtggggca | gacatttttt | ctctctctgt | gatggcggtt | 360 |
| gactgtctaca | tggccatctc  | caagcccctg | cactatgtga | ccatcatgag | tagagggcaa | 420 |

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| tgcactgccc  | tcattctctgc | ctcttggatg  | gggggctttg | tccactccat  | cgtgcagatc | 480 |
| tccctgttgc  | tgcctctccc  | tttctgtgga  | cccaatgttc | ttgacacttt  | ctactgcgat | 540 |
| gtcccccagg  | tcctcaaaact | cacttgcaact | gacacttttg | ctcttgagtt  | cttgatgatt | 600 |
| tccaacaatg  | gcctgggtcac | taccctgtgg  | tttatcttcc | tgcttgtgtc  | ctacacagtc | 660 |
| atcctaata   | gcctgaggtc  | tcaggcagga  | gggggcagga | ggaaagccat  | ctccacttgc | 720 |
| acctccccac  | atcactgtgg  | tgaccctgca  | ttttgtgccc | tgcatctatg  | tctatgcccc | 780 |
| gcccttcaact | gccctcccca  | cagaaaaggc  | catctctgtc | accttcaactg | tcattctccc | 840 |
| tctgctgaac  | cctttgatct  | acactctgag  | gaaccaggaa | atgaagtcag  | ccatgagaag | 900 |
| actgaagaga  | agactcgtgc  | cttctgaaag  | ggaatagaaa | aca         |            | 943 |

&lt;210&gt; 872

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g722 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 872

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| atgctggggc | taaaccacac  | ctccatgtct | gaattcatcc | tcgtcggtt  | ctctgccttc  | 60  |
| ccccacctcc | aactgatgct  | cttctgtctg | ttctgtctga | tgtacctgtt | cacgtgtctg  | 120 |
| ggcaacctgc | tcattcatggc | caccgtctgg | agcgagcgca | gcctccacac | gcccattgtac | 180 |
| ctcttctctg | gcgtcctctc  | agtctccgag | atcctctaca | ccgtggccat | catcccgcg   | 240 |
| atgctggccg | acctgctgtc  | caccagcgc  | tccatcgctt | tcctggcctg | tgccagtcag  | 300 |
| atgttcttct | ccttcagctt  | cggcttcacc | cactccttcc | tgctcacctg | catgggtctac | 360 |
| gaccgctacg | tggccatctg  | ccacccctg  | cgctacaacg | tgctcatgag | cccacggggc  | 420 |
| tgcgcctgcc | tgggtgggctg | ctcctgggct | ggtggctcgg | tcattgggat | ggtgggtgacc | 480 |
| tcggccattt | tccaactgac  | tttctgtgga | tcccatgaga | tccagcattt | tttatgtcat  | 540 |
| gtgccacctc | tgttgaagtt  | ggcctgtgga | aataatgtac | cagctgtggc | cctgggcgtg  | 600 |
| ggcttgggat | gtatcatggc  | actgctgggc | tgttttctcc | tcactcctct | ctcctatgcc  | 660 |
| ttcatcgtgg | cgcacatctt  | gaagatccct | tctgctgaag | gtcggaaaca | ggccttctcc  | 720 |
| acctgtgcct | ctcaccttat  | tgtggtcatt | gtgcactatg | gctttgcctc | tgctcatctac | 780 |
| ctcaagccca | aagggtcccca | ctctcaggag | ggtgacaccc | tgatggccac | cacctacgca  | 840 |
| gtcctcacgc | ccttctctcag | ccccatcatc | ttcagcctca | ggaacaaaga | actgaagggt  | 900 |
| gccatgaaga | ggaccttcct  | cagcacactc | tattcctcag | gc         |             | 942 |

&lt;210&gt; 873

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g723 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 873

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| atgcctgggtc | agaactacag | aaccatatct  | gaatttatcc  | tctctggctt | ctcagccttc | 60  |
| ccccagcagc  | tcctgctgtg | cttgttctctg | ctgtacctcc  | tgatgttctt | gttcacattg | 120 |
| cttggaacac  | ttcttatcat | ggccacagtt  | tggattgaac  | gcagactcca | cacacccatg | 180 |
| tacctcttct  | tgtgtgccct | ctccatctct  | gagattctgt  | tcactgttgc | catcaccctt | 240 |
| cgcattgttg  | ctgatctgct | cttcacccat  | cgttccatca  | cctttgtggc | ttgtgccatt | 300 |
| cagatgttct  | tctccttcat | gtttggcttc  | actcactcct  | tccttctcat | ggtcatgggc | 360 |
| tatgatcact  | acgtgacctt | ctgccaccca  | ctgcattaca  | acatgcta   | gagtcctcgt | 420 |
| ggctgtgccc  | atcttgtggc | ctggacctgg  | gctgggtgct  | cggtcattgg | gatgatgggt | 480 |
| acaatgatgg  | tttttcaact | cactttctgt  | gggtcta     | tgatccacca | ttttctctgt | 540 |
| catgtgcttt  | ccctcttgaa | gttggcctgt  | gggagcaaga  | catcatctgt | catcatgggt | 600 |
| gtgatgctgg  | tgtgtgtcac | agccctgata  | ggctgtttgt  | tcctcatcat | cctctccttt | 660 |
| gtcttcattg  | tggctgccat | cttgaggatt  | ccttctgctg  | agggccggca | caagactttc | 720 |
| tccacttgtg  | tatccacact | cactgtgggtg | gtcatgcact  | atagttttgc | ctcccttata | 780 |
| tacctcaaac  | ccaaggcctt | ccattctatg  | tacagtgtatg | ccttgatggc | caccacctat | 840 |
| actgtcttca  | cccccttctt | cagcccaate  | attttcagtc  | taaggaaaca | ggagctgaag | 900 |
| aatgccataa  | ataaaaactt | ttgcagaagg  | ttctgccttc  | taagctcc   |            | 948 |



<210> 874  
 <211> 484  
 <212> DNA  
 <213> Unknown (H38g724 nucleotide)

<220>  
 <223> Synthetic construct

<400> 874  
 ggatggaaat acaagcacct tcaacatctc ctgcaccaag ttcttcctgg tgggtttccc 60  
 tggacttcga gagggtggc ccttcttggg cctgcctctt gtcttcctct ttgtgaccat 120  
 catctctgcc aatgccctgg tcatccacac agtgggtggc cggcaaaatc tgcacagcc 180  
 tacgtgtatg ctcatcactg tgctcctggc tgtcaatatt cgtgctgcca cagccgtgat 240  
 gcctaaaatg ctggagggct ttgtatatta tgctaacccc atatcgctgc atggccgcct 300  
 ggcctagggtg ttctttatct acctcaccct cctcctggac tacaacttcc tctggccctg 360  
 gccctggact gggtactttg ccatctgcca ccactctgc tttctgacc tgatgacctc 420  
 ccagctgctg ggactgctgg ccattcttgc ctttgaacaa agccctggga gtgacccgcg 480  
 cctt 484

<210> 875  
 <211> 595  
 <212> DNA  
 <213> Unknown (H38g725 nucleotide)

<220>  
 <223> Synthetic construct

<400> 875  
 gtagccatct ggcaccctc tctgttttca aactgaatga cttcccagct ggctgggatt 60  
 ctgggccatt cttgccttga cacagagctg gggagtgaac gtgccttttg tagtactaac 120  
 tgcaaaagcc gatttctgcc ggacagcagt gattcgacac ttcacctgtg agtgcatgac 180  
 actgctgagc atagcttgtg gagacctgac cttcaacaac tggctggggc tggctatgtg 240  
 tttggctact gtaatctctg atatggccct gctggggacc tctacaccc acatcatcta 300  
 tgctgccttc cggatctctt cttggggagc ccaagccaag gccttacaca cgtgtggctc 360  
 ccacctactg gtcacctctt ccatctacgt ctctgggtctt tccacttcca tcaccttctg 420  
 agtagccaag actgtgtccc agaattgtcca gaatctactc agtgccatat acttgctgct 480  
 tccaggagcc ttgaatcctg tcattttatgg ggtgaggact agggagatcc agcaacatgt 540  
 agaaaagatg ctctgtgaaa aggaaacagc ccagaaggct ggggagaagc caaag 595

<210> 876  
 <211> 944  
 <212> DNA  
 <213> Unknown (H38g726 nucleotide)

<220>  
 <223> Synthetic construct

<400> 876  
 ttcagtcaga acttgctgat ctctgggtct gggctcctttg tcttctctggg gatgccggga 60  
 ctggaggctc tgcattgctg gctctctgtg cctgtgtgcc tgctctacat ggcagctttg 120  
 gtaggggaatg ccttcttagt ggggctgggt ggtcgctgac aaggcactct gggcacccat 180  
 gtaccagctg ctgtggcttc tggcagctgc tgattttgtt ctggccacat ccacagtgcc 240  
 caaagctctg gctgtacttt ggggcttgct tagtgagata tcattttggag gctgcttggc 300  
 tcaactcttt gttgcccatt tgtcaatcat tgccacattg ctgagtcctc agtgctgctg 360  
 tccacggccg tagactgcca gcctttgcgc tatggggcgt tgctggccca gtttgtggta 420  
 ggtctagtgg ctctgactac catgaccctg gatgtctgtg tcatgtacac cctgtgatcc 480  
 tgttcaagaa actgccttac tgtggacagt gggccctgcc ccacacctac tgcgaacaca 540  
 tgggtgtggc ttgcctggca tgtggagata cgtgccccat catcaggatg ggactggcca 600  
 ccacactgct ctccccagcc ctggacctag ggctcatagg tgcttcttat gccctcattt 660  
 tccgtgctgt ctgccgtctg ccatcccatg ttgcctgcca caaggctctg ggtaactgctg 720

|   |     |
|---|-----|
| ggacctatgc tagcatcatt ggtctcttct acacacctgc cctcttctcc ttccttgctc | 780 |
| actgttttgg gtgtcacaca gtgccaacc atattcacat cctactggct aacctctacg  | 840 |
| cagtgggtgt cccagcttcc aatcctgtgg tctatggagt gcagactcag cagagctcag | 900 |
| aggctcagga acttgcttca acttttctgg gcaggagcag tgaa                  | 944 |

&lt;210&gt; 877

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g727 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 877

|   |     |
|---|-----|
| atgaattggg aaaatgagag ctccccaaaa gagtttatac tacttggtctt ctcagatagg  | 60  |
| gcttggtctac aaatgcccct ttttgtgggtc ctgttaatat catacacaat caccatattt | 120 |
| ggcaatgtgt ccatcatgat ggtgtgcatt ctggatccca aacttcatac tcccatgtat   | 180 |
| ttctttctca ctaatctctc catcttagat ctctgtata ccacaactac agtccctcat    | 240 |
| atgttggtaa atattggttg caacaaaaag accatcagct atgctggctg tgtggccac    | 300 |
| ctcatcatct tcctggccct aggtgtctca gagtgtctcc ttctggctgt tatgtcctt    | 360 |
| gacagatatg tggctgtttg cagacccctc cactatgtag tcatcatgaa ttattggttc   | 420 |
| tgccaaagga tggcagcctt ctcatggctc attgggttctg gcaactcagt gctgcagtct  | 480 |
| tccttgactc ttaacatgcc acgtgtgggt caccaggaag tggaccactt tttctgtgag   | 540 |
| gtgcctgcac ttctcaagtt gtcattgtgt gacacaaagc ctattgaggc tgagctcttc   | 600 |
| ttcttttagtg tactaattct tctaattcca gtgacattga tctcatctc ctatggcttc   | 660 |
| atagctcaag cagtattaaa aatcagggtca gcagaaggac ggcaaaaagc atttgggaca  | 720 |
| tgtgggtccc acatgattgt ggtgtccctc ttttatggaa cagccattta tatgtatctt   | 780 |
| caaccacctt catccacctc taaggactgg ggaaagatgg tttccctctt ctatggaatc   | 840 |
| atcacatcca tgttgaactc cctcatctac agccttagaa ataaagatat gaaggaggcc   | 900 |
| ttcaagaggc tgatgccaaag aatcttttct tgtaagaaa                         | 939 |

&lt;210&gt; 878

&lt;211&gt; 968

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g728 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 878

|  |     |
|--|-----|
| ggcacattga atttaagtag cttcaatcca ggactcttca ttctgttggg gatcccaggg  | 60  |
| ctggagtggg tctgcatctg gatgggaatt ctctccttta ccagttacct tgtctccctt  | 120 |
| gcagggaatg tcatccttct ctaccttacc actgtggaac acaacctcca taaacctatg  | 180 |
| ttttccttcc tctctatacc ggccctctgca aacctcatat tatgcattac atatttcccc | 240 |
| aaaacatttg ggatattcta gctgaaagct cagaaaataa tatttccttg atgttccacc  | 300 |
| agggtttttt ttttgggtct acttcacttt agctttttt ctggacttgg ccatcttggt   | 360 |
| gggtctggca ttgatcatt acatgaccat tggtttctt ctgagataca ccagtggctt    | 420 |
| gacacctcaa cacttggcaa gattgtgggt agcattgatt gaaggtttaa taacattttg  | 480 |
| cccatgtatt tcctggggaa gcatttgccc ttctgcagaa cacacattaa ttctaacaca  | 540 |
| tactgtgagc acatagggtg ggccctgctt tcctatgctg atatctccat caatatctgg  | 600 |
| tatgacttta ctatattggt aatgactatt atctcagatc tgatcctcac tgatatttcc  | 660 |
| tacacctca cccttcatgc tgttttccac ctcccatcca gtgatgccct tctgaaggcc   | 720 |
| ctaagcacct cgttcttca tgtcagtgtc attctcatgt tgtacacacc aacctgtctt   | 780 |
| tctgccctta ctcatcactt tggccagagt atctcttgca ctttttacct tatgtttgtg  | 840 |
| ggcctctata gggcaatccc tcctgtactc aattccataa ttatggagta aaaacaaagc  | 900 |
| agattggaaa caaggtcata cttttattct ttcttaaagg gatgcagtga tatgaggatg  | 960 |
| agaatatg   | 968 |

&lt;210&gt; 879

&lt;211&gt; 1011

&lt;212&gt; DNA

<213> Unknown (H38g729 nucleotide)

<220>

<223> Synthetic construct

<400> 879

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| atgaaaaaaaa | atgcaagttt  | tgaagacttc  | tttattctac | ttggattttc  | taactggcct  | 60   |
| catctggaag  | tagttctctt  | tgtgggtatc  | ttgatcttct | acttgataac  | actgatagga  | 120  |
| aacctgttca  | tcatcatcct  | gtcataacctg | gactcccac  | tccacactcc  | catgtacttc  | 180  |
| ttcctttcaa  | atctctcatt  | tctggatctc  | tgctacacca | ccagctctat  | ccctcagttg  | 240  |
| ctggtgaatc  | tctggggccc  | ggaaaagacc  | atctcttatg | ctgggtgtac  | agttcâactt  | 300  |
| tactttgttc  | tcgcaactgg  | aaccgcagag  | tgtgtcctac | tgggtggtgat | gtcctatgat  | 360  |
| cgttatgcag  | ctgtgtgtag  | acctttgcat  | tacactgtcc | tcatgcaccc  | tcgtttctgc  | 420  |
| cgcttgttgg  | ctgcggcttc  | ttgggtaagt  | ggttttacaa | cctcagcact  | tcattcctcc  | 480  |
| tttactttct  | ggataccctt  | atgtagacat  | cgcctagtgg | atcacttctt  | ctgtgaagct  | 540  |
| ccagcacttc  | tgcgattatc  | atgtgttgat  | acctaggcaa | atgagctgac  | cctcatggtc  | 600  |
| atgagctcca  | tttttgttct  | catacctctc  | atcctcatcc | tcacttccta  | tgggtgccatt | 660  |
| gcccgggctg  | tactgagcat  | gcaatcaacc  | actgggcttc | agaaagtgtc  | taggacatgt  | 720  |
| ggagcccac   | ttatggttgt  | atctctcttt  | ttcattccag | tcatgtgcat  | gtatctccag  | 780  |
| ccaccatcag  | aaaattctca  | agatcaaggc  | aagtccattg | ccctctttta  | cactgttgtc  | 840  |
| acacctagtc  | ttaaccctct  | aatctacact  | ttcagaaaca | aggatgtaag  | aggggcagtg  | 900  |
| aagagactaa  | tgggggtggga | atgggggatg  | tgacagggaa | atcatgttgg  | ctgttgtttt  | 960  |
| tcctagggtc  | ttatccattt  | tgaaaggttg  | tttccctgct | tctttgtgat  | t           | 1011 |

<210> 880

<211> 956

<212> DNA

<213> Unknown (H38g730 nucleotide)

<220>

<223> Synthetic construct

<400> 880

|            |             |             |            |             |             |     |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| atggccatgt | acaacatgag  | tgaccatggt  | acaggcctgt | tcatacctttt | gggtatccct  | 60  |
| ggacttgagc | agtaccacgt  | ctggatcagc  | atcccatctt | gcttaatcta  | tctcatggct  | 120 |
| gtcgtggcca | agagtatcct  | tctctacctc  | attgtggtag | agcacagtct  | tcatgcaccc  | 180 |
| atgttctttt | tcctttccat  | gctggccatt  | actgatctca | tattgtccac  | cacatgtgtc  | 240 |
| cccaaaacac | ttagcatctt  | ctggtttggg  | cccaaaacag | tttccctggc  | tgtctcacc   | 300 |
| aattattctt | tctgcactat  | agcttttgtg  | tggactcagc | tatactgctg  | gccatggcat  | 360 |
| ttgaccgcta | tatggccatt  | tgtccaccct  | tgagatacac | tactattctg  | actcccaaaa  | 420 |
| ccattgtcaa | aattgctgtg  | ggaatatgtt  | tccgaagttt | ctgtgttttt  | gtcccgtgtg  | 480 |
| ttttccttgt | gaatcgttta  | cccttctgca  | ggacacacat | catttctcac  | acatactgtg  | 540 |
| agcacatagg | tgttgcccag  | cttgccctgtg | ctgatatctc | catcaatata  | tgggtgtggat | 600 |
| tttgtgttcc | catcatgacg  | gtgatgacag  | acgtgatect | cattgtctgtc | tcctacaccc  | 660 |
| tcatgctctg | tgggtgtctt  | tgcctccctt  | cccaagatgc | ccgtcagaag  | gccctttgct  | 720 |
| cctgtggttc | ccatgtctgt  | gttatccctc  | tattctatac | accagcatte  | ttctccatcc  | 780 |
| ttgcccacg  | ctttgggcat  | aatgtccctc  | atacctttca | tattatgttt  | gccaaccttt  | 840 |
| atgtaatcat | tccacctgct  | ctcaacccta  | ttgtctacag | aataaagacc  | aagcaaattcc | 900 |
| agaacagaat | cctttttgctc | tttcccaagg  | gggccagtg  | ataggtgcct  | gagctc      | 956 |

<210> 881

<211> 933

<212> DNA

<213> Unknown (H38g731 nucleotide)

<220>

<223> Synthetic construct

<400> 881

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgaatgatg | atggaaaagt | caatgctagc | tctgaggggt | actttatttt | agttggattt | 60  |
| tctaattggc | ctcatctgga | agtagttatc | tttgtgggtg | tcttgatctt | ctacttgatg | 120 |

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| acactgatag | gaaacctggt  | catcatcatc | ctgtcatacc  | tggactccca  | tctgcacaca  | 180 |
| ccaatgtact | tcttcctttc  | aaacctctca | tttctggatc  | tctgctacac  | caccagctct  | 240 |
| atccctcagt | tgctgggtcaa | tctctggggc | cgggaaaaga  | ccatctctta  | tgctgggtgc  | 300 |
| atgattcaac | tttactttgt  | tctcgactg  | ggaaccacag  | agtgtgtcct  | actgggtggtg | 360 |
| atgtcctatg | accgttatgc  | agctgtgtgt | agacctttgc  | attacactgt  | cctcatgcac  | 420 |
| cctcgtttct | gccacctgct  | ggctgtggct | tcttgggtaa  | gtgggttttac | caactcagca  | 480 |
| cttcattcct | ccttcacctt  | ctgggtacct | ctgtgtggac  | accgccaagt  | agatcacttt  | 540 |
| ttctgtgaag | ttccagcact  | tctgcgatta | tctgtgtgtg  | atacccatgt  | caatgagctg  | 600 |
| accctcatga | tcacaagctc  | catatttgtt | ctcataacctc | tcattcctcat | tctcacttct  | 660 |
| tatggtgcc  | tctgccgagc  | tgtactgagg | atgcagtgca  | ccactgggct  | tcagaaagtg  | 720 |
| tttggaaac  | gtggagctca  | tcttatggct | gtatctctct  | ttttcattcc  | ggccatgtgc  | 780 |
| atatactctc | agccaccatc  | aggaaattct | caagatcaag  | gcaagttcat  | tgccctcttt  | 840 |
| tatactgttg | tcacacctag  | tcttaacctt | ctaattctaca | ccctcagaaa  | caaagttgta  | 900 |
| agaggggcag | tgaagagact  | aatggggtgg | gaa         |             |             | 933 |

&lt;210&gt; 882

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g732 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 882

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tttattcatg | ccctctcagt | cattgaatcc | atcattgtgc | tggccatggc | ctttgagcgt | 60  |
| tatgtggcca | tatgccacc  | actgtgccat | gctgaagtgc | tcaacagtac | agtaacagcc | 120 |
| catattggca | tctagctgg  | ggtaagggga | tccctctttt | tttccccact | ggctctgctg | 180 |
| ataaagacgc | tgggcttatg | ccactcctat | gtgctctcgc | actcctatct | gctccaccag | 240 |
| gatgtagcga | acttgtccta | tgcg       |            |            |            | 264 |

&lt;210&gt; 883

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g733 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 883

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| gttgccatct | gtaacccttt  | gcgctacctt | acagtcatga | acccccagct  | atgccttttg | 60  |
| ttggttcttg | cctgctgggtg | tgggggtttt | atccactcta | tcattgcagg  | catactagtc | 120 |
| atccagctgc | ctttctgtgg  | gcccaatgaa | ctggacaact | tctactgtga  | tgctctacaa | 180 |
| atcatcaagc | tggcctgcat  | ggacacctat | gtggtagagg | tgctgggtgat | agccaacagt | 240 |
| ggctctgctg | ctcttgtctg  | cttcttggct | ttactattct | cttatgctat  | catcctgac  | 300 |
| accctgagaa | cacgcttctg  | ccagggccag | aacaaggctc | tctctacctg  | tgcttctcac | 360 |
| ctgacagtgg | tcagcctgat  | cttcgtgcc  | tgcgtattca | tctatttgag  | gcctttctgc | 420 |
| agcttctctg | tggataagat  | attctccttg | ttttacacag | tgattacacc  | tatggttg   | 477 |

&lt;210&gt; 884

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g734 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 884

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atgtcagctc | ccaaccactc | cactgccaat | catgatattg | ttgtcctcat | tggcgttcct  | 60  |
| ggcctgaagg | agctgcacgt | gtggatctcc | atccccctct | gtctgatgta | cctgggtggct | 120 |
| gtgtcaggaa | atggctctct | tgtctgtgtg | gtggcagtg  | agcacagtct | tcattgaacct | 180 |
| atgtaccttt | tcctctccat | gctggcattt | tgggatctga | ttctatccac | atctgcagta  | 240 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cccaaagcct | tgagcatttt | ctgggttgat | gatgtggaca | tctcctttgg | tggtgtgtgc | 300 |
| actcagctct | tttttatgca | ttttgccttt | gtagcggagt | caggcattct | cttgaccatg | 360 |
| gctttcgacc | gctatgtggc | catctgctac | ccattgaggt | atagcaccat | acttagccac | 420 |
| agtgttattg | gcaaaattgg | gggtgtcgtg | gtgttcagga | gttttgcaac | tgtcttctcc | 480 |
| atcgtcttcc | ttgtgaagcg | tctgcccttc | tgccggacaa | acatcattgc | ccacaccttc | 540 |
| tgtgaacaca | tggggctggc | aaagctaggt | tgttctgaaa | tcaccatcaa | tatttggtat | 600 |
| ggaatctctg | taccactact | cagtgttacg | ttagatatgg | tgacaatagt | catctcctag | 660 |
| gggtcctatg | ttcaagcagt | cttcaggctg | ccctcccttg | gtgcttggat | gaaagcactc | 720 |
| agcacctgtg | gttcccatgg | cagtgtcatc | ctcatgttct | gccttccagg | aattttcact | 780 |
| gtcattgttc | agcgctttgc | ctgaaaattt | cccaagtatg | tccacatcct | gctggccaat | 840 |
| ctctatgttc | ttgttcccc  | catgatgaac | ccaattatct | atggagtaaa | gactaaacag | 900 |
| attcagaaag | gggttgcct  | tgtgttttct | ccaaaaggaa | aattgttgc  |            | 948 |

&lt;210&gt; 885

&lt;211&gt; 1087

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g735 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 885

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| atgccactaa | ctaataaag   | ccaccctgaa  | gaatttattc | tgctaggctt  | tgcagaccgc  | 60   |
| ccttggctag | agcttccctc  | gttcactagt  | cttcttataa | tgtaccctat  | agccgtgatg  | 120  |
| ggaaacatca | caatcattct  | catgtccagg  | ttagactctc | gtcttcatag  | ccccatgtac  | 180  |
| tttttctca  | ccaacctctc  | ctttttggac  | atgtgttata | ccacaagcat  | tgtccctcag  | 240  |
| atgctgttta | acctgggaag  | ctctaagaag  | accatcagct | atatgggggtg | tgcggttcag  | 300  |
| ctttatttct | ttcacataat  | gggggggaaca | gaatgtttgc | ttttggctat  | tatgtccttt  | 360  |
| gatcgctatg | tggtccatctg | cagacctctt  | cactacaccc | tcacatgaa   | tcagcgcgtc  | 420  |
| tgtatcctta | gtttccaccg  | tgtggctaag  | tggaataatc | tatgctgtct  | cagaggccac  | 480  |
| tgccacatta | caattgccac  | tgtgtgctct  | aataaactgg | accacttggg  | gtgtgagatt  | 540  |
| cctgttctga | taaagattgc  | ctgtgggtgaa | aagggttcta | acgagctcac  | actctctgtg  | 600  |
| gtatgcattt | ttatgttagc  | tgtccacta   | tgcttaattc | ttgcttccta  | tgctagtatt  | 660  |
| ggaagtgtcg | tatttaagat  | caaactcttc  | aagggaagga | aaaaggcctt  | tgggacatgc  | 720  |
| tcctcccatc | ttattgtagt  | tttcttattt  | tatggcccag | ccatcagcat  | gtaccttcag  | 780  |
| ccccctcct  | ccatctcaag  | ggatcaaccc  | aagtctcatg | ccctcttcta  | tggagtgggtg | 840  |
| actccctcac | tcaacctctt  | tatctacacc  | ctgcggaata | agaatgtaaa  | gggggcatta  | 900  |
| cgcaacttgg | tgaggagcat  | ttcagcttta  | agtgtatgtg | ggtagacata  | aaatgaagtt  | 960  |
| attgaacagt | tagagttagt  | tgctatggtt  | ttatctaaca | aattcttgtc  | tcataatcaa  | 1020 |
| atatcgcttt | acatgttctt  | gcaaaatatg  | ttatgtctcc | gagactcttt  | gtaaacatgt  | 1080 |
| tcagcaa    |             |             |            |             |             | 1087 |

&lt;210&gt; 886

&lt;211&gt; 498

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g736 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 886

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| tttattcatg | ccctctcagc  | cattgaatcc | accatcctgc | tggtccatggc | ctttgaccgt | 60  |
| tatgtggcca | tctgccaccc  | actgcgccat | gctgcagtgc | tcaacaatac  | agtaacagcc | 120 |
| cagattggca | tcgtggctgt  | ggtccgcgga | tccctctttt | ttttcccaact | gcctctgctg | 180 |
| atcaagcggc | tggtcttctg  | ccactccaat | gtgtctctgc | actcctattg  | tgtccaccag | 240 |
| gatgtactga | agttggccta  | tgcagacact | ttgcccaatg | tggtatatgg  | tcttactgcc | 300 |
| attctgctgg | ccatgggcgt  | ggacgcaatg | ttcatctcct | tgctctattt  | tctgataata | 360 |
| cgaacgggtc | tgcaactgcc  | ttccaagtca | tagcgggcca | aggcctttgg  | aacctgtgta | 420 |
| gtacacattg | gtgtgggtact | cggcttgtat | gtgccactta | ttggcacttc  | aagtggtcac | 480 |
| cggtttggga | acaaactt    |            |            |             |            | 498 |

<210> 887  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g737 nucleotide)

<220>  
 <223> Synthetic construct

<400> 887  
 atgatgatta aaaaaaatgc aagttcggaa gacttcttta ttctacttgg attttctaata 60  
 tggcctcagc tggaagtagt tctcttttggt gttatcttga tcttctacct gatgaactg 120  
 acaggaaacc tgttcatcat catcctgtca tacgtggact cccatctcca cacaccaatg 180  
 tactttcttc tttcaaacct ctcatctctg gatctctgcc acaccaccag ctctatccct 240  
 cagttgctgg tgaatctccg gggcccgaa aagaccatct cgtatgctgg ttgcatgggt 300  
 caactttact ttgttcttgc actgggaatc gcagagtgtg tctacttggg ggtgatgtcg 360  
 tatgatcgtt atgtagctgt gtgtagacct ttgcattaca ctgtctcat gcaccctcgt 420  
 ttctgccact tgttggtctg ggcttcttgg gtaattgggt ttactatctc agcacttcat 480  
 tctctcttta ctttctgggt acccttttgt ggacatcgcc tagtggatca cttcttctgt 540  
 gaagttccag cacttctgcg ttatcatgt gtgacaccc atgcaaatga tgcctatggc 600  
 atggctcatga gctccatttt tgttctcata cctctcatte tgattctcac tgcctatggg 660  
 gccattgccc gggctgtact gagcatgcaa tcaaccactg ggcttcagaa agtgtttagg 720  
 acatgtggag cccatcttat ggttgtatct ctctttttca tccagtcac gtgcatgtat 780  
 ctccagccac catcagaaaa ttctcctgat cagggcaagt tcattgccct cttttatact 840  
 gttgtcacac cgagtcttaa tctctaatc tacactctca gaaacaagca tgtaaaaggg 900  
 gcagcgaaga gactattggg gtgggagtgg ggggag 936

<210> 888  
 <211> 453  
 <212> DNA  
 <213> Unknown (H38g738 nucleotide)

<220>  
 <223> Synthetic construct

<400> 888  
 cggcgcgtgt gcgcgccccg cctgctggac cacttcatct gtgagctgcc ggcgttgctc 60  
 aagctggcct gcggaggcga cggagacact accgagaacc agatgttcgc cgcccgctg 120  
 gtcacctctg tgcggggggt tgccgtcatc ctggcctcct acggtgccgt ggcccgagct 180  
 gtctgttgca tgcggttcaa cggaggccgg aggaggccgg tgggcacgtg tgggtccac 240  
 ctgacagccg tctgcctgtt ctacggctcg gccatctaca cctacctgca gcccgcgag 300  
 cgctacaacc aggcacgggg caagtctgta tcgctcttct acaccgtggc cacacctgt 360  
 cttaaccgcg tcatctacac cctcaggaat aagaaaatga aaggggcacc gaggaggctg 420  
 ctgcggagtc ttgggagagg ccaggctggg cag 453

<210> 889  
 <211> 1014  
 <212> DNA  
 <213> Unknown (H38g739 nucleotide)

<220>  
 <223> Synthetic construct

<400> 889  
 aaagtcaatg ctactctga ggggtacttt attttagttg gattttctaa ttggccttat 60  
 ctggaagtag ttctctttgt gggtattttg atcttctgct tgatgacact gataggaaac 120  
 ctgttcatca tcatcctgac gtacctggac tcccatctcc atactccctt gtatttcttc 180  
 ctttcaaatc tctcatttct ggatctctgc tacaccacca gctctatccc tcagttgctg 240  
 gtcagtctct ggggtgtgga aaagaccatt tcttatgctg gttgcatggg tcaactttac 300  
 ttttttctca cactgggaac cacagagtgt gtctacttgg ttggtgatgtc ctatgaccgt 360  
 tatgcagctg tgtgtagacc ttgtcattac actgtcttca tgcactctcg tttctgccac 420  
 ttgttggctg tggcttcttg ggtaagtggg tttaaaacc cagcacttca ttctccttc 480

```

accttctggtg tacctctgtg tggacaccgc caaatagatc actttttctg tgaagttccg      540
gcacttttat gattatcatt tgtcaatacc cgtgaaaata aactgaccct catgatcaca      600
agctccattht ttgttctgct acttctcacc ctcattttca cttcctatgg tgctattgcc      660
caggctgtac tgaggatgca gtcaaccact gggcttcaga aagtatttgg aacatgtgga      720
gtcatcata ttgttgatc tctctttttc attccggcca tgtgcatgta tctccagcca      780
ccatcagga attctcaaga tcaaggcaag ttcattgtct tctttttatac tgttggtaca      840
cctagtctta accctctaata ctacaccctc agaaacaaag atgtaagagg ggtagtgaag      900
agactaaggg ggtgggagtg agcctgtgtt tgtgtgatat taacaatata atggagtctt      960
tcctcacaat gattcatcca tctgttcatt tatcaacat tctttttatc actc      1014

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&lt;210&gt; 890

&lt;211&gt; 656

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g740 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 890

```

ttgcctgaca tcggtttcac ctccaccacg gtccccaaga tgattgtgga catccaatct      60
cacagcagag tcatctccta tgcaggctgc ctgactcaga tgtctctctt tgccattttt      120
ggaggcatgg aagacagaca tactcctgag tgtgatggcc tatgaccagt ttgtagccaa      180
atgtcaccct ctatatcatt cagccatcat gaaccctgtg tctgtggctt tctacttttg      240
ttgtcttttt tttttccctc agtcttttag atgccagct gtacaatttg attgccttac      300
aaatgacctg cttcaaggat gtggaaattc ctaatttctt ctgtgacct tctcaactcc      360
cccatcttgc atgtttgtgac accttcaaca ataacataat cctgtatttc cctgatgcca      420
tatttggttt tcttcccatc tcggggacac ttttctctta cgataaaaatt gtttctcca      480
ttctgagggt ttcacgtgca ggtgggaggt ataaagccct ctccacctgt gggctctacg      540
tgtcagttgt ttgctgagtt tatggaacag gcgttgagg gtacctcagt tcggatgtgt      600
cattttcccc cagaaagggt gcagtggcct cagtgatgta cgcggttgtc accccc      656

```

&lt;210&gt; 891

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g741 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 891

```

atgattataa tttgcaatga cagccacagt gatttcatcc ttctgggctt ctctaacaag      60
ccacatttgg agaagatact ttttggatca tttttattht ttattttttg actcttgcag      120
gaaatatggt catagttht gtgtccttga aggatccaaa actccacatc cctatgtatt      180
tctttctttc caacctttcc ttggtagacc tctgtttgac cagcagctgt gttccacaga      240
tggtgattaa cttctggggc ccagaaaaga ccatcagcta cattggctgt gccattcaac      300
tctatgtttt tttgtggctt gggggcacgg aatatgtcct tcttgttgtc atggctgtgg      360
attgttatgt agcagtgtgt catccactgc aaaataccat gatcatgcac ccaaaacttt      420
gtctgcagct ggctatcttg gcatggggga ctggcttggc ccagtctctg atccagtccc      480
ctgccaccct ccggttaccc ttctgtctcc agcggatggt ggatgatgtt gtttgtgaag      540
tcccagctct gattcagctc tccagtactg atactaccta cagtgaatc cagatgtcta      600
tcgccagtgt tgtcctcctg gtgatgccct tgatcattat ctttctctct tctgggtgta      660
ttgctaaggc tgttgagaga attaatgcaa ctgcaggaca gaagaaagca tttggcacct      720
gcatctctca cttctttgtg gtttctctct tttatggcac tgtcacagg gtctaccttc      780
aaccaaaaaa tcaactatct catgaatggg gcaaatttct cactcttttc tacactgtag      840
taacccaac tcttaatccc ctcatctaca ctctaaggaa caaggaggta aaggagcac      900
taataagatt ggggaggagg acctgggatt ccagaataa ctaacaagg taacatatgt      960
ttacctttgc t

```

&lt;210&gt; 892

&lt;211&gt; 651

&lt;212&gt; DNA

<213> Unknown (H38g742 nucleotide)

<220>

<223> Synthetic construct

<400> 892

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| ttgcctgaca | ttggtttcac | cttggccacg | gtccccaaga | tgatggagac  | atgcaatcac  | 60  |
| atagcagagt | catctcccat | gcaggctgtc | tgacacagat | acctttcttt  | gtcctttttg  | 120 |
| tatgtataga | tgacatgctc | ctgactgtga | tggcctataa | ctgatttggtg | gccatctgtc  | 180 |
| acccctgca  | ctaccagtc  | atcatgaatc | ctcacctctg | tgtcttctta  | gttttggtgt  | 240 |
| cctttttcct | tagcctgttg | gattcccagc | tgcacagctg | gattgtgtta  | caacaactcac | 300 |
| cttcttcaag | aatgtggaaa | tctataattt | ttttctgtg  | acccatctca  | acttctcaac  | 360 |
| cttgctgtt  | ctgacagcat | catcaataac | atattatgta | ttttagatat  | ccctatat    | 420 |
| ggttttcttc | ccatttcagg | gattcctttg | tcttactata | aaattgtctc  | ctccattcca  | 480 |
| agaattccat | cgtcagatgg | gaagtataaa | gccttctcca | cctgtggctc  | tcacctggca  | 540 |
| gttgtttgct | tattttatgg | aacagggctt | gtagggtacc | tcagttcagc  | tgtgttacca  | 600 |
| tccccagga  | agagtatggt | ggcttcagtg | atgtacactg | tggtcacccc  | c           | 651 |

<210> 893

<211> 373

<212> DNA

<213> Unknown (H38g743 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(373)

<223> n = A,T,C or G

<400> 893

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttcctccttt | aggccaactt | acagcgcaga | ggagcgcttt | ctcctgctgg | gtttctccga | 60  |
| ctggccttcc | ctgcagccgg | tctctctcgc | ccttgctctc | ctgtgctacc | tcttgacctt | 120 |
| gacgggcaat | tcgggcgctg | gtgctgcttg | gcngngnngg | acccacgcct | gcanaacnac | 180 |
| gatgtatgna | ctacttcctc | tgccacctgg | ccttggtaga | cgcgggcttc | actactagcg | 240 |
| tggtgcccgc | gctgctggcc | aacctgcgcg | gaccagcgct | gctntgncgc | gcagccactg | 300 |
| cacggcccga | gctgtgcgca | tcgctggctc | tgggttcggc | cgaatgcgct | ctctggcggt | 360 |
| gatggctctg | gan        |            |            |            |            | 373 |

<210> 894

<211> 648

<212> DNA

<213> Unknown (H38g744 nucleotide)

<220>

<223> Synthetic construct

<400> 894

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| atattagaaa | tttcgttcac  | aaccgtcagt  | ataccaagt  | ttctgggtaa | cattatttca | 60  |
| ggagataaaa | ccatttcctt  | taataattgc  | atagttcagt | tatttttctt | cattctcttg | 120 |
| ggagtcacag | agttttacct  | tctggctgcc  | atgtcctatg | accgctatgt | ggccatctgc | 180 |
| aagcctctgc | attacttgag  | tatcatgaat  | cgaagagtct | gcacactgct | tgtttttact | 240 |
| tcttggtgtg | tttcattctt  | aatcatattc  | ccagcactca | tgttgctttt | aaagcttgat | 300 |
| tactgtaggt | ctaattattat | tgaccatttt  | acctgtgatt | attttccact | gctgcaactt | 360 |
| gcttgttcag | acacaaaatt  | cttagagggtg | atgggatttt | cttggtgtgc | gtttactcta | 420 |
| atgttcactt | tggcattaat  | atttctgtcc  | tacatataca | ttatcagaac | aattttgaga | 480 |
| attccttcta | ctagtcagag  | gacaaaggcc  | ttttccacat | gttcttccca | catgggtgtt | 540 |
| atctccatct | cttatggcag  | ctgcattttt  | atgtacatta | aaccttcagc | aaaagataga | 600 |
| gtgtccttga | gcaagggagt  | ggcaatacta  | aacacctcag | tagcccc    |            | 648 |

<210> 895



<211> 659  
 <212> DNA  
 <213> Unknown (H38g745 nucleotide)

<220>  
 <223> Synthetic construct

<400> 895  
 ttctctgaca tcggtttcac ctccaccaca gtccccaaga tgattgtgga catccagtct 60  
 cacagcagag tcatctccta tgcaggctgc ctgactcaga tgtctctctt tgccattttt 120  
 ggaggcatgg aagagagaca tgctcctgag tgtgatggcc tatgaccggg ttgtâgcat 180  
 ctgtcaccct ctatatcgct cagccatctt gaaccctgtg ttctgtggct tcttagattt 240  
 gttgtctttt ttttttttcc ctcaagtctt tagactccca gctgcacaac ttgattgcct 300  
 taaaaatgac ctgcttcaag gatgtggaaa ttctaattt cttctgtgac cttctcaac 360  
 tccccatct tgcattgtgt gacacctca ccaataacat aatcatgtat ttccctgctg 420  
 ccatttttg tttcttccag atctcgggga cccttttctc ttactataaa attgtttcct 480  
 ccattctgag ggtttcatca tcagggtggga actataaagc cttctccacc tgtgggtctc 540  
 acctgtcagt tgtttgctga ttttatggaa caggcggttg agggtagctc agttcagatg 600  
 tgtcatcttc cctgagaaag gctgcagtgg cctcagtgat gtacatgggtg gtacacacc 659

<210> 896  
 <211> 804  
 <212> DNA  
 <213> Unknown (H38g746 nucleotide)

<220>  
 <223> Synthetic construct

<400> 896  
 atgatggcac tcatcttcac agactcccat ctccaaagcc caatgtattt cttcctcaat 60  
 gtcctctcgt ttcttgatat ttgttactct tctgtgggtca cacctaagct cttgggtcaac 120  
 ttcttgggtc ctgacaagtc catctctttt gagggtctgt tgggtccagct cgccttctt 180  
 gtagtgcatg tgacagctga gagcttccctg ctggcctcca tggcctatga ccgcttccca 240  
 gccatctgtc aaccctccca ttatggttct atcatgacca gggggacctg tctccagctg 300  
 gtagctgtgt cctatgcatt tgggtggagcc aactccgcta tccagactgg aaatgtcttt 360  
 gccctgcctt tctgtgggce caaccagcta acacactact actgtgacat accaccctt 420  
 ctccacctgg cttgtgccaa cacagccaca gcaagagtgg tcctctatgt cttttctgct 480  
 ctggtcaccc ttctgcctgc tgcagtcatt ctacctcct actgcttggg cttgggtggcc 540  
 attgggagga tgcgctcagt agcaggagg gagaaggacc tctccacttg tgccctccac 600  
 tttctggcca ttgccatttt ctatggcacc gtggttttca cctatgttca gccccatgga 660  
 tctactaaca ataccaatgg ccaagtagtg tccgtcttct acaccatcat aattcccatg 720  
 ctcaatccct tcatctatag cctccgcaac aaggaggtga agggcgctct gcagaggaag 780  
 cttcaggtca acatctttcc cggc 804

<210> 897  
 <211> 949  
 <212> DNA  
 <213> Unknown (H38g747 nucleotide)

<220>  
 <223> Synthetic construct

<400> 897  
 atggacttgg gaaatcaaac aagagtttca gaatttttac tcttgggatt ttcccaagac 60  
 cttagaggatc aacagtgtgt ctttgcactg tttctgtcca tgtacctggg caccgttctg 120  
 gggaacctgc tcatcatcct ggccatcagc tctgactccc acctccacac ccccaggtac 180  
 ttcttctct ccaatctgtc cctggctgac atcgggtttca cctccaccgc agtccccaag 240  
 atgctggtga acatccagggt gcagagcaat gccatcagct atgcagactg catcgcccag 300  
 atgtatgttt tcatgtgttt ttggaggcat ggacacattt ctctcaccg tgaaggccta 360  
 tgacctgtat gtggccatct gtcacccct gtactactgt gtcaccagga accctgcct 420  
 ctgtggcctg ctggttcttg tgtcctgggt cctcagcttg tcatactccc tgatccagag 480

|            |             |            |             |             |            |     |
|------------|-------------|------------|-------------|-------------|------------|-----|
| tctgttggtg | ctgcggggtg  | ccttctgcac | cagttgagtc  | attcagcact  | tttactgtga | 540 |
| gcttgctcag | gtccctcaggc | ttacctgctc | agacacacat  | gtcaattaca  | tcctgctcta | 600 |
| cgtggtggcc | ggccttctgg  | actttgtgcc | cttctcaggg  | atccttttct  | cctacaccca | 660 |
| aattgtctcc | tacatcctga  | gaatctcate | cacagatggg  | aaacacaaag  | ccttttctac | 720 |
| ctgtggatct | catctgtttg  | tggtttcttt | attctatggg  | acaggccttg  | gtgtgtatct | 780 |
| tagttccaat | gcacgtcctc  | cttcttggtg | gggcatgggtg | gcctcgggtca | tgtacactgt | 840 |
| ggtcaccccc | atgctgaacc  | ccttcactta | ttgcttgctg  | aacagggaca  | tcaagaggac | 900 |
| cctagaaaca | ctgcttgggg  | gaatgctgta | tgctcaatga  | cggggacat   |            | 949 |

&lt;210&gt; 898

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g748 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 898

|            |            |             |             |            |             |     |
|------------|------------|-------------|-------------|------------|-------------|-----|
| atggagaatt | gtacggaagt | gacaaagttc  | attcttctag  | gactaaccag | tgtcccagaa  | 60  |
| ctacagatcc | ccctctttat | cttggtcacc  | ttcatctacc  | tcctcactct | gtgtgggaac  | 120 |
| ctggggatga | tgttgctgat | cctgatggac  | tcttgctctc  | acacccccat | gtactttttc  | 180 |
| ctcagtaacc | tgtctctggt | ggactttgga  | tactcctcag  | ctgtcactcc | caagggtcatg | 240 |
| gctgggttcc | ttagaggaga | caagggtcatc | tcctacaatg  | catgtgctgt | tcagatgttc  | 300 |
| ttctttgtag | ccttggccac | ggtggaaaat  | tacttggttg  | cctcaatggc | ctatgaccgc  | 360 |
| tatgcagcag | tgtgcaaacc | cctacactac  | accaccacca  | tgacggccag | tgtaggtgcc  | 420 |
| tgtctggccc | taggctcata | tgtctgtggc  | ttcctaaatg  | cctcattcca | cattgggggc  | 480 |
| atattcagtc | tctctttctg | taaatccaat  | ctggtacatc  | actttttctg | tgatgttcca  | 540 |
| gcagtcattg | ctctgtcttg | ctctgataaa  | cacactagtg  | aggtgattct | ggttttttacg | 600 |
| tcaagcttta | atatcttttt | tgttcttcta  | gttatcttta  | tctcctactt | gttcataatc  | 660 |
| atcaccatct | tgaagatgca | ttcagctaa   | ggacacccaaa | aagcattgtc | cacctgtgcc  | 720 |
| tctcatttca | ctgcagtctc | cgtcttctat  | gggacagtaa  | tcttcatcta | cttgcagccc  | 780 |
| agctccagcc | actccatgga | cacagacaaa  | atggcatctg  | tgttctatgc | tatgatcatc  | 840 |
| cccatgctga | accctgtggt | ctacagcctg  | aggaacagag  | aagtcagaa  | tgcattcaag  | 900 |
| aaagtgttga | gaaggcaaaa | atttcta     |             |            |             | 927 |

&lt;210&gt; 899

&lt;211&gt; 938

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g749 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 899

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| atgcacacca  | tgggtggagaa | ccacacccaa | gtcacctggt | tccgcctgct | gggacttaca | 60  |
| gagcaggagg  | agctcagagg  | catectcttt | gtgctcttcc | tgtcatgca  | ttcagtcact | 120 |
| gttatgggca  | acctgggaat  | gatcactctg | atccatgcag | acccacagct | ccacaccccc | 180 |
| atgtatttct  | tcctgagcgt  | cctatecttc | atagactcct | cgttttccac | agtggacacc | 240 |
| cccaggctgc  | tggagagctt  | cctcatctca | agccaatcca | tctcctttgc | aggctgtatg | 300 |
| gtccagatgg  | ccctcatgat  | cctccatggg | actgctgagt | gtctgctcct | ggccatcatg | 360 |
| gcctatgacc  | gattcaccgc  | catctgccac | cctctcctct | atcacactat | tatatcccaa | 420 |
| tgtctgtgtg  | ccctgctggt  | ggtgacctgc | tatactgttt | ctggtgccaa | ttcagctttg | 480 |
| ctgactgggt  | gcatctttaa  | gctgccctac | tgtggcccca | atgtcattaa | ccactatttc | 540 |
| tgtgacatcc  | ccccgtgtgt  | ccaacttgcc | ggtgcagata | ctacgaggtt | gagaccatta | 600 |
| tcttctcatt  | gtgtgccttg  | ctcatcctct | ttaccatcac | cattatccca | gtctcctatg | 660 |
| cctacatcct  | cgtgaccatt  | tgcaggatgc | gtcccttgca | agcccagagc | aaagctctct | 720 |
| ccacctgtgc  | ctcccacctc  | accatcatct | gcctcttcta | tagcaccatc | accttcatgt | 780 |
| atgctcagcc  | aagctctcac  | aattccatgg | aacacaacaa | ggtcatgtct | gtcttctaca | 840 |
| ctgtgggtcat | cgcaggctg   | aacctctgta | tctacagcct | gaggaataaa | gatgtaaaat | 900 |
| atgctttgaa  | gaggagatgc  | ctgtgcaagc | tgtcttca   |            |            | 938 |

<210> 900  
 <211> 942  
 <212> DNA  
 <213> Unknown (H38g750 nucleotide)

<220>  
 <223> Synthetic construct

<400> 900  
 atggaaaata agacagaagt aacacaattc attcttctag gactaaccaa tgactcagaa 60  
 ctgcagggtc ccctctttat aacgttcccc ttcatctata ttatcactct gggttggaac 120  
 ctgggaatta ttgtattgat attctgggat tcctgtctcc acaatcccat gtactttttt 180  
 ctcaagtaact tgtctctagt ggacttttgc tactcttcag ctgtcactcc catcgatcatg 240  
 gctggattcc ttatagaaga caaggtcatc tcttacaatg catgtgctgc tcaaagtgtat 300  
 atctttgtag cttttgccac tgtggaaaat tacctcttgg cctcaatggc ctatgaccgc 360  
 tatgcagcag tgtgcaaacc cctacattac accacaacca tgacaacaac tgtgtgtgct 420  
 cgtctggcca taggttccta cctctgtggt ttctggaatg cctccatcca cactggggac 480  
 acatttagtc tctctttctg taagtccaat gaagtccatc actttttctg tgatattcca 540  
 gcagtcattg ttctctcttg ctctgataga catattagcg agcttgttct tatttatgtt 600  
 gtgagcttca atatctttat agctctcctg gttatcttga taccctacac attcattttt 660  
 atcaccatcc taaagatgca ctcaagcttca gtataccaga agcctttgtc cacctgtgcc 720  
 tctcatttca ttgcagtcgg catcttctat gggactatta tcttcattga cttacaaccc 780  
 agctccagtc actccatgga cacagacaaa atggcacctg tgttctatac aatgggtcatc 840  
 cccatgctga accctctggt ctatagtctg aggaacaagg aagtgaagag tgcattcaag 900  
 aaagttgttg agaaggcaaa attgtctgta ggatgggtcag tt 942

<210> 901  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g751 nucleotide)

<220>  
 <223> Synthetic construct

<400> 901  
 atgaacaact ctgacactcg catagcaggc tgccttctca ctggcatccc tgggctggag 60  
 caactacata tctggctgtc catcccttcc tgcacatgt acatcgctgc cctggaaggc 120  
 aatggcatcc taatttgtgt catcctctcc caggcaatcc tgcattgagc catgtacata 180  
 ttcttatcta tgcctggccag tgcctgatgc ttgctctcta ccaccaccat gcctaaggcc 240  
 ctggccaatt tgtggctagg ttatagccac atttcccttg atggctgcct cactcaaaaag 300  
 ttcttcattc acttctctt cattcactct gctgtcctgc tggccatggc ctttgaccgc 360  
 tatgtggcca tctgtctccc cctgcgatat gtcacaatcc tcacaagcaa ggtcattggg 420  
 aagatcgta ctgccaccct gagccgcagc ttcatcatta tgtttccatc catctttctc 480  
 cttgagcacc tgcactattg ccagatcaac atcattgcac acacattttg tgagcacatg 540  
 ggcattgccc atctgtcctg ttctgatata tccatcaatg tctgggatgg gttggcagct 600  
 gctcttctct ccacaggcct ggacatcatg cttattactg ttccctacat ccacatcctc 660  
 caagcagtc tccgcctcct ttctcaagat gcccgctcca aggccttgag tacctgtgga 720  
 tcccatatct gtgtcatcct actcttctat gtccctgccc tttttctgt ctttgccctac 780  
 aggtttggtg ggagaagcat cccatgctat gtccatattc tcctggccag cctctacgtt 840  
 gtcattcctc ctatgctcaa tcccgttatt tatggagtga ggactaagcc aatactggaa 900  
 ggggctaagc agatgttttc aaatcttgcc aaagga 936

<210> 902  
 <211> 994  
 <212> DNA  
 <213> Unknown (H38g752 nucleotide)

<220>  
 <223> Synthetic construct

<400> 902

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| agcattcttt  | tcctttat   | ctcattgctg | caggcatcct | ctgattttct | aataacattg | 60  |
| atgaagaact  | gtacagaagt | gacagagttc | atcctcctgg | gactaaccac | tgctccagag | 120 |
| ctacaagtcc  | ccctccttat | catgttcact | ctcatatacc | ttgtcaatgt | ggttggaaac | 180 |
| ctggggatga  | ttgtttta   | tggttgggac | attcatctcc | acactcccat | gtattttttc | 240 |
| ctcagtcacc  | tgtctctagt | ggacttttgt | tactcttcag | ctgtcactcc | cacagtcata | 300 |
| gctgggctcg  | ttataggaga | caaggtcatc | tcttacaatg | catgtgctgc | tcaaatgttc | 360 |
| ttttttgcag  | cctttgccac | tgtggaaaat | ttcctcttgg | cctcaatggc | ctatgaccgc | 420 |
| tatgatgcag  | tgtgcaaac  | cctacattac | accaccacca | tgacaacaag | tgtgtgtgca | 480 |
| tgtctggcta  | taatctgtta | tgtctgtggt | ttcttgaatg | cctccataca | cattggggaa | 540 |
| acattgtctc  | tctttctgta | tgtccaatga | agtccattgc | tttttctgtg | atgttccacc | 600 |
| agtcattggc  | ctgtcttgct | gtgatagaca | tgtgaatgag | ctagtcttca | tttatgtagc | 660 |
| cagtttcaat  | atcttttctg | ccatcctagt | tatcttgatc | tcctacctat | tcataattat | 720 |
| caccatccta  | aagatgcact | cagcttcagg | ataccagaag | gctttgtcca | cctgtgcctc | 780 |
| ccacctcact  | gcagtcac   | tcttctatgg | gactattatc | ttcatgtact | tacagcccag | 840 |
| ctctgggtcac | tccatggaca | cagacaaact | ggcatctgtg | ttctatacta | tgatcatccc | 900 |
| catgctgaac  | cccctggctc | atagcctgag | gaacaacgaa | gtgaagagcg | cattcaagaa | 960 |
| agttattgag  | aaggcaaaat | tgtctctatt | attg       |            |            | 994 |

&lt;210&gt; 903

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g753 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 903

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| atgtcagatt | ccaacctcag  | tgataaccat  | cttccagaca  | ccttcttctt | aacagggatc | 60  |
| ccagggctgg | aggctgcccc  | cttctggatt  | gccatccctt  | tctgtgccat | gtatcttgta | 120 |
| gcactgggtg | gaaatgctgc  | cctcatcctg  | gtcattgcc   | tggacaatgc | tcttcatgca | 180 |
| cctatgtacc | tcttctctg   | ccttctctca  | ctcacagacc  | tggtctctag | ttctaccact | 240 |
| gtgcccaga  | tgctggccat  | tttgtggctc  | catgctgggt  | agatttctct | tggtggatgc | 300 |
| ctggcccaga | tgttttgtgt  | ccattctatc  | tatgctctgg  | agtcctcgat | tctacttgcc | 360 |
| atggcctttg | ataggtatgt  | ggctatctgt  | aaccatttaa  | ggtacacaac | cattctcaac | 420 |
| catgctgtca | taggcagaat  | tggtttgtt   | gggtatttcc  | gtagtgtggc | tattgtctcc | 480 |
| cccttcatct | tcttgtctgag | gcgactcccc  | tactgtgggtc | accgtgtcat | gacacacaca | 540 |
| tactgtgagc | atatgggcat  | cgcccagactg | gcctgtgcc   | acatcactgt | caatattgtc | 600 |
| tatgggctaa | ctgtggctct  | gctggccatg  | ggactggatt  | ccattctcat | tgccatttcc | 660 |
| tatggcttta | tcttccatgc  | agtccttcc   | cttccatctc  | atgatgccc  | gcacaaagct | 720 |
| ctgagtacct | gtgggtccca  | cattggcatc  | atcctggttt  | tctacatccc | tgcccttctc | 780 |
| tcttctctca | cccaccgctt  | tggtcaccac  | gaagtcccca  | agcatgtgca | catctttctg | 840 |
| gctaattctc | atgtgctgg   | gcctcctgta  | ctcaatccta  | ttctctatgg | agctagaacc | 900 |
| aaggagattc | ggagtcgact  | tctaaaactg  | cttcacctgg  | ggaagacttc | aata       | 954 |

&lt;210&gt; 904

&lt;211&gt; 989

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g754 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 904

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| cacatagaac | caggggaatga | tacacagatt  | tcagaatttc | ttcttctggg | actttcagat | 60  |
| aaaccagaat | tgcagccctt  | cctcttttggg | ctgttcttct | ccatgtacct | ggtcactgtg | 120 |
| cttgggaatc | tgctcatcat  | cctggccaca  | atctcagact | cccacctcca | caccccatgt | 180 |
| acttcttctc | ctccaacctg  | tcctttgcgg  | acatctgttt | catctctact | acaatcccaa | 240 |
| agatgctcgt | aaacatccag  | acacagagca  | gagtcatcac | ttatgcaggc | tgcatcacc  | 300 |
| agatgtgctt | ttttgtactc  | ttagaagcac  | tggacagctt | actcctgacc | gtgatggcct | 360 |
| atgaccagtt | tgtggccatc  | tgtaaccccc  | tgcactacat | ggtcacatg  | agccctgggt | 420 |
| tctgtggact | gctgggtctg  | gcatacctgga | tcacatcatg | ccctgggtc  | tgtggactgc | 480 |

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| tggttctggc | atcctggatt  | atcagtgatc | tggattcctc | attacatagc | ttgatgggtgc | 540 |
| tgctactgcc | cttctgcaca  | gatttccaaa | ttccacattt | tgtctatgaa | cttaatcagg  | 600 |
| tcatccgcct | tgcgggttct  | gatacctttc | ttaatgacat | ggcgatgtat | tttgacgtag  | 660 |
| ggccactggg | tggagttccc  | ctcgtctgga | tctgtacttt | gtactgtaag | atagttttct  | 720 |
| ccatacgtgc | aatctcatca  | gctcagggga | agtacaaggc | attttccacc | tgtgcatctc  | 780 |
| atctctcagt | tgtctcctta  | ttttatggta | ggagcctagg | ggtgtacttt | agttctgctc  | 840 |
| ctacccaaaa | ctctcactca  | ggtgctgcag | cttcagtgat | gtacactgtg | gtcaccccca  | 900 |
| tgctgaaccc | cttcactctgc | agtctgagga | ataaagacat | aaagagagct | ctgaatcaat  | 960 |
| tcatcagggt | agtgccattc  | ttcaggaag  |            |            |             | 989 |

&lt;210&gt; 905

&lt;211&gt; 932

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g755 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 905

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| accacatcta  | tagatgataa | tacagaggta  | aatgaattca  | tatgactagg  | actaaccaaa  | 60  |
| gccccagaac  | tacaggtcca | cctctttgtc  | ttattttaact | tcatctacct  | cttcactctg  | 120 |
| agtgggaacc  | tggggatgat | gctgctgac   | ctgctggact  | ctcgtctcca  | cacttccatg  | 180 |
| tactttttcc  | tcagtaacct | gtctctggtg  | gacttttgtc  | actcagaaac  | tgctactcca  | 240 |
| aagatgatgg  | ctgggttgct | gatagctcac  | aaggctcatc  | cctacaatgt  | atgtgctgct  | 300 |
| cagatgttct  | tttttgcagt | ctttgctact  | gtggaaagtt  | acttcttgac  | ttcagtggcc  | 360 |
| tatgattgct  | acagagtaat | gtgtaaaccc  | ctacattaca  | ccaccaccat  | gacaacaaat  | 420 |
| gtgtgtgctt  | ctctggccat | acatgcatgt  | cttaggttta  | ctgactgctg  | ctgttgacat  | 480 |
| tggagacatt  | ttatgtccaa | tgagatccat  | cactttttct  | gtgatattct  | ggcagtcatg  | 540 |
| actctgactt  | gctctaataa | acatattaat  | gagttgatcc  | ttgttccctac | ttcaagctat  | 600 |
| atttttttacc | ctcctagtta | tcttgatttc  | ctgcttggtt  | gtatttgtat  | ttgtcaccat  | 660 |
| tttaaagatg  | ctctctttta | gtatacaaga  | aggttttatc  | tacctatggt  | tctcacctca  | 720 |
| ctgcagttcc  | tttattttat | gagactgtcc  | tcatcacata  | tgtgcagcca  | agttctatca  | 780 |
| tttcatgaac  | acagaaaaaa | ttgtatctgt  | gtttcatatt  | atggttatcc  | ccatgctaata | 840 |
| ccctgtgggt  | tatagcctga | gaaacaacga  | gggtcaagagt | gcattcaaga  | ctgtttgttg  | 900 |
| aggaaacaaa  | atattttctg | ggttttagtct | tt          |             |             | 932 |

&lt;210&gt; 906

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g756 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 906

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| atgggggggct | ttgggactaa  | catctcaagt | actaccagct  | tcactctaac  | aggcttccct  | 60  |
| gagatgaagg  | gtctggagca  | ctggctggct | gcccttctgc  | tgctgctttg  | tgctatttcc  | 120 |
| ttcctgggca  | acatccctcat | cctctttatc | ataaagggaag | agcagagctt  | gcaccagcca  | 180 |
| atgtactact  | tcctgtctct  | tttttctggt | aatgacctgg  | gtgtgtcctt  | ttctacattg  | 240 |
| cccactgtac  | tggctgctgt  | gtgttttcat | gccccagaga  | caacttttga  | tgctgtcctg  | 300 |
| gcccagacgt  | tcttcatcca  | cttttctccc | tggacagagt  | ttggcatcct  | actggccatg  | 360 |
| agttttgacc  | actatgtggc  | catctgtaac | ccgctgcgct  | atgccacagt  | gctcactgat  | 420 |
| gtccgtgtgg  | cccacaatgg  | catatccatt | gtcatccgca  | gcttctgcat  | ggtattccca  | 480 |
| cttcccttcc  | tcctgaagag  | actgccttcc | tgtaaggcca  | gtgtgggtact | ggccccattcc | 540 |
| tactgtctgc  | atgcagacct  | gattcggctg | ccctgtggag  | acactaccat  | caacagcatg  | 600 |
| tatggcctgt  | tcattgtcat  | ctctgccttt | ggtgtagatt  | cactgctcat  | cctcctctcc  | 660 |
| tatgtgtcca  | ttctacattc  | tgtgtgccca | ttgcctccag  | gggtgagagg  | cttaagacac  | 720 |
| tcgaacacat  | gtgtgtcaca  | tatctatgca | gtgtgtatct  | tctatgtgcc  | tatgggttagt | 780 |
| gtgtccatgg  | ttcatcgatt  | tgggaggcat | gctcctgaat  | atgtgcacaa  | gttcatgtct  | 840 |
| ctttgtacct  | gccaatgtct  | taccgcaatt | atctattcca  | tcaagactaa  | ggagattcgc  | 900 |
| aggagactac  | acaagatggt  | attgggagct | aagttctgat  | cgaag       |             | 945 |

<210> 907  
 <211> 989  
 <212> DNA  
 <213> Unknown (H38g757 nucleotide)

<220>  
 <223> Synthetic construct

<400> 907  
 atggaaccag agaatgatac acgaatttca gaatttcgac ttctgggatt ttcagaagaa 60  
 cccagactgc aacgatttcg atttctcttt ggagtgttct tatccatgta cctcatcatt 120  
 gtatttggaa acttgcttat cactctgggt atcattttat gctccacct ccacacctcc 180  
 atgtacttct ttctctccaa cctgtccttt gtagacatct gttttgcctc caccagggtc 240  
 ccaaagatgc tggatgaatat ccaggcacag agcaaagtca tcacctctgc aggtgcatc 300  
 acccagatgt actttttcat acatttttga ggattggaca gcttctcct gactgtgatg 360  
 gcctatgacc ggtttgtggc catctgtcac cccctgtact acacgggtcat catgaaccct 420  
 caactctgtg gattgcttgt tctggatcc tggatcacia gtgtcttgca ttccttatta 480  
 catagcttaa tgggtgtgca gttgtcctta tgcagagagt tggaaatccc ccactttttc 540  
 tgtgaactta atcagggtcat ccaccttgcc tgttctgaca cttttcttaa tgacatgggtg 600  
 atgtatctgg cagctgtgct gctgggtggg gggatgtctc gctgggatcc tttactctta 660  
 ctctaagaca gtttctccca tatgtgcaat ctcacagct caagggaggt ataaggcatt 720  
 ttccacctgt ccactctacc tctcagttgt ctccttgttt tactgtacaa gcctaggagt 780  
 gtaccttagc tgggtgtcat cccacaactc acactcaggt gcaatagcct cagtgatgta 840  
 cactgtgtgc acccccatgc tgaaccctt catctacagc ctgaggaata aggacataaa 900  
 gagggctctg aagaattctt tgggagggaa actagaaaag ggccagttgt cctagggctg 960  
 aagctatata catgattgca aggtcaaa 989

<210> 908  
 <211> 960  
 <212> DNA  
 <213> Unknown (H38g758 nucleotide)

<220>  
 <223> Synthetic construct

<400> 908  
 atggaaagag gaaaccaaac agaagttgga aactttctcc tcttgggatt cgcagaggac 60  
 tctgacatgc agcttctcct ccatgggctg ttcctctcca tgtacctggt taccatcatc 120  
 ggaaacctgc tcatcactct gaccatcagt tcagactccc acctccacac ccccatgtac 180  
 ttcttctctt ccaacctgtc ctttgtgtac atctgtttca catccacgac tgtcccaaag 240  
 atgctgggtga atatccaaac acaaagcaaa atgatcactt ttgcaggctg cctcactcag 300  
 atattttttt tcattgcatt tggatgcctg gacaatttgc tctgacctat gacggcctat 360  
 gaccgcttgc tggccatctg ttacccctgc cactacacgg tcatcatgaa ccccggtctc 420  
 tgtggactgc tggttctggg gtccctgtgc atcagtgtca tgggttcctt gcttgagacc 480  
 ttgaccattt tgaggctgtc ctccctgcaca aatatggaaa ttccgcactt tttttgtgat 540  
 ccttccgaag tcttgaagct ggccgtgtct gacaccttca tcaataacat cgtgatgtgt 600  
 tttgtgacca ttgtcctggg tgtttttcct ctctgtggaa tctattctc ttattctcag 660  
 attttctcct cgtcctaag agtatcatct gccagaggcc agcacaagc ctttaccacc 720  
 tgtgggtccc acctctcagt ggtcagcttg ttctatggca ctggccttgg ggtctatctc 780  
 agttctgcag ttacaccacc ttctaggaca agtctggcag cctcgggtgat gcacaccatg 840  
 gtcaccccca tgcgaaccc cttcatctac agcctgagga acaaggacat gaaggggtca 900  
 ctggggagac tctcctcag ggcaacgtct ctcaaagagg ggaccattgc taagctctca 960

<210> 909  
 <211> 981  
 <212> DNA  
 <213> Unknown (H38g759 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 909

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| tatacagacc  | cacagaatct  | aacagatgtc | tttatattcc  | tcctcctaga  | actctcagag  | 60  |
| gatccagcac  | tgcagctggg  | cgctactggg | ctgtgcctgt  | gtgcctgggc  | acgggtgctgt | 120 |
| ggaacctgct  | cagcatcctg  | gccgtcagcc | ctgactccca  | cctccacacc  | cccatgcact  | 180 |
| tcttcctctg  | caacctgtcc  | ttgcctgaca | tcgggtttcac | ctccaccacg  | gtccccaaga  | 240 |
| tgatcgtgga  | catccaatct  | cacagcagag | tcatctccta  | tgcaggctgc  | ctgactcaga  | 300 |
| tgtctctctc  | tgccattttt  | ggaggcatgg | aagagagaca  | tgctcctgag  | tgtgatggcc  | 360 |
| tatgaccagt  | ttgtagccat  | ctgtcaccct | ctgtatcatt  | cagccatcat  | gaaccctgtg  | 420 |
| ttctgtggct  | tcctgggtttt | gttgtctttt | tttttctcag  | tcttttagac  | tcccagctgc  | 480 |
| aaaacttgat  | cgccttaca   | atcacctgct | tcaaggatgt  | ggaaattcct  | aattttctct  | 540 |
| gtgacccttc  | tcaactcccc  | catcttgcac | gttgtgacac  | cttcaccaat  | aacattatca  | 600 |
| tgtatttccc  | tgctgccata  | tttgggtttc | ttcccatctc  | ggggaccctt  | ttctcttact  | 660 |
| ataaaaattgt | ttcctccatt  | ctgagggttt | catcatcagg  | tgggagctat  | aaagccttcg  | 720 |
| ccacctgtgg  | atctcacctg  | tcagttgttt | gctgatttta  | tggaaacaggc | gttggagggt  | 780 |
| acctcagttc  | agatgtgtcg  | tctccctga  | gaaagcgtgc  | agtggcctca  | gtgatgtaca  | 840 |
| cagtggtcac  | ccccatgctg  | aatcccttga | tctacagcct  | gagaaacagg  | gatattaaag  | 900 |
| gtgtcctgtg  | gcagccgtgc  | agccgcacgg | cagcacagtc  | tcattctcaat | atcttatctg  | 960 |
| ttccattcct  | tttgaggat   | g          |             |             |             | 981 |

&lt;210&gt; 910

&lt;211&gt; 628

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g760 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 910

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| tcagtgaagt  | acttgaatga | aagtttccca | gaggatttca | ttctcatggg  | ctttgtcaaa | 60  |
| tatccatggc  | tggattttct | tctcttctgt | gtcctcttga | ccttctacat  | gttcacattg | 120 |
| ttgggaaata  | gtgctattat | tctggctctc | caactagatt | cccaacttca  | tagtcctatg | 180 |
| tatttccttc  | tcaccagtct | ttccgtctta | tatctctgtt | tcaccaccac  | aacagtacct | 240 |
| caaattgctgt | tcaatttagg | gggcccaaca | agaacatcac | ttaaattaggc | tgtatggccc | 300 |
| aggcctatgt  | atttcaactg | ctagcctgta | ttgaatgtgt | ccttcttggc  | atcgtggcct | 360 |
| tagactgcta  | tgtggctgtc | tgtaaagctc | caaggtacac | tataatcata  | gaccataagg | 420 |
| tctgcctgca  | cctgtccagc | actgcttggc | taattggctc | ggccaattca  | ctgctgcagt | 480 |
| caacaatcac  | aattcagttg | cccctgtaga | ggtgtatagc | tcagatcttc  | ctttagttag | 540 |
| agtctgtcac  | ctaacagtct | ctaactgtaa | caacctttga | gatctgctac  | agcattctat | 600 |
| ctgaggccaa  | cttcatgctg | gggagctc   |            |             |            | 628 |

&lt;210&gt; 911

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g761 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 911

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atggaaccag | aaaagcaaac | cgaaatctca | gaattcttcc | tccagggact | ctcagaaaaag | 60  |
| ccagagcatc | agaccctcct | cttcacaatg | ttcctctcca | catacctggg | caccatcatt  | 120 |
| ggaaatgccc | tcattatcct | ggccatcacc | acggactctc | acctccacac | acccatgtac  | 180 |
| ttctttctct | tcaacctctc | actcgttgac | acctatttat | cctccaccac | cgtccccaag  | 240 |
| atgctagcga | acatccaggc | tcagagcaga | gccatccctt | ttgtgggctg | cctcaccag   | 300 |
| atgtatgcct | tccacctgtt | cgggaccatg | gacagctttc | tcctggcagt | aatggccatc  | 360 |
| gaccgcttcg | tggccattgt | ccacccacag | cgttacttgg | ttctcatgtg | ctccctgtc   | 420 |
| tgtgggctgc | tgtggggagc | atcatggatg | atcaccacac | tccagtctct | catacacacc  | 480 |
| tgcctcatgg | ctcaactgac | cttctgcgcc | ggctctgaaa | tctccactt  | cttctgtgac  | 540 |
| ctcatgcccc | tgtgaagct  | ctccggctca | gacacgcaca | ccaacgagct | ggtgatcttt  | 600 |
| gcttttggca | ttgtcgtggg | caccagccca | ttctcctgca | tccttctctc | gtacatccgc  | 660 |

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| atcttcttga  | cagtccttta | gatcccttct | actcggggca | agtggaaagc | cttctccacc  | 720 |
| tgtggcttac  | acctcactgt | ggtgtcactg | tcctatggga | ccatctttgc | tgtgtactta  | 780 |
| cagccacacat | ccccagctc  | ctcccagaag | gacaaggcag | ccgcccta   | gtgtgggggtg | 840 |
| ttcatcccca  | tgtcaaccc  | ctttatctac | agcatagcga | acaaggatat | gaaggcagcc  | 900 |
| ctggggaagc  | tcacggcaa  | agtggcgcgc | ccctgtccta | ggcca      |             | 945 |

&lt;210&gt; 912

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g762 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 912

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| atggctccga  | ccaacctcac  | atctgcccc   | gtgttctctc | tcctcggcct | ggtggacgga | 60  |
| acagacgccc  | acccgctgct  | gttctctgctc | tgccttggca | tctatctgct | caacgccctg | 120 |
| agcaacctga  | gcattggtggc | gctggtgaga  | tccgacgggg | ccctccgctc | ccccatgtat | 180 |
| tacttcttgg  | gtcacctgag  | cctcgtggac  | gtctgtctta | ccaccgtcac | ggtccccagg | 240 |
| ctgctggccg  | gcctgtctca  | cccgggccag  | gccatatact | tccaggcgtg | ctttgccgag | 300 |
| atgtacttct  | tcgtggctct  | gggcatcacc  | gagagctacc | tcctggcggc | catgtcctac | 360 |
| gaccgcgcga  | cggcggcgtg  | ccggccccctg | cgctacggcg | cgctggtgac | gccatgggag | 420 |
| tgcgcctcgc  | tgggtgcgtgc | gtcgtgggccc | gtgacgcacc | tgcactcgtc | gctgcacacg | 480 |
| ctgctcctct  | ccgcgtcttc  | ctacccctac  | cccacccccg | tgcgccccct | cttttgcgac | 540 |
| atgacgggtga | tgctgagctt  | ggcgacctcg  | gacacgtccg | ccgcggagac | ggccatcttc | 600 |
| tccgagggcc  | tggccgtggt  | gttggccccg  | ctgctcctcg | tgttcccttt | cctacgcgcg | 660 |
| catcctggtc  | gcggtgctcg  | gcttgccgcg  | gccggcgccg | cgcttctctc | tactgcgggg | 720 |
| cccacctagt  | ggcggtggcg  | gtggcgcttt  | tctttggctc | tgtcctctcc | gtgtatttcc | 780 |
| cgcgctcgtc  | tgcctactca  | gcccgtctacg | accgcctggc | cagcgtggtc | tacgctgtca | 840 |
| tcacgccgac  | cttgaaccct  | ttcatcaaca  | gccttcgcaa | caaagaggtc | aagggcgccc | 900 |
| tgaaggggg   | gctcagatgg  | agggctgcac  | cccaagaggc | gtgagggca  |            | 949 |

&lt;210&gt; 913

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g763 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 913

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| atggatggag | agaatcactc  | agtggatatct | gagtttttgt  | ttctgggact  | cactcattca  | 60  |
| tgggagatcc | agtcctctct  | cctagtgttt  | tcctctgtgc  | tctatgtggc  | aagcattact  | 120 |
| ggaaacatcc | tcattgtgtt  | ttctgtgacc  | actgaccctc  | acttacactc  | ccccatgtac  | 180 |
| tttctactgg | ccagtctctc  | cttcattgac  | ttaggagcct  | gctctgtcac  | ttctcccaag  | 240 |
| atgatttatg | acctgttcag  | aaagcgcaaa  | gtcatctcct  | ttggaggctg  | catcgctcaa  | 300 |
| atcttcttca | tccacgtcat  | tgggtggtgtg | gagatggtgc  | tgtcatagc   | catggccttt  | 360 |
| gacagatatg | tggccctatg  | taagccccctc | cactatctga  | ccattatgag  | cccaagaatg  | 420 |
| tgcctttcat | ttctggctgt  | tgcctggacc  | cttgggtgtca | gtcactccct  | gttccaactg  | 480 |
| gcatttcttg | ttaatttagc  | cttctgtggc  | cctaattgtgt | tggacagctt  | ctactgtgac  | 540 |
| cttctctggc | ttctcagact  | agcctgtacc  | gacacctaca  | gattgcagtt  | catgggtcact | 600 |
| gttaacagtg | ggtttatctg  | tgtgggtact  | ttcttcatac  | ttctaatactc | ctacgtcttc  | 660 |
| atcctgttta | ctgtttggaa  | acattcctca  | ggtggttcat  | ccaaggccct  | ttccactctt  | 720 |
| tcagctcaca | gcacagtggg  | ccttttgttc  | tttgggtccac | ccatgtttgt  | gtatacacgg  | 780 |
| ccacacccta | attcacagat  | ggacaagttt  | ctggctatatt | ttgatgcagt  | tctcactcct  | 840 |
| tttctgaatc | cagttgtcta  | tacattcagg  | aataaggaga  | tgaaggcagc  | aataaagaga  | 900 |
| gtatgcaaac | agctagtgtat | ttacaagagg  | atctca      |             |             | 936 |

&lt;210&gt; 914

&lt;211&gt; 954

&lt;212&gt; DNA



<213> Unknown (H38g764 nucleotide)

<220>

<223> Synthetic construct

<400> 914

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| atgtggcaga | agaatcagac | ctctctggca | gacttcatcc | ttgaggggct  | cttcgatgac  | 60  |
| tccettaccc | accttttcc  | tttctccttg | accatgggtg | tcttcccttat | tgcggtgagt  | 120 |
| ggcaacaccc | tcaccattct | cctcatctgc | attgatcccc | agcttcatac  | accaatgtat  | 180 |
| ttcctgctca | gccagctctc | cctcatggat | ctgatgcatg | tctccacaac  | catcctgaag  | 240 |
| atggctacca | actacctatc | tggcaagaaa | tctatctcct | ttgtgggctg  | tgcaatccag  | 300 |
| cacttctct  | atttgtgtct | aggtggtgct | gaatgttttc | tcttagctgt  | catgtcctat  | 360 |
| gaccgctatg | ttgccatctg | tcatccactg | cgctatgctg | tgctcatgaa  | caagaagggtg | 420 |
| ggactgatga | tggctgtcat | gtcatgggtg | ggggcatccg | tgaactccct  | aattcacatg  | 480 |
| gcgatcttga | tgcacttccc | tttctgtggg | cctcggaaag | tctaccactt  | ctactgtgag  | 540 |
| ttcccagctg | ttgtgaagtt | ggtatgtggc | gacatcactg | tgtatgagac  | cacagtgtac  | 600 |
| atcagcagca | ttctcctcct | cctccccatc | ttcctgattt | ctacatccta  | tgtcttcac   | 660 |
| cttcaaagt  | tcattcagat | gcgctcatct | gggagcaaga | gaaatgcctt  | tgccacttgt  | 720 |
| ggctcccacc | tcacgggtgg | ttctcttttg | tttgggtgct | gcactttctc  | ctacatgaga  | 780 |
| cccaggtccc | agtgcactct | attgcagaac | aaagttgggt | ctgtgttcta  | cagcatcatt  | 840 |
| acgcccacat | tgaattctct | gatttatact | ctccggaata | aagatgtagc  | taaggctctg  | 900 |
| agaagagtgc | tgaggagaga | tgttatcacc | cagtgcattc | aacgactgca  | attg        | 954 |

<210> 915

<211> 309

<212> DNA

<213> Unknown (H38g765 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(309)

<223> n = A,T,C or G

<400> 915

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| acgctgtgcg | ccacagcctn | gctgggccac | ttcatctgtg | agctgccggc  | gttgtctcaag | 60  |
| ctggcccgcg | gagcatcgga | gacactaccg | agaaccagat | gttcgcccgc  | cgcgtgggtca | 120 |
| tctgtgtgct | gcccgtttgc | gtcatcctgg | cctcctacgg | tgccgtggcc  | gagctgtctg  | 180 |
| ttgtatgcgg | ttcagcggag | gccggagagg | gcggtgggca | cggtgtgggtc | ccactgacag  | 240 |
| ccgtctgcct | gttctacggc | tcggcatcta | cacctacctg | cagcccgcgc  | agctaacaac  | 300 |
| caggcacgg  |            |            |            |             |             | 309 |

<210> 916

<211> 313

<212> DNA

<213> Unknown (H38g766 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(313)

<223> n = A,T,C or G

<400> 916

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| attcatgccc | tctcagccat | tgaatccacc | atcctgctgg  | ccatggcctt | tnaccgttat  | 60  |
| gtggccatct | gccaccact  | gcgccatgct | gcagtgtctca | acaatacagt | aacagcccag  | 120 |
| attggcatcg | tggctgtggt | cgcgggatac | ctcttttttt  | tcccactgcc | tctgtgtgatc | 180 |
| aagcggctgg | ccttctgcca | ctccaatgtc | ctctgcact   | cctattgtgt | ccaccaggat  | 240 |
| gtaatgaagt | tggcctatgc | aagacanttt | gcccgaatgtg | gtatatggtc | ttaactgncc  | 300 |

attttgggtg gtc

313

&lt;210&gt; 917

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g767 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 917

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| atggaaacag | gaaatcaaac | acatgcccaa | gaattttctcc | tcctgggatt  | ttcagcaacg | 60  |
| tcagagattc | agttcattct | ctttgggctg | ttcctctcca  | tgtacctagt  | cactttcacc | 120 |
| gggaacctgc | tcatcatcct | ggccatatgc | tcagactccc  | acctccacac  | ccccatgtac | 180 |
| ttcttcctct | ccaacctgtc | ttttgctgac | ctctgtttta  | cctccacgac  | tgtcccaaag | 240 |
| atgttactga | atatactgac | acagaacaaa | ttcataacat  | atgcaggctg  | tctcagtcag | 300 |
| atTTTTTTTT | tcacttcatt | tggatgcctg | gacaatttac  | tcttgaccgt  | gatggcctat | 360 |
| gaccgcttcg | tggcgcgtcg | tcacccctg  | cactatacgg  | tcatcatgaa  | ccccagctc  | 420 |
| tgtggactgc | tggttctggg | gtcctgggtc | atcagtgta   | tgggttcct   | gctcgagacc | 480 |
| ttgactgttt | tgaggctgtc | cttctgcacc | aaaatggaaa  | ttccacactt  | tttttgtgat | 540 |
| ctacttgaag | tcctgaagct | cgcctgttct | gacaccttca  | ttaataacgt  | ggtgatatac | 600 |
| tttgcaactg | gcgtcctggg | tgtgatttcc | ttcactggaa  | tattttttctc | ttactataaa | 660 |
| attgttttct | ctatactgag | gatttcctca | gctgggagaa  | agcacaaagc  | gttttccacc | 720 |
| tgtggttccc | acctctcagt | ggtcaccttg | ttctatggca  | cgggcttttg  | ggtctatctc | 780 |
| agttctgcag | ccacaccatc | ttctaggaca | agtctggtgg  | cctcagtgat  | gtacaccatg | 840 |
| gtcaccccca | tgtgaaccc  | cttcatctac | agcctgagga  | acacggacat  | gaagagggcc | 900 |
| ctggggagac | tcctcagtag | ggcaacattt | tttaatggtg  | acatcactgc  | aggactttca | 960 |

&lt;210&gt; 918

&lt;211&gt; 937

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g768 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 918

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| atgggggaca  | accaatcacg  | ggtcacagaa  | ttcatcctgg  | ttggattcca | gctcagtggtg | 60  |
| gagatggaag  | tgtcctctct  | ctggatcttc  | tccctgttat  | atctcttcag | cctgctggca  | 120 |
| aatggcatga  | tcttggggct  | catctgtctg  | gatcccagac  | tgcgcacccc | catgtacttc  | 180 |
| ttcctgtcac  | acttggccgt  | cattgacata  | tactatgctt  | ccagcaattt | gctcaacatg  | 240 |
| ctggaaaacc  | tagtgaaaca  | caaaaaaac   | tatctcgctc  | atctcttgca | ttatgcagat  | 300 |
| ggctttgtat  | ttgacttttg  | ctgctgcagt  | gtgcatgatt  | ttggtggtga | tgtcctatga  | 360 |
| cagatttgtg  | gcgatctgcc  | atccccctgca | ttacactgtc  | atcatgaact | ggagagtgtg  | 420 |
| cacagtactg  | gctattactt  | cctgggcatg  | tggattttcc  | ctggccctca | taaatctaata | 480 |
| tctccttcta  | aggctgccct  | tctgtgggcc  | ccaggagggtg | aaccacttct | tcgggtgaaat | 540 |
| tctgtctgtc  | ctcaaaactgg | cctgtgcaga  | cacctggatt  | aatgaaattt | ttgtctttgc  | 600 |
| tgggtggtgtg | tttgtcttag  | tcggggccct  | ttccttgatg  | ctgatctcct | acatgcgcac  | 660 |
| cctcttggcc  | atcctgaaga  | tccagtcaaa  | ggaggggccgc | aaaaaagcct | tttccacctg  | 720 |
| ctcctcccac  | ctctgtgtgg  | ttgggcttta  | ctttggcatg  | gccatggtgg | tttacctggt  | 780 |
| cccagacaac  | agtcaacgac  | agaagcagca  | gaaaattctc  | accctgtttt | acagcctttt  | 840 |
| caaccatttg  | ctgaaccccc  | tcatctacag  | cctgcggaat  | gctcaagtga | agggtgcctt  | 900 |
| atacagagca  | ctgcagaaaa  | agaggaccat  | gtgaatg     |            |             | 937 |

&lt;210&gt; 919

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g769 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 919

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atggaaccag | gaaatgatac | acaaatttca | gaattttcttc | ttctgggatt | ttcacaagaa | 60  |
| cctggactgc | aacccttctc | ctttgggctg | ttcctgtcca  | tgtacctggt | caactgtgtc | 120 |
| gggaacctgc | tcatcatcct | ggccacaatc | tcagactccc  | acctccacac | ccccatgtac | 180 |
| ttcttctctc | ccaacctgtc | ctttgctgac | atctgtgtta  | cttccaccac | cattccaaaa | 240 |
| atgctgatga | acatccagac | acagaacaaa | gtcatcacct  | acatagcctg | cctcatgcag | 300 |
| atgtattttt | tcatactctt | tgctggattt | gaaaacttcc  | tcctgtccgt | gatggcctat | 360 |
| gaccggtttg | tggccatctg | tcaccccctg | cactacatgg  | tcattatgaa | ccctcacctc | 420 |
| tgtggactgc | tggttctagc | atcctggacc | atgagtgtc   | tgtattcctt | gctacaaatc | 480 |
| ttaatggtag | tacggctgtc | cttctgcaca | gccttagaaa  | tcctccactt | tttctgtgaa | 540 |
| cttaatcagg | tcatccaact | tgcttgttct | gatagctttc  | ttaatcacat | ggtgatatat | 600 |
| tttacagttg | cgtgctggg  | tggaggctcc | ctgactggga  | tcctttactc | ttactctaag | 660 |
| ataatttctt | ccatacatgc | aatctcatca | gtcagggga   | agtacaaggc | atcttccacc | 720 |
| tgtgcatctc | acctctcagt | tgtctcctta | ttttatgggt  | caatcctagg | ggtgtacctt | 780 |
| agttctgctg | ccaccgcgaa | ctcacactca | agtgaacag   | cctcagtgat | gtacactgtg | 840 |
| gtcaccccca | tgctgaacct | ctttatctat | agtctgagga  | ataaagacat | aaagagggtc | 900 |
| ctgggaatac | atctgttgtg | gggaacaatg | aaagggaat   | tttcaagaa  | gtgccca    | 957 |

&lt;210&gt; 920

&lt;211&gt; 222

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g770 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 920

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggagacacta | cagagaacca | gatgttcgcc | gcccgcgtgg | tcatectgct | gctgccgtat | 60  |
| gacgtcatac | tggcctccta | aggtgccgtg | gcccagactg | tctgttgcac | gcggttcagc | 120 |
| ggaggaccga | ggagggcgct | gggcacgtgt | gggtcccacc | cgacagccgt | ctggctgttc | 180 |
| taaggctcgg | gcaataaac  | ctatctgcaa | gccgcgcagc | ta         |            | 222 |

&lt;210&gt; 921

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g771 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 921

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| atgaaatcat  | ggaacaatac  | aataatttta  | gaattttcttc | tcctgggaat | ttcagaggaa | 60  |
| ccagaattgc  | aggccttctc  | ctttgggctg  | ttcctgtcca  | tgtacctggt | caactgtgtc | 120 |
| gggaacctgc  | tcatcatcct  | ggccacaatc  | tcagactccc  | acctccacac | ccccatgtac | 180 |
| ttcttctctc  | ccaacctgtc  | cttcgtaggc  | atctgttttg  | tctctaccac | tgtcccgaag | 240 |
| atgctgggtga | acatccagac  | acacaacaaa  | gtcatcacct  | atgcaggctg | catcacccag | 300 |
| atgtgctttt  | tcttactctt  | tgtaggattg  | gataacttcc  | ttctgaccgt | gatggcctat | 360 |
| gaccggtttg  | tggccatctg  | tcacccctctg | cactacatgg  | tcattatgaa | ccctcaactc | 420 |
| tgtggactgc  | tggttctggc  | atcctggatc  | atgagtgttc  | tgaattccat | gttacaaagc | 480 |
| ttaatgggtg  | tggcactgcc  | cttttgtaca  | cacatggaaa  | tccttcattt | tttctgtgaa | 540 |
| attaatcagg  | tggctccacct | tgctgtttct  | gacacctttc  | ttaatgacat | agtgtatgat | 600 |
| ttcgcagtag  | cgctgctggg  | cggtgggtccc | ctcactggga  | tcctgtactc | ttactctaag | 660 |
| atagtttctc  | ccatacgtgc  | aatctcatca  | gtcagggga   | agtataaggc | atcttccacc | 720 |
| tgtgcatctc  | acctctcagt  | tgtctcctta  | ttttatggta  | catgcttagg | ggtgtacctt | 780 |
| agttctgctg  | ccaccacaaa  | ttcacacaca  | ggtgctgcag  | cctcagtgat | gtacactgtg | 840 |
| gtcaccccca  | tgctgaacct  | cttcatctac  | agtctgagga  | ataaacacat | aaagggtgct | 900 |
| atgaaaacat  | tcttcagagg  | aaagcaa     |             |            |            | 927 |

&lt;210&gt; 922

&lt;211&gt; 246

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g772 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 922

|  |     |
|--|-----|
| atgggtcacag agttcctccc actgggattt ctcctggggc caaggattca gatgctcctc | 60  |
| cttgggctct tctccctggt ctatgtcttc accccgctgg ggaatgggac catccccggg  | 120 |
| ctcatctcac tggactccag actccacacc cccatgtact tcttcctctc acacctggcc  | 180 |
| gtcgtcaaca tcgctatgc ctgcaacaca gtgccccaga tgctggtgaa cctcctgcat   | 240 |
| ccagcc   | 246 |

&lt;210&gt; 923

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g773 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 923

|  |     |
|--|-----|
| ctcatggacc tcaagctcat ctgcaccacc gtacccaaga tggccttcaa ctacctgtct  | 60  |
| ggcagcaagt ccatttctat ggctggttgt gtcacacaaa ttttcttcta tatatcactg  | 120 |
| tctggctctg aatgttttct tttggctggt atggcttatg accgctatat tgctatttgc  | 180 |
| cacctctaa gatataccaa tctcatgaat cctaaaattt gtggacttat ggctaccttc   | 240 |
| tcttggtacc tgggctctac agatggaatc attgatgctg tagccacatt ttccttctcc  | 300 |
| ttttgtgggt ctcgggaaat agcccacttc ttctgtgaat tcccttccct actaatcttc  | 360 |
| tcatgcaatg acacatcaat atttgaagag gttattttca tctgctgtat agtaatgctt  | 420 |
| gttttccctg ttgcaatcat cattgcttcc tatgctcgag ttattctggc tgatcattcac | 480 |
| atgggatctg gagagggtcg ttgcaaagct ttcacgacct gttcctctca cctcatggtg  | 540 |
| gtgggaatgt actatggagc agctttgttc atgtacatac ggcccacatc tgatcactcc  | 600 |
| ccaacgcagg acaagatggt gtctgtattc tacaccatcc tcaactccc              | 648 |

&lt;210&gt; 924

&lt;211&gt; 916

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g774 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 924

|   |     |
|---|-----|
| atgaaaccag ggaatgatac acgaatttca gaattttctc ttctaggact ttcagcagaa | 60  |
| ccagaattgc agcccttctt ctttgggctg ttctgttcca tgtacctggg caccgtgtct | 120 |
| gggaacctgc tcatcatcct ggccacaatc tcagactccc acctccacac ccccatgtac | 180 |
| ttcttctctt ccaacctgtc ctttgcagat atcagttttg tgtctaccac tgtcccgaag | 240 |
| atgctggtga atatccagac gcagagcaga gtcatcacct atgcaggctg catcaccag  | 300 |
| atgtgctttt tctactatt tgcagtgttg gacagccttc tctagctgtg gatggcctat  | 360 |
| gatcggtttg tggccatctg tcatcctctg tactacacaa tcatcatgaa cctcagttc  | 420 |
| tatagactgg attcttagtg tctgaattc tctgttaca agcttaatgg tgttgccact   | 480 |
| gcccttctat acagacatag caatccccca ctttttctgt gaacttaatc agataatctg | 540 |
| cattgcctgt tctgacacct ttcttaatga catcatgata tattgtgcaa ctgtgtgtct | 600 |
| gggcggtggt cccctcactg gaatccttta ctcttactct aagatagttt cctccatag  | 660 |
| tgcaatctca tcagctcagg ggaagtacaa ggcattttcc acctgtgcat ctcacctctc | 720 |
| agttgtctcc ttgttttatg gtacaagcct aggaatgtac cttagtcttg ctgcaaccca | 780 |
| caactcacc tcaagtgcaa cagcctcagt gatgtacact gtggtcaccc ccatgctgaa  | 840 |
| cccctttatc tacagtctga ggaataaaga cctaaaggat gctctgaaac gcttcttcag | 900 |
| aaggaagcaa taaaag   | 916 |

&lt;210&gt; 925

<211> 360  
 <212> DNA  
 <213> Unknown (H38g775 nucleotide)

<220>  
 <223> Synthetic construct

<400> 925  
 ttttcctct cacacctggc ggttggtgac attgcctacg cctgcaacac ggtgccccgg 60  
 atgctgggtga acctcctgca tccagccaag cccatctcct ttgcggggccg catgatgcag 120  
 acctttctgt tttccacttt tgcgtgcaca gaatgtttcc tctggtggt gaagtccaat 180  
 gatttgtaag tggccatctg ccacccctcc cgatatttgg ccatcatgac ctggagagtc 240  
 tgcacacccc tcgcggtgac ttctgggacc actggagtcc ttttatcctt gattcatctt 300  
 gtgttacttc tacctttacc cttctgtagg cccagaaaaa tttatcactt tttttgtgaa 360

<210> 926  
 <211> 643  
 <212> DNA  
 <213> Unknown (H38g776 nucleotide)

<220>  
 <223> Synthetic construct

<400> 926  
 ttgcctgaca tcggtttcac ctccaccacg gtccccaaga tgattgtgga atccaatctc 60  
 acagcagagt catctcctat gcaggctgcc tgactcagat gtctctcttt gccatttttg 120  
 gaggcagatga agagagacat gctcccgagt gtgatggcct atgaccgggt tgtagccatc 180  
 tgtcacccctc tatatcattc agccatcatg aaccggtgtt tctgtggctt cctagttttg 240  
 ctgtcttttt tttctttctt tttctcagct gcacaacttg attgccttac aaatgacctg 300  
 cttcaagaat gtgggaattc ctaatttctt ctgtgacctc tctcaactcc cccatctcac 360  
 atgttggtgac accttcacca atcacataat catgtatttc cccgctgcca tatttggett 420  
 tcttcccatc tcgggggaccc tttctcttta ccagtgaatt gtttcctcca ttctgagggt 480  
 ttcacatca ggtgggaagt ataaagcctt ctccacctat ggggtctacc tgcagatgt 540  
 ttcttgattt tatggaacag gcgttgagg gtacctcagt tcagatgtgt catcttcccc 600  
 gagaaagact gcagtggcct cagtgatgta cgcagtgggtc acc 643

<210> 927  
 <211> 498  
 <212> DNA  
 <213> Unknown (H38g777 nucleotide)

<220>  
 <223> Synthetic construct

<400> 927  
 gtgaaaaatc agacaatggt cacagagttc cttctatttg gatttttctt gagcccaagg 60  
 atacacatgc tctcttttg gctcttctac ctgttctatg tcttcaccct gctgggggaat 120  
 gggaccatcc tggggctcat ttcactggac tccatactcc acaccccat gtacttcttc 180  
 ctataacacc tgcctgctgt caacatcgcc tatgcctgca acacagtgcc ccagatgctg 240  
 gtgaacctcc tgcattcagc caagcccat tactttgctg gctgcatgac atataccttt 300  
 ctctttttga gatttgacac tactgaatgc ctctgttgg tgctgatgtc ctacgattgg 360  
 tacgtggcca tcttgacacc tctccgatat atcatatta tgacctgtaa agtcttcac 420  
 atctctgcca tcaatttcat gtacatgtgg ttcctttctg tcttggtcca tgtaagcctc 480  
 atactaagac tgcctttt 498

<210> 928  
 <211> 276  
 <212> DNA  
 <213> Unknown (H38g778 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 928

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| caaattgagct | tgtttgtaat | ctttgcctct | ggctgaatgc | aatttggtta | aactcgcaact | 60  |
| ggcctataga  | cccctgttac | tgccatctgt | gcacccaccc | gttctaccac | attgaccatg  | 120 |
| tctaagaggc  | cattatcttt | ttcttggtag | caggatgcta | ccttggtggg | ttagttaaga  | 180 |
| tggtcactgt  | gacaacttcc | atcacacaac | tatcgctttg | tcaaccatgt | gtccacctgc  | 240 |
| cttctctgtg  | acattccctc | attttgtage | tattcg     |            |             | 276 |

&lt;210&gt; 929

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g779 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 929

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| ttctctgac   | tctgcttttc  | ctctgtcaca  | atacctaaat | tgcttcagaa | catgcagagc | 60  |
| caagtaccaa  | cgatataccta | tgcagattgc  | ctgacacagc | tgtacttctt | tatgggtttt | 120 |
| ggagatatgg  | agagcttcct  | tcttggtggtc | atggcctatg | accgctatgt | ggccatctgc | 180 |
| tttccctttgc | attataaccag | catcatgagc  | accaaatttt | gtgctttact | agtgtacta  | 240 |
| ctgtggatgc  | tgacaataac  | ccatgccctg  | ctgcataccc | tactcatggc | tagattgtct | 300 |
| ttttgtgaga  | agaatgtcat  | tcttcacttt  | ttctgtgata | tttctgctct | tctgaagttg | 360 |
| tcctgtctcag | acacttatgt  | taatgagttg  | atgatattta | tcatgggagg | gatcatcagt | 420 |
| attattccat  | ttctactcat  | tgttatgtct  | tatgtaagga | tttttttctc | cattctcaag | 480 |
| gttccatctt  | ctcaggacat  | ccacaaggtc  | ttctctacct | gtggttccca | tctgtctgtg | 540 |
| gtgaccttgt  | tttatgggac  | aattattggt  | ctctacttat | gtccatcagg | caataattct | 600 |
| actgtgaatg  | agatttccat  | ggccatgatg  | tacacagtgg | tggct      |            | 645 |

&lt;210&gt; 930

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g780 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 930

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| agcaacctat | ccttcaactga | cctctaattt | tcctctgtca | caatgcccaa  | gttgctgcag | 60  |
| aacatgcaga | gccaagttcc  | ttcaatcccc | tatgcaggct | gcctgacaca  | aatgtacttc | 120 |
| cttttggttt | ttggagatct  | tgagagcttc | ctccttggtg | ccatggccta  | tgaccgctat | 180 |
| gtagccatct | gcttccctct  | tcattacacc | agcatcatga | gccccaggct  | ctgtgtgagt | 240 |
| cttgtgctgc | tgctctgggt  | gctgaccatg | tcccatccca | tgtctgcacac | tttgcctcta | 300 |
| actaggttgt | ctttctgtga  | aaacaatgtg | atccccatt  | ttttctgtga  | tctgtctgcc | 360 |
| ctgctgaagc | tggcctgctc  | tgatattcac | attaatgaat | tggatgatt   | gatcatagga | 420 |
| gggcttggtg | ttatacttcc  | atctctactc | atcacagtgt | cttatgcacg  | catcatctcc | 480 |
| tccattctca | aggctccctc  | aactcaaggc | atccacaagg | tcttctccac  | ttgtgggtct | 540 |
| cacctgtctg | tgggtgtcact | gttctatggg | acaattattg | gcctctactt  | atgtccatct | 600 |
| gctaataact | ctactctaaa  | ggacactgtc | atgtctatga | tgtacaccgt  | ggtaact    | 657 |

&lt;210&gt; 931

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g781 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 931

|            |            |            |            |             |           |    |
|------------|------------|------------|------------|-------------|-----------|----|
| atggagaaca | acacagaggt | gactgaattc | atccttggtg | gggttaactga | tgaccagaa | 60 |
|------------|------------|------------|------------|-------------|-----------|----|

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ctgcagatcc  | cactcttcat | agtcttccct | ttcatctacc | tcactactct | ggttggaac  | 120 |
| ctggggatga  | ttgaattgat | tctactggac | tctgtctcc  | acaccccat  | gtacttcttc | 180 |
| ctcagtaacc  | tctccctggg | ggactttggg | tattcctcag | ctgtcactcc | caaggtgatg | 240 |
| gtgggggttc  | tcacaggaga | caaattcata | ttatataatg | cttgtgccac | acaattcttc | 300 |
| ttcttttag   | cctttatcac | tgcagaaagt | ttcctcctgg | catcaatggc | ctatgaccgc | 360 |
| tatgcagcat  | tgtgtaaacc | cctgcattac | accaccacca | tgacaacaaa | tgtatgtgct | 420 |
| tgccctggcca | taggctccta | catctgtggg | ttcctgaatg | catccattca | tactgggaac | 480 |
| actttcaggc  | tctccttctg | tagatccaat | gtagttgaac | actttttctg | tgatgtcctc | 540 |
| cctctcttga  | ctctctcatg | ttcagacaac | tacatcagtg | agatgggtat | tttttttgtg | 600 |
| gtgggattca  | atgacctctt | ttctatcctg | gtaatcttga | tctcctactt | atttatattt | 660 |
| atcaccatca  | tgaagatgcg | ctcacctgaa | ggacgccaga | aggccttttc | tacttgtgct | 720 |
| tcccacctta  | ctgcagtttc | catcttttat | gggacaggaa | tctttatgta | cttacgacct | 780 |
| aactccagcc  | atttcatggg | cacagacaaa | atggcatctg | tgttctatgc | catagtcatc | 840 |
| cccattgtga  | atccactggg | ctacagcctg | aggaacaaag | aggttaagag | tgccctttaa | 900 |
| aagactgtag  | ggaaggcaaa | ggcctctata | ggattcatat | tt         |            | 942 |

&lt;210&gt; 932

&lt;211&gt; 562

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g782 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 932

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gcaacaaagg | agctgtgttt | tcttggggta | tatattccca | aaggcgatgc | ctgctggaaa  | 60  |
| tgactcctct | gggcctgcat | ttactcttgc | taggttgaca | agttgtctcc | atgggtggga  | 120 |
| acctggcctt | gattgctcta | attggctgaa | attcatacct | tcccaccccc | aagctctgtt  | 180 |
| ttctttcacc | cagtccttcc | ctgatctcta | ttgtcctggt | tgcaccccca | gaatgctcat  | 240 |
| gacttttgta | tcaaagaaaa | acatcttcta | tgtcagggtc | atgactcagc | tgctgcagct  | 300 |
| ttctttctc  | tttattgtcc | tactctatta | aataccacgt | gttgatgttc | atagcctgtg  | 360 |
| gttgcttagt | ggccatctac | aatccatcat | tgcattgagg | caccatgtct | cctcagggtga | 420 |
| gagagagaga | gagagtggat | ttgctggaac | cactcccaca | cagggcacat | acttaggccg  | 480 |
| aacttggtga | atattgatgt | catcaatcat | catcttatga | cagcctcttg | gtcctctaag  | 540 |
| ttctttgtac | cagcacctgt | gc         |            |            |             | 562 |

&lt;210&gt; 933

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g783 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 933

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| atgactgggg | gaggaaatat  | tacagaaatc | acctatttca | tcctgctggg  | attctcagat  | 60  |
| tttcccagga | tcataaaaagt | gctcttcaat | atattcctgg | tgatctacat  | tacatctctg  | 120 |
| gcctggaacc | tctccctcat  | tgttttaata | aggatggatt | cccacctcca  | tacacccatg  | 180 |
| tatttcttcc | tcagtaacct  | gtccttcata | gatgtctgct | atatcagctc  | cacagtcccc  | 240 |
| aagatgctct | ccaacctctt  | acaggaacag | caaactatca | cttttggttg  | ttgtattatt  | 300 |
| cagtacttta | tcttttcaac  | gatgggactg | agtgagtctt | gtctcatgac  | agccatggct  | 360 |
| tatgatcggt | atgctgcat   | ttgtaacccc | ctgctctatt | catccatcat  | gtcaccacc   | 420 |
| ctctgtgttt | ggatgggtact | gggagcctac | atgactggcc | tcactgcttc  | tttattccaa  | 480 |
| attgggtgct | tgcttcaact  | ccacttctgt | gggtctaatg | tcattcagaca | tttcttctgt  | 540 |
| gacatgcccc | aactgttaat  | cttgctctgt | actgacactt | tctttgtaca  | ggctcatgact | 600 |
| gctatattaa | ccatgttctt  | tgggatagca | agtgccttag | ttatcatgat  | atcctatggc  | 660 |
| tatattggca | tctccatcat  | gaagatcact | tcagctaaag | gcaggccaaa  | ggcattcaac  | 720 |
| acctgtgctt | ctcatctaac  | agctgtttcc | ctcttctata | catcaggaat  | ctttgtctat  | 780 |
| ttgaggtcca | gctctggagg  | ttcttcaage | tttcagagat | ttgcatctgt  | tttctacact  | 840 |
| gtggtcattc | ccatgttaaa  | tcccttgatt | tacagtttga | ggaacaaaga  | aattaaagat  | 900 |
| gccttaaaga | ggttgcaaaa  | gagaaagtgc | tgc        |             |             | 933 |

<210> 934  
 <211> 935  
 <212> DNA  
 <213> Unknown (H38g784 nucleotide)

<220>  
 <223> Synthetic construct

<400> 934  
 atgactgggg aaaggaacag tacgagaatt acaaagttca ttctcttggg attctctgaa 60  
 ttccaaaga accctatttt cctcttttca atattcctag ggatctacct cctgacagtg 120  
 tcctggaaca taaacctcat cacccttatac aggacgactc ccatctgcat acacctatgt 180  
 actttttcct tagtaatctg tcgtttctgg acatctgcta tgtttccact atagcccca 240  
 agatgctctc agacttcttc aagaagcata aattcatctc ctttatgggg tgcagtatgc 300  
 agtacttttt cttctctagc ctaggtctaa ctgagtgtctg tcttctggca gccatggctt 360  
 atgatcgata tgctgccatt tgcaaccctc tgctctacag ggccatcatg ttcccccacc 420  
 tctgctgca gatggtggca ggatcttgta taactggatt cttaggctca tttatccaac 480  
 tctgtgcctt gcttcagctc catttctgtg ggccaaatgt catcaaccat ttcttctgtg 540  
 atctgcccc gctgctgatt ctatctgtt ctgacacctt tttctttcaa gtcatgacct 600  
 ctgttctcac agtgatcttt ggactcacgt ctgtcttagt tatcatgata tcttatgggt 660  
 atatcattgc caccattctg aagatcacct cagctgaagg cagagccaaa tctttcaaca 720  
 cttgtgcttc tcaccttaca gcagtgatec ttttcttgg ctcaggatc tttgtttata 780  
 tgtatcctaa tgctggtgat tccctgagcc aaaacaagtt ggcatcagtc ttatacacag 840  
 ttacaatccc catgttaaat ccagtgatct acagcctgag gaacaaggaa atcaaagatg 900  
 ctctaaacag atggaagaag agaattcttct cctgg 935

<210> 935  
 <211> 1330  
 <212> DNA  
 <213> Unknown (H38g785 nucleotide)

<220>  
 <223> Synthetic construct

<400> 935  
 atgactgtgg aaaggagtag catgacaatt acaaagttca ttctcttggg attctctgaa 60  
 tattcaaaga ccactatttt tctcttttca gtattcctag ggatataacct cctgaccatg 120  
 tcctgaaacg tgagtctcat cgcccttatac aggacggact cccatctaca tgcacctgtg 180  
 tactttttcc ttagtaatcc gtcttttctg gacatctgct gtgtttccac tatagcccc 240  
 aagatgccct cagacttttt caagaagcat aaattcattt cctttatggg gtgcaccatg 300  
 cagtacttct ctagecctgaa tgtgactgag tgctgtcttc ttacagccat ggcttatgat 360  
 taatatgctg ccatttgtga tctctgtctc tacacagcca tcatgtcacc tgctctctgt 420  
 atgccaatgg tggcaggatc ttgtacaact ggatactttg tctcatttat ccaactctgt 480  
 gccttgcttc tgctccattt ctgtgagtca aatagcagcc atttcttttg tgacctgccc 540  
 caactgctga ttctatcctg ttctcatact gttttttttt tctcaagtca tgaccactat 600  
 gctcacagta acctttatac tcacctctat cttgggttatc atgataactt atgggttatat 660  
 cattgccaac attcatctct tttatgggat gcaccatgta atacttcttc tctagcctgg 720  
 gtctgactga gtgctgtctt ctggaagcta tggcttataa ttgatatgct gccatttgtg 780  
 acctctgct ctacatggcc atccatgtcc ccaacctctg tgtgcacata atgggtggaa 840  
 cctgtataac tattatcttt ggctcattta tccaactatg tgctttgctt cagctccatt 900  
 tctgtgggcc aaatagcaac catttcttct gtgacctgcc ccaactcttg atcctatctt 960  
 gctatgacac ctttttctgt caagtcatga catccatgct tacagtggta tttggactca 1020  
 catctgtctt agttatcatg atattttatg gctatgtcat tgctaccatt ctgaagatca 1080  
 tctcagttga aggcaggtct aaggcttctca acactggtgg ttctccctga tagcagtgac 1140  
 tctcttctat tgctcaagaa tctttgtcta tatgtgctct cactctgatg cttctctgag 1200  
 tagaaacaag gtggattcta ttgtatacac tgtggtgatc cccagggtga atccattgat 1260  
 ctacagcctg agtgacaagt aaatcaaaga tgccctaaag agatggacga agagaatatt 1320  
 ctctggcct 1330

<210> 936



<211> 930  
 <212> DNA  
 <213> Unknown (H38g786 nucleotide)

<220>  
 <223> Synthetic construct

<400> 936  
 atgggggaaa atcagacaat ggtcacagag ttctctctac tgggatttct cctggggccca 60  
 aggattcaga tgctcctctt tgggctcttc tccctgttct atatcttcac cctgctgggg 120  
 aacggggcca tcctggggct catctcactg gactccagac tccacacccc catgtacttc 180  
 ttctctctac acctggctgt cgtcgacatc gcctacaccc gcaacacggg gccccagatg 240  
 ctggcgaacc tcctgcatcc agccaagccc atctcctttg ctggctgcat gacgcagacc 300  
 tttctctgtt tgagtttttg acacagcgaa tgtctcctgc tgggtgctgat gtcctacgat 360  
 cgttacgtgg ccactctgcca cctctctccga tactccgtca tcatgacctg gagagtctgc 420  
 atcacccctg ccgtcacttc ctggacgtgt ggctccctcc tggctctggc ccattgtggtt 480  
 ctcatcctaa gactgccctt ctctgggccc catgaaatca accacttctt ctgtgaaatc 540  
 ctgtctgtcc tcaggctggc ctgtgctgac acctggctca accagggtgt catctttgca 600  
 gcctgcgtgt tcttctctgt gggggccacc agcctgggtg ttgtctctca ctgcacatc 660  
 ctggcggcca tcctgaggat ccagtctggg gagggccgca gaaaggcctt ctccacctgc 720  
 tcctccacc tctgctgtgt gggactcttc tttggcagtg ccatcatcat gtacatggcc 780  
 cccaagtccc gccatcctga ggagcagcaa aaggctcttt ttctatttta cagttttttc 840  
 aacccaacac ttaacccctt gatttacagc ctgaggaacg gagagggtcaa ggggtgccctg 900  
 aggagagcac tgggcaagga aagtcattcc 930

<210> 937  
 <211> 942  
 <212> DNA  
 <213> Unknown (H38g787 nucleotide)

<220>  
 <223> Synthetic construct

<400> 937  
 atggaaagac aaaatcaaag ctgtgtggtt gaattcatcc tcttggggctt ttctaactat 60  
 cctgagctcc aggggcagct ctttgtggct ttcttggtta tttatctggt gaccctgata 120  
 ggaaatgcca ttattatagt catcgtctcc ctgaccaga gcctccacgt tcccatgtac 180  
 ctgtttctcc tgaacttata tgtggtggac ctgagtttca gtgcagttat tatgcctgaa 240  
 atgctgggtg tcctctctac tgaaaaaact acaatttctt ttgggggctg ttttgacag 300  
 atgtatttca tccttctttt tgggtggggct gaatgtttt ttctgggagc aatggcttat 360  
 gaccgatttg ctgcaatttg ccactccttc aactaccaa tgattatgaa taaaggagtt 420  
 tttatgaaat taattatatt ttcatgggcc ttaggtttta tggtaggtac tgttcaaaca 480  
 tcatgggtat ctagttttcc ctttgtggc cttaatgaaa ttaaccatat atcttgtgaa 540  
 accccagcag tgttagaact tgcagtgcga gacacgtttt tgtttgaaat ctatgcattc 600  
 acaggcacct ttttgattat tttggttctt ttcttgttga tactcttgc ttacattcga 660  
 gttctgtttg ccactcctga gatgccatca accactggga gacaaaaggc cttttccacc 720  
 tgtgccgctc acctcacatc tgtgacctta ttctatggca cagccagtat gacttattta 780  
 caacccaaat ctggctactc accggaaacc aagaaagtga tgtcattgtc ttactcactt 840  
 ctgacaccac tgctgaatct gcttatctac agtttgcgaa atagttagat gaagagggtc 900  
 ttgatgaaat tatggcgaag gcgagtgggt ttacacacaa tc 942

<210> 938  
 <211> 993  
 <212> DNA  
 <213> Unknown (H38g788 nucleotide)

<220>  
 <223> Synthetic construct

<400> 938  
 atggtcacag agttcctcct actgggattt ctctggggcc caaggattca gatgtcctc 60

|             |            |             |             |             |            |     |
|-------------|------------|-------------|-------------|-------------|------------|-----|
| tttgggctct  | tctccctggt | ctatgtcttc  | accctgctgg  | ggaatgggac  | catcctgggg | 120 |
| ctcatctcac  | tggactccag | actccacacc  | cccattgtact | tcttcctctc  | acacctggcc | 180 |
| gtcgtcaaca  | tcgcctatgc | ctgcaacaca  | gtgcccaga   | tgctgggtgaa | cctcctgcat | 240 |
| ccagccaagc  | ccatctcctt | tgctgggtgc  | atgacataga  | cctttctctt  | tttgagtttt | 300 |
| gcacatactg  | aatgcctcct | gttgggtgctg | atgtcctacg  | atcgggtacgt | ggccatctgc | 360 |
| cacctctctc  | gatatttcat | catcatgacc  | tggaaagtct  | gcatcactct  | ggccatcact | 420 |
| tcctggacat  | gtggctccct | cctggctatg  | gtccatgtga  | gcctcatcct  | aagactgccc | 480 |
| ttttgtgggc  | ctcgtgaaat | caaccacttc  | ttctgtgaaa  | tcctgtctgt  | cctcaggctg | 540 |
| gcctgtgctg  | atacctgggt | caaccagggtg | gtcatctttg  | cagcctgcat  | gttcatcctg | 600 |
| gtgggaccac  | tctgcctggt | gctgggtctcc | tactcacaca  | tcctggcggc  | catcctgagg | 660 |
| atccagtctg  | gggagggccg | cagaaaggcc  | ttctccacct  | gctcctccca  | cctctgcgta | 720 |
| gtgggactct  | tctttggcag | cgcacccgtc  | atgtacatgg  | cccctaagtc  | ccgccatcct | 780 |
| gaggagcagc  | agaaggtcct | ttttctattt  | tacagttctt  | tcaacccgat  | gctaaacccc | 840 |
| ctgattttaca | acctgaggaa | tgtagaggtc  | aagggtgccc  | tgaggagagc  | actgtgcaag | 900 |
| gaaagtcatt  | cctaagaggt | gtgacatttg  | aactgccagc  | ctcagttgtc  | acgtggactc | 960 |
| ttgatgcccc  | attattgcct | caatccagaa  | aag         |             |            | 993 |

&lt;210&gt; 939

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g789 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 939

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| atgggggaca  | atataacatc  | catcacagag | ttcctcctac  | tgggatttcc  | cgttgggcca | 60  |
| aggattcaga  | tgctcctctt  | tgggctcttc | tcctgtttct  | acgtcttcac  | cctgctgggg | 120 |
| aacgggacca  | tactggggct  | catctcactg | gactccagac  | tgacacgccc  | catgtacttc | 180 |
| ttcctctcac  | acctggcggt  | cgtcgacatc | gcctacgcct  | gcaacacggt  | gccccggatg | 240 |
| ctggtgaacc  | tccctgcatt  | agccaagccc | atctcctttg  | cgggccgcat  | gatgcagacc | 300 |
| tttctgtttt  | ccacttttgc  | tgtcacagaa | tgctcctccc  | tggtgggtgat | gtcctatgat | 360 |
| ctgtacgtgg  | ccatctgcca  | ccccctccga | tatttggtcca | tcattgacctg | gagagtctgc | 420 |
| atcacccctg  | cggtgacttc  | ctggaccact | ggagtccctt  | tatccttgat  | tcattctgtg | 480 |
| ttactttctac | ctttaccctt  | ctgtaggccc | cagaaaattt  | atcacttttt  | ttgtgaaatc | 540 |
| ttggctgttc  | tcaaacttgc  | ctgtgcagat | accacatca   | atgagaacat  | ggtcttggcc | 600 |
| ggagcaattt  | ctgggctgggt | gggacccttg | tccacaattg  | tagtttcata  | tatgtgcac  | 660 |
| ctctgtgcta  | tccttcagat  | ccaatcaagg | gaagttcaga  | ggaaagcctt  | ctgcacctgc | 720 |
| ttctcccacc  | tctgtgtgat  | tggactcttt | tatggcacag  | ccattatcat  | gtatgttggg | 780 |
| cccagatatg  | ggaaccccaa  | ggagcagaag | aaatatctcc  | cgctgtttca  | cagcctcttt | 840 |
| aatcccatgc  | tcaatcccct  | tatctgtagt | cttaggaact  | cagaagtga   | gaatactttg | 900 |
| aagagagtgc  | tgggagtaga  | aagggtttaa |             |             |            | 930 |

&lt;210&gt; 940

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g790 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 940

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| atgaaaagac | aaaatcaaa   | ctgtgtgggt  | gaattcatcc | tcctgggctt  | ttctaacttt | 60  |
| cctgagctcc | agggtgcagct | ctttgggggt  | ttcctagtta | tttatgtgggt | gacctgatg  | 120 |
| ggaaatgcc  | tcattacagt  | catcatctcc  | ttaaaccaga | gcctccacgt  | tcccatgtac | 180 |
| ctgttctctc | tgaacctatc  | tgtgggtggag | gtgagtttca | gtgcagtcac  | tacgcctgaa | 240 |
| atgctgggtg | tgctctctac  | tgagaaaact  | atgatttctt | ttgtgggctg  | ttttgcacag | 300 |
| atgtatttca | tccttctttt  | tgggtgggact | gaatgttttc | tcctggggagc | gatggcttat | 360 |
| gaccgatttg | ctgcaatttg  | ccatcctctg  | aactaccag  | tgattatgaa  | cagaggggtt | 420 |
| tttatgaaat | ctcatgaatt  | ctcatggatc  | tcagggatca | tggtgggtac  | tgtcagacc  | 480 |
| acttgggtat | ttagttttcc  | attttgtggc  | cccaatgaaa | ttaatcatct  | cttctgtgag | 540 |

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| actcccccg  | tactagagct  | tgtgtgtgca | gacacettct | tatttgaaat | ctatgccttc | 600 |
| acaggcacca | ttttgattgt  | tatggttcct | ttcttgttga | tcctcttgte | ttacattcga | 660 |
| gttctgtttg | ccatccctgaa | gatgccatca | actactggga | gacaaaaggc | ctttccacc  | 720 |
| tgtgcctctc | acctcacatc  | tgtgacctg  | ttctatggca | cagccaatat | gacttattta | 780 |
| caacccaaat | ctggctactc  | acccgaaacc | aagaaactga | tctcattggc | ttacacgttg | 840 |
| cttaccctc  | tgctcaatcc  | gctcatctat | agcttacgaa | acagtgagat | gaagaggact | 900 |
| ttgataaaac | tatggcgaag  | aaaagtgatt | ttacacacat | tc         |            | 942 |

&lt;210&gt; 941

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g791 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 941

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| atgagtgcaa | acacctccat | ggtgactgag  | tttctcttc   | tcggtcttc   | ccacctggcc | 60  |
| gacctccagg | gcttgetctt | ctctgtcttt  | ctcactatct  | acctgctgac  | cgtggcaggc | 120 |
| aatttctca  | ttgtgggtgt | ggctctccact | gatgctgccc  | tccagtcccc  | tatgtacttc | 180 |
| ttctctgcga | ccctctcggc | cttgagatt   | ggctatacgt  | ctgtcacggg  | ccccctgcta | 240 |
| cttcaccacc | tccttactgg | cgggcgccac  | atctctcgct  | ctggatgtgc  | tctccagatg | 300 |
| ttctctctcc | tcttcttttg | cgccacggag  | tgctgcctcc  | tggcagccat  | ggcctatgac | 360 |
| cgctatgcag | ccatctgtga | acccctccgc  | taccactgc   | tgctgagcca  | ccgggtgtgt | 420 |
| ctacagctag | ctgggtcggc | gtgggcctgt  | gggtgctgg   | tggggtggg   | ccacaccct  | 480 |
| ttcatcttct | ctttgccctt | ctgggcctcc  | aataccatcc  | cgcagttctt  | ctgtgagatc | 540 |
| cagcctgtcc | tgcagctggg | atgtggagac  | acctcgctta  | atgaactgca  | gattatcctg | 600 |
| gcaacagccc | tcctcatcct | ctgccccttt  | ggcctcatcc  | tgggctccta  | cgggcgtatc | 660 |
| ctcgttacca | tcttcgggat | cccctctgtt  | gcgggccgcc  | gcaaggcctt  | ctccacctgc | 720 |
| tctctccacc | tgatcgtggg | ctccctcttc  | tatggcaccg  | cactctttat  | ctatatctgc | 780 |
| cctaaggcca | gctacgatcc | ggccactgac  | cctctgggtg  | ccctcttcta  | tgctgtgggc | 840 |
| acccccatcc | tcaaccccat | catctacagc  | ctgcgggaaca | cagagggtcaa | agctgcctta | 900 |
| aagagaacca | tccagaaaac | ggtgcctatg  | gagatt      |             |            | 936 |

&lt;210&gt; 942

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g792 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 942

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atgtacctgg | tcactgtgct  | cggaacctg  | ctcatcatcc | tggccgcaat | ctcagactcc | 60  |
| tgctccacca | cccccatgta  | cttctttctc | tccaacctgt | ccttcgtaga | tatctgtttt | 120 |
| gcctccacca | tggtcccaaa  | gatgttggtg | aacatccaga | cacagagcaa | agtcattacc | 180 |
| tatgcagggt | gcatcaccca  | gatgtgcttt | tttgtactct | ttatagtgtt | ggacagctta | 240 |
| ctcctgaccg | tgatggccta  | tgaccagttt | gtggccatct | gtcaccctcc | gcactacacg | 300 |
| gtcatcatga | gccctcagct  | ctgtggactg | ctgggtctgg | tgctctggat | catgagtgtc | 360 |
| ctaaactcca | tgttacaaaag | cttagtgaca | ttgcagttgt | ccttctgcac | agacttgga  | 420 |
| atccctcact | ttttctgtga  | acttaatgag | atgatccacc | ttgcctgttc | tgacaccttt | 480 |
| gtgaacaaca | tggatgatga  | ttttgcagct | gtgctgtctg | acgggtggtc | tctcgttggg | 540 |
| atcctttatt | cttactgtag  | gatagtttcc | tccatacgtg | caatctcgtc | aactcagggg | 600 |
| aagtacaagg | cactttccac  | ctgtgcactc | cacctctcag | ttgtctccat | attttatggt | 660 |
| acggggctag | gggtgtacct  | tagctctact | atgacccaaa | acttacactc | aactgctgtc | 720 |
| gcctcgggtg | tgtacactgt  | ggtcaccccc | atgctcaacc | ccttcattta | cagtctgagg | 780 |
| aataaagaca | taaagggggg  | tctgacacaa | ttcttcagag | ggaaacaa   |            | 828 |

&lt;210&gt; 943

&lt;211&gt; 950

&lt;212&gt; DNA

<213> Unknown (H38g793 nucleotide)

<220>

<223> Synthetic construct

<400> 943

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| tcaattacct  | gggaaaatca  | ctcagtggtg | atggaatttg | tgttcctggc | ctatccctcc | 60  |
| tgcccagaac  | tgcataattct | gtccttcctt | ggggtcagcc | tgggttatgg | tttgatcatc | 120 |
| actgggaaca  | ttctcattgt  | ggtgtccatt | cacacagaaa | cctgtctatg | cacatccatg | 180 |
| tactatttcc  | tgggcagcct  | ttctgggatt | gaaatatgct | acactgcagt | ggtgggtgcc | 240 |
| catatcctgg  | ccaacaccct  | acagtcagag | aagacatcac | tctcctgggc | tgtgccaccc | 300 |
| agatggcttt  | cttcattgca  | ctgggcagtg | ctgattgctt | cctcttggct | gccatggcct | 360 |
| atgaccgcta  | tgtggccatt  | tgccaccctg | tgcagtaccc | tctcctcatg | acattgactc | 420 |
| tttgtgtcca  | cttgggtgtg  | gcatcagtc  | tcagtggtct | gttcctgtcc | ttacaactgg | 480 |
| tggccttcat  | cttctctctg  | ccattctgcc | aggctcaggg | cattgagcac | ttcttttgtg | 540 |
| atgtgccacc  | agtcattgcat | gttgtttgtg | ctcagagtca | cattcatgag | cagtcagtgc | 600 |
| tgggtggcagc | catactagcc  | attgctgtgc | ctttcttctt | catcaccacc | tcctacacct | 660 |
| tcatagtggc  | tgctctgctc  | aagatccact | cggtctgtgg | ccgccaccgg | gccttctcca | 720 |
| cctgctcttc  | ccacctcact  | gtgggtgctg | tgcagtatgg | ctgctgtgcc | ttcatgtacc | 780 |
| tgtgccccag  | ctccagctac  | aaccccaagc | aagatcgggt | catctcactg | gtgtacacat | 840 |
| tgggaacccc  | actgctcaac  | ccacttatct | atgccctgag | gaacagttag | atgaaagggg | 900 |
| ccgtaggggag | agttcttacc  | aggaactgcc | tttcccagaa | cagctaggaa |            | 950 |

<210> 944

<211> 927

<212> DNA

<213> Unknown (H38g794 nucleotide)

<220>

<223> Synthetic construct

<400> 944

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggaaccag | agaatgacac | agggatttca | gaatttggtc | ttctgggact | ttctgaggaa | 60  |
| ccagaattgc | agcccttctt | ctttgggctg | tttctgtcca | tgtacctggg | cactgtgctc | 120 |
| gggaattctg | tcatactcct | ggccacaatc | tcagactccc | acctccacac | ccccatgtac | 180 |
| ttcttctctt | ccaacctgtc | ctttgcagac | atctgtttca | tctccactac | aatcccaaag | 240 |
| atgctcatta | acatccagac | acagagcaga | gtcatcacct | atgcaggctg | catcacccag | 300 |
| atgtgctttt | ttgtactttt | tggagggtta | gacagcttac | tcctggctgt | gatggcctat | 360 |
| gatcggtttg | tggccatctg | tcactctctg | cactacacag | tcatactgaa | ccctcggctc | 420 |
| tgtggactcc | tggttctggc | atcctggatg | attgctgccc | tgaattcctt | gtcacaaagc | 480 |
| ttaatgggat | tgtggctgtc | cttctgcaca | gacttggaaa | tccccactt  | tttctgtgaa | 540 |
| cttaatcagg | tcataccact | tgctgtttct | gacacctttc | ttaatgacat | ggggatgtat | 600 |
| tttgcagcag | ggctgctggc | tgggtgtccc | cttgtgggga | tcctttgtct | ttactctaag | 660 |
| atagtttctt | ccatacgtgc | aatctcatca | gctcagggga | agtacaaggc | attttccacc | 720 |
| tgtgcatcac | acctctcagt | tgtctcttta | ttttgttgta | cgggcctagg | tgtgtacctt | 780 |
| acttctgctg | caaccacaaa | ctcacacaca | agtgaacag  | cctcagtgat | gtacactgtg | 840 |
| gccaccccca | tgctgaaccc | ctttatctac | agtctgagga | ataaagacat | aaagagggct | 900 |
| ctgaaaatgt | ccttcagagg | aaagcaa    |            |            |            | 927 |

<210> 945

<211> 942

<212> DNA

<213> Unknown (H38g795 nucleotide)

<220>

<223> Synthetic construct

<400> 945

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggagaata | atacagaggt | gagtgaattc | atcctgcttg | gtctaacc   | tgccccagaa | 60  |
| ctacaggttc | ccctctttat | catgtttacc | ctcatctacc | tcatactct  | gactgggaac | 120 |
| ctggggatga | tcataatta  | cctgctggac | tctcatctcc | acactcccat | gtactttttt | 180 |

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ctcagtaacc  | tgtctcttgc | aggcattggt | tactcctcag | ctgtcactcc | aaaggtttta  | 240 |
| actgggttgc  | ttatagaaga | caaagccatc | tcctacagtg | cctgtgctgc | tcagatgttc  | 300 |
| ttttgtgcag  | tctttgccac | tgtggaaaat | tacctcttgt | cctcaatggc | ctatgaccgc  | 360 |
| tacgcagcag  | tgtgtaaccc | cctacattat | accaccacca | tgacaacacg | tgtgtgtgct  | 420 |
| tgtctggcta  | taggctgtta | tgtcattggt | tttctgaatg | cttctatcca | aattggagat  | 480 |
| acatttcgcc  | tctctttctg | catgtccaat | gtgattcatc | actttttctg | tgacaaaacca | 540 |
| gcagtcatta  | ctctgacctg | ctctgagaaa | cacattagtg | agttgattct | tgttcttata  | 600 |
| tcaagtttta  | atgtcttttt | tgcacttctt | gttaccttga | tttcctatct | gttcatattg  | 660 |
| atcaccattc  | ttaagaggca | cacaggtaag | ggataccaga | agcctttatc | tacctgtggt  | 720 |
| tctcacctca  | ttgccatttt | cttattttat | ataactgtca | tcatcatgta | catacgacca  | 780 |
| agttccagtc  | attccatgga | cacagacaaa | attgcatctg | tgttctacac | tatgatcatc  | 840 |
| cccattgctca | gtcctatagt | ctataccctg | aggaacaaag | acgtgaagaa | tgcattcatg  | 900 |
| aaggttgttg  | agaaggcaaa | atattctcta | gattcagtct | tt         |             | 942 |

&lt;210&gt; 946

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g796 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 946

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| atgtaaaata | actcaaagtt | tactgatttc | atcctggtag  | gtctaaccaa  | tgccacagaa | 60  |
| cttcagatcc | ccctctttat | cttggttcac | ctcatccacc  | tcctcattct  | gactaggaac | 120 |
| ctggagatca | tactgttgat | cctgctggac | tcttgtctcc  | aattcccatg  | tactttttcc | 180 |
| tcagtaacct | gtctctgctt | ggatacttaa | ctgtcactcc  | caggggtcacg | gctagcaggg | 240 |
| ctaggttact | tagagggtag | gaggctaagt | tcctcgtaca  | atgcttgtgc  | tgctcagatg | 300 |
| ttcttttttg | tagccttggc | cacagtggaa | aatatcgctg  | ttgacatcaa  | tgccctatga | 360 |
| ccactatata | gcagtgtgca | aacccttaca | ctacactacc  | accacgatag  | ccagtgtatg | 420 |
| tgctcatctg | gtcataggct | cctatgtctg | tggttttcta  | aatgcctccc  | tcgcatttgg | 480 |
| ggacatatcc | agtctctctt | tctgtaagtc | caatcttgtc  | catcaccttt  | tctgtgatgt | 540 |
| tccaccagtc | atggctgtgt | cttgcctctg | ttaacacatt  | agcaagaaga  | ttctggtttt | 600 |
| tatgtcaagc | ttcaatgtct | ttttggctct | tctagttatc  | ttgacctcct  | acctgttcat | 660 |
| attcatcacc | atcttgaaga | tgcactcagc | tcagggacac  | ttaaaagctt  | tgtccacctg | 720 |
| tgccctcacc | ctcattgcag | tctccatctt | ctatggaaact | actatcttta  | tgcacttaca | 780 |
| gcctagctcc | agccattcca | tggacacaga | tgaattggca  | tccttgttct  | atgctgtgtt | 840 |
| catctccatg | ctgaaccttg | tgttctacag | cctgaggagc  | aaagaagtca  | agaatgcatt | 900 |
| caaaaaggcg | gttgagaagg | caaaattttt | cttagaactg  | tgattt      |            | 946 |

&lt;210&gt; 947

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g797 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 947

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| atggacaaca  | gcaactggac  | cagtgtgtcc  | cattttgttc | tcttgggcat  | ttccacccac  | 60  |
| ccagaagagc  | aaatcccact  | cttccttgtt  | ttctcactca | tgtaacgcaat | caatattttct | 120 |
| ggcaacttgg  | ccatcatcac  | actgattctc  | tctgtctcac | gcctccacat  | ccccatgtac  | 180 |
| atcttctctca | gtaacttggc  | cttgacagac  | atctgtctca | cctccaccac  | ggcccccaag  | 240 |
| atgctgcaga  | ttattttctc  | ccctacaaaag | gtaatttctc | acacaggctg  | tttagcccaa  | 300 |
| acttattttct | tcattttgctt | cgccgtcatg  | gaaaacttca | tcctggctgt  | gatggcctat  | 360 |
| gacagggtaca | ttgccatctg  | ccaccctttc  | cactacacta | tgatcctgac  | tagaatgctg  | 420 |
| tgtgtgaaga  | tggttggtcat | gtgccatgct  | ctctcccacc | ttcatgccat  | gctgcatacc  | 480 |
| ttctctatgg  | gccaactaat  | cttctgtgca  | gataacagaa | tcctccactt  | cttctgtgac  | 540 |
| ctctacgctc  | tgatgaagat  | ctcctgcacc  | agcacctacc | tcaacacctc  | tatgattcac  | 600 |
| acagaagggtg | ctgttgtaat  | cagtggagct  | ctggccttca | ttactgcctc  | ctatgcctgc  | 660 |
| atcatcctgg  | tggtcctccg  | gatcccttca  | gccaagggca | ggcggaaaac  | cttttctacc  | 720 |

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| tgcggctccc | acctcactgt | ggtggccata  | ttctatggca | ccctcagttg | ggtctacttc | 780 |
| cgggcccttt | ccagctatcc | agtgaccaag  | ggtcgcatta | taacagtcgt | gtacacagtg | 840 |
| gtgactccca | tgctgaaccc | cttcactctac | agcctgagga | atggggatgt | caagggaggc | 900 |
| ttcatgaaat | ggatgagcag | aatgcagact  | ttttcttta  | ga         |            | 942 |

&lt;210&gt; 948

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g798 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 948

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| atggttaacc | aaagctcccc  | catgggcttc | ctccttcttg  | gcttctctga | acaccagca  | 60  |
| ctggaaagga | ctctctttgt  | ggttgtcttc | acttcctacc  | tcttgaccct | ggtgggcaac | 120 |
| acactcatca | tctgtctgtc  | tgtactgtac | cccaggctcc  | actctccaat | gtactttttc | 180 |
| ctctctgacc | tctccttctt  | ggacctctgc | tttaccacaa  | gttgtgtccc | ccagatgctg | 240 |
| gtcaacctct | ggggcccaaa  | gaagaccatc | agcttcctgg  | gatgctctgt | ccagctcttc | 300 |
| atcttcctgt | ccctggggac  | cactgagtgc | atcctcctga  | cagtgatggc | ctttgaccga | 360 |
| tacgtggctg | tctgccagcc  | cctccactat | gccaccatca  | tccacccccg | cctgtgctgg | 420 |
| cagctggcat | ctgtggcctg  | ggttatgagt | ctgggtccaat | cgatagtcca | gacaccatcc | 480 |
| accctccact | tgcccttctg  | tccccaccag | cagatagatg  | actttttatg | tgagggtcca | 540 |
| tctctgattc | gactctcctg  | tggagatacc | tcctacaatg  | aaatccagtt | ggctgtgtcc | 600 |
| agtgtcatct | tcgtggttgt  | gcctctcagc | ctcatccttg  | cctcttatgg | agccactgcc | 660 |
| caggcagtgc | tgaggattaa  | ctctgccaca | gcatggagaa  | aggcctttgg | gacctgtccc | 720 |
| tcccatctca | ctgtggtcac  | cctcttctac | agctcagtca  | ttgctgtcta | cctccagccc | 780 |
| aaaaatccgt | atgcccaagg  | gaggggcaag | ttctttggtc  | tcttctatgc | agtgggcact | 840 |
| ccttcactta | accctctcgt  | atacaccctg | aggaacaagg  | agataaagcg | agcactcagg | 900 |
| aggttactag | ggaaggaaaag | agactccagg | gaaagctgga  | gagctgct   |            | 948 |

&lt;210&gt; 949

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g799 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 949

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| cacacagagc  | cacggaatct | cacagggtgc | tgagaattcc  | tcctcctggg  | actctcagag  | 60  |
| gatccagaac  | tgcagccggg | cctcgctttg | ctgtccctgt  | ccctgtccat  | gtatatgggc  | 120 |
| acgggtgctga | ggaacctgct | cagcatcctg | gctgtcagct  | ctgactcccc  | gctccacacc  | 180 |
| cccatgtgct  | tcttctcttc | caaactgtgc | tgagctgaca  | tcggtttcac  | cttgggccatg | 240 |
| gttcccaaga  | tgattgtgaa | catgcagtcg | catagcagag  | tcactctcta  | tgagggtctgc | 300 |
| ctgacacgga  | tgtctttctt | tgtccttttt | gcatgtatgg  | aagacatgct  | cctgactgtg  | 360 |
| atggcctatg  | actgctttgt | agccatctgt | cgccctctgc  | actaccaggt  | catcgtgaat  | 420 |
| cctcacctct  | gtgtcttctt | cgtcttgggt | tcctttttcc  | ttagcccgtt  | ggattcccag  | 480 |
| ctgcacagtt  | ggattgtgtt | actattcacc | atcatcaaga  | atgtggaaat  | cactaatttt  | 540 |
| gtctgtgaac  | cctctcaact | tctcaacctt | gcttgttctg  | acagcgtcat  | caataacata  | 600 |
| ttcataatatt | tcgatagtac | tatgtttggg | tttcttccca  | tttcagggat  | cctttttgtct | 660 |
| tactataaaa  | tgtccccctc | cattctaagg | atgtcatcgt  | cagatgggaa  | gtataaaggc  | 720 |
| ttctccacct  | gtggctctta | cctggcagtt | gtttgtgat   | ttgatggaaac | aggcattggc  | 780 |
| atgtacctga  | cttcagctgt | gtcaccaccc | cccagggaatg | gtgtggtggc  | gtcagtgatg  | 840 |
| tatgctgtgg  | tcacccccat | gctgaacctt | ttcatctaca  | gcctaggaaa  | gagggatata  | 900 |
| caaagtgtcc  | tgcggaggct | gtgcagcaga | acagtcgaat  | ctcatgatat  | gttccatcct  | 960 |
| ttttcttctg  | t          |            |             |             |             | 971 |

&lt;210&gt; 950

&lt;211&gt; 474

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g800 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 950

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atggaaccag | agaatggtac | gaggatttta | ggattttcttc | ttctgggact | ttcagaggaa | 60  |
| ccagaattgc | agcccgttat | gtttggactc | ttcctctcca  | tgtatctgac | aactgtgttt | 120 |
| ggaaacctgc | tcatcatcct | ggccatctgc | tctgggtccc  | acctccacac | ccccatgtac | 180 |
| ttcttctctc | ctaacctgtc | ctttgtagac | atctgtgtta  | cctccaccac | agtcccaaag | 240 |
| acactgtcaa | acatccggac | acagagtaaa | gtcatcacct  | atgcagggtg | catcacccag | 300 |
| atgtactttt | ttgtactctt | tatagtgttg | gacagcttac  | tcttgaccgt | gatggcctat | 360 |
| gaccagtttg | tggccatctg | tcacccctg  | cactacacgg  | tcacgtgaa  | ccctcggctc | 420 |
| tgtggactgc | tggttctggc | gtcctggatc | atgagtgcc   | tgaattcctt | gata       | 474 |

&lt;210&gt; 951

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g801 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 951

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| atgatgagct  | ttgcccctaa | tgttcacac  | tctccggttt  | ttttgtcct   | tgggttctcg | 60  |
| agagctaaca  | tctcctacac | tctcctcttc | ttcctgttcc  | tggctattta  | cctgaccacc | 120 |
| atactgggga  | atgtgacact | ggtgctgctc | atctcctggg  | actccagact  | gcactcacc  | 180 |
| atgtattatc  | tgtctcgttg | cctctctgtg | atagacatgg  | ggctatccac  | agttacactg | 240 |
| ccccagttgc  | tggcccattt | ggtctctcat | tacccaacca  | ttcctgctgc  | ccgtgcttg  | 300 |
| gctcagttct  | ttttcttcta | tgcatttggg | gttacagata  | cacttgctcat | tgtgtctatg | 360 |
| gctctggatc  | gctatgtggc | catctgtgac | cccctgcact  | atgctttggg  | aatgaatcac | 420 |
| caacgggtgtg | cctgcttact | agccttgagc | tgggtggtgt  | ccatactgca  | caccatgttg | 480 |
| cgtgtgggac  | tgtcctgcc  | tctttgctgg | actggggatg  | ctgggggcaa  | cgtaaacctt | 540 |
| cctcacttct  | tttgtgacca | ccggccactt | ctgcgagcct  | cctgttctga  | catacattct | 600 |
| aatgagctgg  | ccatattctt | tgagggtggc | ttccttatgc  | tggggccctg  | tgccctcatt | 660 |
| gtactctctt  | atgtccgaat | tggggccgct | attctacgtt  | tgccttcagc  | tgtgtgtcgc | 720 |
| cgccgagcag  | tctccacctg | tggatcccac | ctcaccatgg  | tgggttctct  | ctacggcacc | 780 |
| atcatttgtg  | tctacttcca | gcctcccttc | cagaactctc  | agtatcagga  | catggtggct | 840 |
| tcagtaatgt  | atactgccat | tacacctttg | gccaaacctat | ttgtgtatag  | cctccacaat | 900 |
| aaggatgtca  | agggtgcact | ctgcaggctg | cttgaatggg  | tgaaggtaga  | cccc       | 954 |

&lt;210&gt; 952

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g802 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 952

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| atgctgaata | caacctcagt | caccgaattt | ctcctcttgg  | gagtgcacaga | cattcaagaa | 60  |
| ctgcagcctt | ttctcttcgt | ggttttcttc | accatctact  | tcatcagtgt  | gactgggaat | 120 |
| ggagccgttc | tgatgattgt | catctccgat | cctagactcc  | attcccttat  | gtatttcttc | 180 |
| ctgggaaacc | tgtctacct  | ggatatctgt | tactctacgg  | tgacactgcc  | aaaaatgctg | 240 |
| cagaactttc | tctctacaca | caaagcaatt | tctttcttgg  | gatgcataag  | ccagcttcat | 300 |
| ttcttccact | tcctgggcag | cacggagtcc | atgttggttcg | ccgtgatggc  | atttgacctc | 360 |
| tctgtggcta | tcgcaagcc  | acttcgtac  | actgtcatca  | tgaacctca   | gctctgtacc | 420 |
| cagatggcca | tcacaatctg | ggtcattggg | ttttccatg   | ccctgctgca  | ctccgtaatg | 480 |
| acttctcgct | tgaacttctg | tggttccaac | cgtatccatc  | attttctctg  | tgatattaag | 540 |
| ccattgctaa | agctggcctg | tgggaacact | gagcttaatc  | agtggctact  | cagtactgtc | 600 |
| acggggacaa | ttgccatggg | ccccttcttt | ctgacacttc  | tctcctattt  | ctacattatc | 660 |

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| acttatctct | tcttcaagac | ccgttcttgt | agcatgctct | gtaaagcact  | gtccacttgt  | 720 |
| gcctcccact | tcattgtagt | tattcttttc | tatgcacctg | ttctttttcac | ctatatccat  | 780 |
| cctgcgttag | agagcttcat | ggaccaggac | cggattgttg | ccatcatgta  | cactgtgggtc | 840 |
| actcctgtac | taaaccact  | gatctatact | ttgaggaaca | aggaagtga   | gggggccttg  | 900 |
| ggtagagtga | tcagaaggct | t          |            |             |             | 921 |

&lt;210&gt; 953

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g803 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 953

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| cagccacgga | atctcacaga | tgtctgagaa | ttcctcctca | tgggactctc | agaggatcca  | 60  |
| gaactgcagc | ccgtcctcgc | tgggctgtcc | ctgtccatgt | atctggtcac | ggtgctgagg  | 120 |
| aacctgctca | gcaccttggc | tgtcagctct | gactcccacc | tccacacccc | catgtacttc  | 180 |
| ttcctctcca | acctgtgctg | ggctgacatc | ggtttcacct | cggccacggt | tcccaagata  | 240 |
| attgtggaca | tgcagtcgca | tagcagagtc | atctcttatg | tgggctgcct | gacacggatg  | 300 |
| tcttttttgg | tcctttttgc | atgtatagaa | gacatgcttc | tgactgtgat | ggcctatgac  | 360 |
| tgtttttag  | ccatctgtcg | ccctctacac | taccagtc   | tcgtgaatgc | tcacctccgt  | 420 |
| gtcttcttag | ttttggtgtc | ctttttcctt | agcctgttgg | attcccagct | gcacagttag  | 480 |
| attgtgttac | aattcacctt | cttcaagaat | gtggaaatct | ctaattttgt | ctgtgagcca  | 540 |
| tctcaacttc | tcaagcttgc | ctgttctgac | agcatcatca | atagcatatt | catatatctc  | 600 |
| gatagtacta | tgtttggttt | tcttccatt  | tcagggatcc | ttttgtctta | ctgtaaaatt  | 660 |
| gttccctcca | ttctaaggat | ttcaacatca | gatgggaaat | ataaagcctt | ctccacctgt  | 720 |
| ggctctcacc | tggcacttgt | ttgcttattt | tatggagcag | gcattggcgt | gtacctgact  | 780 |
| tcagctgtgt | caccaccccc | caggaatggt | gtgggtggtg | cagtgatgta | cactgtgggtc | 840 |
| accccatgc  | tgaaccctt  | catctacagc | ctgagaaaca | gggacattca | aagcaccctg  | 900 |
| cggaggctgc | tcagcagaac | agtcgaatct | catgatctgt | tccatccttt | ttcttgtgt   | 959 |

&lt;210&gt; 954

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g804 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (984)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 954

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| atggcacctg | gaaatggctc | tttcgtgact  | gaattcattc  | tggcgggatt  | aacacatcag | 60  |
| ccagatctcc | agtccctctc | gttcttctctg | tttctagtaa  | tctatgtggg  | cactctgttg | 120 |
| ggaaacttgg | gcttggtaac | tctaattggg  | ctgaactcac  | accttcatac  | ccccatgtac | 180 |
| ttcttctctc | tttaacttgc | cttcatagat  | ctctgttatt  | cttctgtgtt  | tatacccaaa | 240 |
| atgctaata  | actttatttc | agagaagaat  | attatgtcct  | tcaaggggtg  | catgacccaa | 300 |
| ctttcctttt | nctgattttt | ttgggtcattt | ctgaagggtta | tgtgctgacg  | tcaatggcgt | 360 |
| atgatcgctg | tggccatctg | taccccaactt | ctgtatcaca  | ttgccatgtc  | tcctacagtg | 420 |
| tgtccagacc | ttatgttttg | ttcctatttg  | atgccttttt  | ctgggtgccat | ggcccacact | 480 |
| ggatgcatgc | tgagactgac | tttctgtgat  | gcgaacacca  | tcgatcacta  | cttctgtgac | 540 |
| atcctccctc | tgtccagct  | ctcctgcacc  | agcacctaca  | tcaatgagct  | ggtgggtttc | 600 |
| actgtgggtg | gcacaaacat | cattgtgccc  | actgttacca  | tctttatctc  | ttatgggttc | 660 |
| atcctctcca | gcacccctca | tatcagttcc  | aaggagggtca | ggtccaaagc  | tttcagcact | 720 |
| tgcagttccc | atataattgc | tgtttctctg  | ttctttggat  | caggtgcatt  | tatgtatctc | 780 |
| aaccatctt  | ctgctgggtc | catggataag  | agaaaattat  | cttctgtctt  | ttatacaaat | 840 |
| gtggttccca | tgttgaaacc | cttaatctac  | agcctgagga  | acaaagatgt  | taaatttgcc | 900 |
| ctaagaaaag | ccctgagtag | taggaaactt  | tgataagtaa  | tagtatgtgt  | ctgtgtgtat | 960 |



agtcacaaga cagggatatt ctgt

984

&lt;210&gt; 955

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g805 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 955

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| atgggaagaa  | ataacctaac  | aagaccctct | gaattcatcc | tccttggact | ctcctctcga  | 60  |
| cctgaggatc  | agaagccgct  | ctttgctgtg | ttcctcccca | tctaccttat | cacagtgata  | 120 |
| ggaaacctgc  | ttatcatcct  | ggccatccgc | tcagacactc | gtctccagac | gcccatgtac  | 180 |
| ttctttctaa  | gcatcctgtc  | ttttgttgac | atttgctatg | tgacagtcac | tatccctaag  | 240 |
| atgctgggtga | acttcttata  | agagacaaag | accatctctt | acagtgaagt | tctgaccagg  | 300 |
| atgtactttt  | tcttagcctt  | tggaaacaca | gacagttacc | tgctagcagc | catggccatt  | 360 |
| gaccgctatg  | tggccatatg  | taatcccttc | cactacatca | ccattatgag | tcacagatgc  | 420 |
| tgtgtcctgc  | ttctggttct  | ctccttctgc | attccacatt | ttcactccct | cctgcacatt  | 480 |
| cttctgacta  | atcagctcat  | cttctgtgcc | tcaaagtgtc | tccatcactt | tttctgcgat  | 540 |
| gatcaaccag  | tgtctaaaatt | gtcctgttcc | tcccattttg | tcaaagaaat | cacagtaattg | 600 |
| acagaaggct  | tggctgtcat  | aatgaccccg | ttttcatgca | tcacatcttc | ttatttaaga  | 660 |
| atcctcatca  | ctgttctgaa  | gattccttca | gctgctggaa | agcgtaaagc | attttctacc  | 720 |
| tgtggctctc  | atctcacagt  | ggtgaccctg | ttttatggaa | gcattagcta | tctctatttt  | 780 |
| cagccctgtg  | ccaactatac  | tgtcaaggat | caaatagcaa | caattatcta | caccgtactg  | 840 |
| actcctatgc  | taaatccatt  | tatctatagt | ctgaggaaca | aagacatgaa | gcaggggttg  | 900 |
| gcaaagttga  | tgcacaggat  | gaaatgtcag |            |            |             | 930 |

&lt;210&gt; 956

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g806 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 956

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atggaaattg | tctccacagg | aaacgaaact | attactgaat  | ttgtcctcct | tggcttctat | 60  |
| gacatccctg | aactgcattt | cttggttttt | attgtattca  | ctgctgtcta | tgtcttcatc | 120 |
| atcataggga | atatgctgat | tattgtagca | gtgggttagct | cccagaggct | ccacaaacct | 180 |
| atgtatattt | tcttggcgaa | tctgtccttc | ctggatatcc  | tctacacctc | cgcagtgatg | 240 |
| caaaaaatgc | tggagggctt | cctgcaagaa | gcaactatct  | ctgtggctgg | ttgcttgctc | 300 |
| cagttcttta | tcttcggctc | tctagccaca | gctgaatgct  | tactgctggc | tgtcatggca | 360 |
| tatgaccgct | acctggcaat | ttgctaccca | ctccactacc  | cactcctgat | ggggcccaga | 420 |
| cgggtacatg | ggctgggtgg | cacaacctgg | ctctctggat  | ttgtggtaga | tggactgggt | 480 |
| gtggccctgg | tggcccagct | gaggttctgt | ggccccaacc  | acattgacca | gttttactgt | 540 |
| gactttatgc | ttttcgtggg | cctggcttgc | tggatccca   | gagtggctca | ggtgacaact | 600 |
| ctcattctgt | ctgtgttctg | cctcactatt | ccttttggac  | tgattctgac | atcttatgcc | 660 |
| agaattgtgg | tggcagtgtc | gagagttcct | gctggggcaa  | gcaggagaag | ggctttctcc | 720 |
| acatgctcct | cccacctagc | tgtagtgacc | acattctatg  | gaacgctcat | gatcttttat | 780 |
| gttgaccctt | ctgctgtcca | ttcccagctc | ctctccaagg  | tcttctccct | gctctacact | 840 |
| gtggtcaccc | ctctcttcaa | tctgtgatc  | tataccatga  | ggaacaagga | ggtgcatcag | 900 |
| gcacttcgga | agattctctg | tatcaaacaa | actgaaacac  | ttgat      |            | 945 |

&lt;210&gt; 957

&lt;211&gt; 565

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g807 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 957

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cactggaaaa | ttttaagaag | aaacagcaag | atgatacatg | aaattatata | gaccttatgc | 60  |
| caaatccttt | actcagagga | caaaacttgt | tacatacaga | tacaaagctt | gtttgtact  | 120 |
| gacttgga   | tcccaaactt | tttctgtgaa | cttaattagg | tggccacct  | tgctgttct  | 180 |
| gacacctttc | tcaaagacat | agtgaggtat | tgtacaacta | tgctgtgag  | tgggtgtccc | 240 |
| attgctggta | tttttttact | ctttctctaa | gatcatttca | tccatatgtg | caatcccatc | 300 |
| agctcagggg | aagcataaag | catttccac  | ctgcgtgtct | cacctctcaa | atatgtcctt | 360 |
| attttattgt | aggagcacag | gattgtacct | tagttttgct | gctaccaca  | actcatgctc | 420 |
| taatgcaact | gcctcagtga | ggcacactgt | ggttaaaccc | ttactaaacg | ttttcatctt | 480 |
| aaagtcaagt | aataaagaca | taaaatgagc | tctgaaagta | ttcttcagag | gaaagcaatg | 540 |
| gaagcatcat | ttttcaaaaa | gtgca      |            |            |            | 565 |

&lt;210&gt; 958

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g808 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 958

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| atggaaaaaa  | gaaatctaac  | agttgtcagg | gaattcgtcc | ttctgggact  | tcctagctca  | 60  |
| gcagagcagc  | agcacctcct  | gtctgtgctc | tttctctgta | tgtatttagc  | caccaccttg  | 120 |
| gggaacatgc  | tcattcattgc | gacgattggc | tttgactctc | acctccattc  | ccctatgtac  | 180 |
| ttcttccctta | gtaacttggc  | ctttgttgac | atctgcttta | cgctcgactac | agtcccccaa  | 240 |
| atggtagtga  | atatcttgac  | tggcaccaag | actatctctt | ttgcaggctg  | cctcaccacag | 300 |
| ctcttcttct  | tcgtttcttt  | tgtgaatatg | gacagcctcc | ttctgtgtgt  | gatggcgat   | 360 |
| gatagatatg  | tggcgatttg  | ccaccctta  | cattacaccg | ccagaatgaa  | cctgtgcctt  | 420 |
| tgtgtccagc  | tagtggctgg  | actgtggcct | gttacttacc | tccacgccct  | cctgcatact  | 480 |
| gtcctaatag  | cacagctgtc  | cttctgtgcc | tccaatatca | tccatcattt  | cctctgtgat  | 540 |
| ctcaatcctc  | tectgcagct  | ctctgtcctc | gacgtctcct | tcaatgtaat  | gatcattttt  | 600 |
| gcagtaggcg  | atctattggc  | tctcacgccc | cttctctgta | tctcgtatc   | ttatggactt  | 660 |
| atcttctcca  | ctgttctgaa  | gatcacctct | actcagggca | agcagagagc  | tgtttccacc  | 720 |
| tgcagctgcc  | acctgtcagt  | ggtggtgttg | ttttacggca | cagccatcgc  | cgtctatttc  | 780 |
| agcccttcat  | ccccccatat  | gcctgagagc | gacactctgt | caaccatcat  | gtattcaatg  | 840 |
| gtggctccga  | tgctgaatcc  | tttcatctat | accctaagga | acaggggat   | gaagagggga  | 900 |
| cttcagaaaa  | tgcttctcaa  | gtgcacagtc | tttcagcag  |             |             | 939 |

&lt;210&gt; 959

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g809 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 959

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| atggatggag  | gcaaccagag  | tgaaggttca  | gagttccttc | tcctggggat  | gtcagagagt  | 60  |
| cctgagcagc  | agcagatcct  | gttttggtatg | ttcctgtcca | tgtacctggg  | cacggtgggtg | 120 |
| ggaaatgtgc  | tcattcattc  | ggccatcagc  | tctgattccc | gcctgcacac  | ccccgtgtac  | 180 |
| ttcttctctg  | ccaacctctc  | cttcaactgac | ctcttctttg | tcaccaaacac | aatccccaaag | 240 |
| atgctgggtga | acctccagtc  | ccataacaaa  | gccattctct | atgcagggtg  | tctgacgcag  | 300 |
| ctctacttcc  | tgggtctcctt | ggtggccctg  | gacaacctca | tcctggctgt  | gatggcatat  | 360 |
| gaccgctatg  | tggccatctg  | ctgccccctc  | cactacacca | cagccatgag  | ccctaagctc  | 420 |
| tgtatcttac  | tcctttcctt  | gtgttggtgc  | ctatccgtcc | tctatggcct  | catacacacc  | 480 |
| ctcctcatga  | ccagagtgc   | cttctgtggg  | tcacgaaaaa | tccactacat  | cttctgtgag  | 540 |
| atgtatgtat  | tgctgaggat  | ggcatgttcc  | aacattcaga | ttaatcacac  | agtgtgtatt  | 600 |
| gccacaggct  | gcttcatctt  | cctcattccc  | tttggattcg | tgatcatttc  | ctatgtgctg  | 660 |
| attatcagag  | ccatcctcag  | aataccctca  | gtctctaaga | aatacaaagc  | cttctccacc  | 720 |
| tgtgcctccc  | atgtgggtgc  | agtctccctc  | ttctatggga | cactttgtat  | ggtataccta  | 780 |

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| aagccccctcc | atacctactc | tgtgaaggac | tcagtagcca | cagtgatgta | tgctgtgggtg | 840 |
| acacccatga  | tgaatccctt | catctacagc | ctgaggaaca | aggacatgca | tggggctctg  | 900 |
| ggaagactcc  | tagataaaca | ctttaagagg | ctgaca     |            |             | 936 |

&lt;210&gt; 960

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g810 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 960

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| atgggaatgt  | ccaacctgac | aagactctct | gaattttatct | tcttgggact | ctcctctcgg | 60  |
| tctgaagacc  | agaggccact | ctttgcccct | tttcttatca  | tatacctggg | cactttgatg | 120 |
| ggaaatctgc  | tcatcatctt | ggctatccac | tctgatccct  | gacttcaaaa | ccctatgtat | 180 |
| tttttcttaa  | gcatcttgtc | ctttgctgat | atttgctaca  | caacagtcac | agtcccaaa  | 240 |
| atgctcgtga  | acttcttatc | agagaaaaag | accatttctc  | atgctgaatg | tctggcacag | 300 |
| atgtatttct  | tcctgggttt | tggaacata  | gatagttatc  | tcctggcggc | tatggccatc | 360 |
| aaccgctgtg  | tagccatttg | taacccattc | cattatgtca  | ctgttatgaa | ccgcagatgc | 420 |
| tgtgtgttgc  | tactagcatt | ccccatcact | ttctcctatt  | tccactctct | cctacatgtc | 480 |
| ctcctgggtga | atcggtcac  | cttttgtaca | tcaaatgtta  | tccatcattt | tttttgtgat | 540 |
| gtcaaccctg  | tgctgaaact | gtcctgtctc | tccacctttg  | tcaatgaaat | tgtggccatg | 600 |
| acagaagggc  | tggtctctgt | gatggctcca | tttgtctgta  | tcatcatctc | ttatctaaga | 660 |
| attctcatcg  | ctgttctcaa | gattccctca | gcagctggaa  | aacacaaagc | cttctccacc | 720 |
| tgagctccc   | atctcactgt | ggtgattctg | ttttatggga  | gtattagcta | tgctctattg | 780 |
| cagcctttgt  | ccagctatac | tgtcaaggac | cgaatagcaa  | caatcaacta | cactgtgttg | 840 |
| acatcagtg   | tgaacccatt | tatctacagt | ttaagaaaca  | aagacatgaa | acggggctta | 900 |
| cagaaattga  | taaacaagat | taagtctcaa | atgagtaggt  | tctctacaaa | g          | 951 |

&lt;210&gt; 961

&lt;211&gt; 926

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g811 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 961

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atgctgaata | caacctcagt | cactgaattt | ctccttttgg | gagtgcaga  | cattcaagaa  | 60  |
| ctgcagcctt | ttctcttcgt | tgttttcctt | accatctact | tcatcagtg  | ggctgggaat  | 120 |
| ggagccattc | tgatgattgt | catctctgat | cctagactcc | attccccat  | gtattttctt  | 180 |
| ctgggaacc  | tgctctgctt | ggacatctgc | tactccagcg | taacactgcc | aaaaatgctg  | 240 |
| cagaacttcc | tctctgcaca | caaagcaatt | tctttcttgg | gatgcataag | ccaactccat  | 300 |
| ttcttccact | tcctgggcag | cacagaggcc | atgttgttgg | ccgtgatggc | atttgaccgc  | 360 |
| tttgtggcta | tttgcaagcc | acttcgctac | actgtcatta | tgaacctca  | gctctgtacc  | 420 |
| cagatggcca | tcacaatctg | gatgattgg  | tttttccatg | ccctgctgca | ctccctaattg | 480 |
| acctctcgct | tgaacttctg | tggttctaac | cgtatctatc | acttcttctg | tgatgtgaag  | 540 |
| ccattgctaa | agctgagctt | aatcagtggc | tgctcagtac | tgctcacagg | acaatcgcca  | 600 |
| tgggcccctt | ctttctcaca | ttactctcct | atttctacat | tatcacccat | ctcttcttca  | 660 |
| agactcatte | ttttagcatg | ctccgcaaag | cactgtccac | ttgtgctccc | cacttcatgg  | 720 |
| tagttattct | tttgtatgca | cctgttctct | tcacctatat | tcatcatgcc | tcagggaact  | 780 |
| ccatggacca | ggaccggatc | actgccatca | tgtatactgt | ggctactcca | gtactaaacc  | 840 |
| cactgatcta | cactttgagg | aacaaggaag | tgaaaggggc | ctttaataga | gcaatgaaaa  | 900 |
| ggtggctttg | gcctaaagaa | atcttg     |            |            |             | 926 |

&lt;210&gt; 962

&lt;211&gt; 983

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g812 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 962

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| tcagtggacc | aagtaaata  | ctctctggta | acagaatttg | tattacttgg | acttgcacaa  | 60  |
| tccttggaaa | tgcagttttt | cctttttctc | ttcttctctt | tattctatgt | gggaattatc  | 120 |
| ctgggaaacc | tcttcattgt | gttcacagtg | atctttgatc | ctcacttaca | ctcccccattg | 180 |
| tatattctgc | tggccaacct | atcgctcatt | gacttgagcc | tttcatctac | cacagttcct  | 240 |
| aggttgatct | acgatctttt | tactgattgt | aaagtatttt | ccttccataa | ttgtatgata  | 300 |
| caaaagttct | ttatccatgt | tacgggagga | gttgaaatgg | tgctgctgat | agtcattggaa | 360 |
| tatgataggt | acactgcgat | ctgcaagcct | ctccactatc | caactattat | gaatcccaaa  | 420 |
| atgtgcatgt | ttttggtagc | agcagcttgg | gtcattgggg | tgattcatgc | tatgtctcag  | 480 |
| tttgtttttg | tcataaatta | accttctgtg | gccctaataa | tgtggggagc | ttttattgtg  | 540 |
| atcttctctg | ggttattaaa | cttgcattga | tggacactta | cgggctagaa | tttgtggtca  | 600 |
| ctgccaacag | tggattcata | tcgatgggca | ccttcttttt | cttaattgta | tcatacattt  | 660 |
| ttattctggg | cactgtccaa | cgacattcct | caaattgatt | atccaaagca | ttcttcactt  | 720 |
| cgtaggctca | catcaccgta | gtggttttgt | tttttgcctc | atgcatgttt | ctctacgtgt  | 780 |
| ggcctttccc | tactaagtca | ttggataaat | tttttggcat | catgaacttt | gttgtcacc   | 840 |
| ctgtcttaaa | tcctgccatc | tatactttaa | ggaacaaaga | tatgaagttt | gcaatgagaa  | 900 |
| ggctgaatca | acataattta | aattctatgg | agacgacata | acacatttgg | ttgatgagag  | 960 |
| cacaggataa | atgccatgga | cca        |            |            |             | 983 |

&lt;210&gt; 963

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g813 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 963

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| atgtggatca  | acaatcaaag | ctcgctagat | gattttatcc  | tattgggatt | ttctgaccgt | 60  |
| ccctggctag  | agacacccct | ctgtaatctt | tctgggtggc  | tacatctttt | ccctatttgg | 120 |
| aaatatctcc  | attatcctag | tttcccatct | ggatccccag  | cttgacagtc | ccatgtactt | 180 |
| ttttgtctct  | aattctatct | ttctggacct | ctgctatacc  | accagcactg | tcccacagat | 240 |
| gctgggtcaac | ctccggggac | cagaaaagac | catttagctat | gggggttgtg | ttgcccact  | 300 |
| ctatatatct  | ttggccctgg | gttctactga | atgcatactt  | ctagccatca | tggcctttga | 360 |
| ccgttacgct  | gccatagca  | agcccttca  | ctaccagtc   | atcatgaacc | atagacgctg | 420 |
| tatccacatg  | gctgctggca | cttggatcag | tggctttgct  | aactcccttg | tccagtccac | 480 |
| tctcacagtg  | gtggccccaa | gatgtggaca | gaggggtgtg  | gaccatttct | tctgtgaagt | 540 |
| tccagccctt  | ttgaaactag | cctgtattga | tattcgtgtg  | aatgaaatgg | agctcaatgt | 600 |
| actagggcgt  | ttgcttctcc | tgatgccact | caccctcatc  | ctgggcactt | atgtgttcat | 660 |
| tgctcaggca  | gtaatgagaa | tctgctctgc | tgaaagtcgc  | tggagggtct | tcaatacctg | 720 |
| tgctcaccat  | ttgctggtgg | tctccctctt | ctacttcaca  | gccatcagta | tgtatgtcca | 780 |
| gcctccctct  | agctattctc | atgaccgggg | gaagatc     |            |            | 817 |

&lt;210&gt; 964

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g814 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 964

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| atgaatgtct | ctgagccaaa  | ttccagcttt | gcttttgtaa  | atgaatttat | actccaaggt  | 60  |
| ttctcttgtg | agtggacaat  | tcagatcttc | ctcttctcac  | tctttactac | aacatattgca | 120 |
| ctgactataa | cagggaaatgg | agccatttgc | tttgtcctgt  | gggttgaccg | gcgacttcac  | 180 |
| actcccatgt | acatgttctt  | gggaaatttc | tccttttttag | agatatggta | tgtctcttct  | 240 |
| acagttccca | agatgttggg  | caacttctct | tcagagaaaa  | aaaacatctc | ctttgctgga  | 300 |
| tgttttctcc | agtttttattt | cttcttctct | ttgggtacat  | cagaatgctt | gcttttgact  | 360 |

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| gtgatggcct | ttgatcagta  | ccttgcctatc | tgccgtccct | tgctctatcc  | taatatcatg | 420 |
| actgggcatc | tctatgccaa  | actgggcata  | ctgtgctggg | tttgtggatt  | tctgtgggtc | 480 |
| ctgateccca | ttgttctcat  | ctctcagatg  | cccttctgtg | gccccaaacat | tattgaccat | 540 |
| gttgtgtgtg | accaggggcc  | acgatttgca  | ttggattgtg | tttctgcccc  | aagaatccaa | 600 |
| ctgttttctg | acactcctaag | ctcattagtt  | atTTTTggtg | acttctctct  | tattattgga | 660 |
| tcctatactc | ttgtcctgaa  | agctatgttg  | ggtatgcctt | caagcactgg  | gagacataag | 720 |
| gccttctcta | cctgtgggtc  | tcatttggct  | gtggtatcac | tgtgctatag  | ctctcttatg | 780 |
| gtcatgtatg | tgagcccagg  | actcggacat  | tctacaggga | tgcagaaaat  | tgaaactttg | 840 |
| ttctatgcta | tggtgacccc  | actcttcaat  | ccccttatct | atagcctcca  | gaataaggag | 900 |
| ataaaggcag | ccctgaggaa  | agttctgggg  | agttccaaca | taatc       |            | 945 |

&lt;210&gt; 965

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g815 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 965

|             |             |             |             |             |            |     |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| atggtgactg  | aattcatttt  | tctgggtctc  | tctgattctc  | agggactcca  | gaccttccta | 60  |
| tttatgttgt  | tttttgtatt  | ctatggagga  | atcgtgtttg  | gaaaccttct  | tattgtcata | 120 |
| acagtgggat  | ctgactccca  | ccttcactct  | cccattgtact | tcctgctagc  | caacctctca | 180 |
| ctcattgata  | tgtctctgtc  | ttcagtcaca  | gcccccaaga  | tgattactga  | cttttccagc | 240 |
| cagcgcaaag  | tcattctctt  | caagggctgc  | cttgttcaga  | tatttctcct  | tcacttcttt | 300 |
| ggtgggagtg  | agatgggtgat | cctcatagcc  | atgggctatg  | acagatatat  | agcaatatgc | 360 |
| aaaccactaa  | actacactac  | aattatgtgt  | ggcaacgcat  | gtgtcggcat  | tatggctgtc | 420 |
| gcatggggaa  | ttggctttct  | ccattcgggtg | agccagttgg  | cctttgccgt  | gcacttaccc | 480 |
| ttctgtggtc  | ccaatgaggt  | cgatagtttt  | tattgtgacc  | ttcctagggt  | aatcaaactt | 540 |
| gcctgtacag  | atacctacag  | gctagatatt  | atggtcattg  | ctaacagtgg  | tgtgctcact | 600 |
| gtgtgtttct  | ttgttcttct  | aatcatctca  | tacactatca  | tcctaattgac | catccagcat | 660 |
| cgcccttttag | ataagtcgtc  | caaagctctg  | tccactttga  | ctgtctacat  | tacagttagt | 720 |
| cttttgttct  | ttggaccatg  | tgtctttatt  | tatgcctggc  | cattccccat  | caagtcatta | 780 |
| gataaattcc  | ttgctgtatt  | ttattctgtg  | atcacccctc  | tcttgaacce  | aattatatac | 840 |
| acactgagga  | acaaagacat  | gaagacggca  | ataagacagc  | tgagaaaatg  | ggatgcacat | 900 |
| tctagtgtaa  | agttt       |             |             |             |            | 915 |

&lt;210&gt; 966

&lt;211&gt; 953

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g816 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 966

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| atgacattac | ccagcgatga | ctccactgtc  | ccagtctctg | aattcctcct  | catctgcttc | 60  |
| cccaactttc | agagttggca | gcacttgctg  | tccttgcccc | tcagcctcat  | ttcctcctgg | 120 |
| ccatggggac | caacacccac | cccccccatc  | accatccacc | tgagggcctc  | tctgcacctg | 180 |
| cccctgtact | acctgcccag | cctcctctcc  | ctgctggaca | tcgtgctctg  | cctcaccgtc | 240 |
| atccccagg  | tcctggccat | cttctggttt  | gatcttaggt | cgatcggett  | ccctgcctgc | 300 |
| ttccttcaga | tgttcatcat | gaacagtttc  | ctccccatgg | agtcctgcac  | attcatggtc | 360 |
| aaggactatg | atcattatgt | ggccatctgc  | cacccactgc | agtacctgtc  | catcatcact | 420 |
| catcaatttg | tggccaaagc | tagtgtcttc  | attgtgggtg | agaatgcttt  | gctgctttca | 480 |
| cctgttccta | ttctctctgc | ccagctccat  | tactgtagga | aaaatgtgat  | tgagaactgc | 540 |
| atctgtgcca | acctgtctgt | gtccaggctc  | tcctgtgata | atttcaccct  | taacagactc | 600 |
| taccaatttg | tggctgggtg | gaccttctctg | ggctcggatt | tcatectcat  | cttctctctc | 660 |
| tacaccttca | ttctaagagc | tgtgcttaga  | ttcaagggtg | aggggggtggc | agtgaaggcc | 720 |
| ctgagcacat | gtggctccca | ctttatectc  | atcctcttct | tcagcacctg  | ctggttgttg | 780 |
| tgttgacaaa | tgtggccaga | aagaaggtec  | ccatggacat | cctgatectg  | tttaatgtcc | 840 |
| ttcatccctt | tagtctctct | gcattaaacc  | ctatcatatg | tggatttcaa  | actaaagagt | 900 |

taaagaagga attttagaag ttgctgcaga ggggcctttg aaaacacgga agg

953

<210> 967

<211> 954

<212> DNA

<213> Unknown (H38g817 nucleotide)

<220>

<223> Synthetic construct

<400> 967

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| aaacacaatc | acacggcagt | gaccaagggtg | actgaattta  | ttctcatggg  | gattacagac  | 60  |
| aaccctgggc | tgcaggctcc | actgttttga  | ctcttctca   | tcatatatct  | ggtcacagt   | 120 |
| ataggcaatc | tgggcatggg | tatctttgac  | ctactttgga  | ctccaagcta  | cacaccccca  | 180 |
| tgtacttttt | ccttaaacad | ttggcaatca  | ctgatctttg  | gttactccac  | tgtcattggg  | 240 |
| ccccaaagat | gtttagtga  | acctcatatg  | tgcacaaaga  | acacaatttc  | ttttacaatt  | 300 |
| ggtatgcaa  | tcacagagca | cgttttgaga  | ggaacatcat  | ctctcaccgc  | ggcattctat  | 360 |
| cagcaacgaa | caatgagccc | tacaaacca   | tcactaaaca  | acttctgaac  | ccgatcatca  | 420 |
| tgccagagaa | aatacgggag | gagcaataaa  | ccgttcccga  | gctcgataaa  | acgtgtgcgc  | 480 |
| cactatttct | caaaaggaag | tgagtcaaaa  | cagtctccac  | caaccacagac | acaaccaaca  | 540 |
| attgtcacgg | tgaagggacc | gctaaaatgt  | gaatactccg  | ttctgaaaaa  | aagaaaataa  | 600 |
| caataataaa | ggcgatgacc | gcaggaaacc  | aacatgctca  | tctccctctc  | aattgttctc  | 660 |
| atatectaca | tgtttattct | agtggccaat  | ctcagaatga  | actcaaggaa  | agggagggtac | 720 |
| aaagccttct | ccacctgtag | ctctcatctg  | acagtgggtga | tcatgttcta  | tgggacattg  | 780 |
| ttattttatt | acttgcaacc | caagtccagt  | catactttgg  | ctattgataa  | aatggcctca  | 840 |
| gtgttttata | ccctgttgat | tcctatgctg  | aatccgttga  | tctacagcct  | aaggaacaaa  | 900 |
| gaagtaaaag | atgctctaaa | gagaacttta  | accaatcgat  | tcaaaattcc  | catt        | 954 |

<210> 968

<211> 660

<212> DNA

<213> Unknown (H38g818 nucleotide)

<220>

<223> Synthetic construct

<400> 968

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| tccaacctgt | gctgggctga  | catcggtttc  | acctcgggcca | tgggtcccaa | gatgattgtg | 60  |
| gacatgcagt | ctcatagcag  | agtcattccct | tatgcgggct  | gcctgacacg | gatgtctttc | 120 |
| ttggctcctt | ttgcatgtat  | agaagacatg  | ctcctgactg  | tgatggccta | tgactgcttt | 180 |
| gtagccatct | gtcgccctct  | gcactacca   | gtcatcatga  | atcctcacct | ctgtgtcttc | 240 |
| ttcgtttttg | tgtccttttt  | ccttagcctg  | ttggattccc  | agctgcacag | ttagattgtg | 300 |
| ttacaattca | ctttcttcag  | taatgtggaa  | attgctaatt  | ttgtctatga | gccatctcaa | 360 |
| cttctcaacc | ttgactgttc  | tgacaccgtc  | atcaatagca  | tatttatata | tttcgatagt | 420 |
| actgttttgt | tttcttccca  | tttcagggat  | cctttgtctt  | agtataaaat | tgtccctctc | 480 |
| attctaagga | tgatcatcgt  | agatgggaag  | tataaagcct  | tcgccacctg | tggtctctac | 540 |
| ctagcagttg | tttgctgatt  | tgatggaaca  | ggcattggca  | tgtacctgac | ttcagctgtg | 600 |
| tcaccacccc | ccagggaatgg | tgtggcgggc  | tcagtgtatg  | acgtgtgggt | caccccatg  | 660 |

<210> 969

<211> 933

<212> DNA

<213> Unknown (H38g819 nucleotide)

<220>

<223> Synthetic construct

<400> 969

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atggaaaaaa | gcaataatag  | cactttgttt | attctcttgg | ggttttccca | aaataagaac | 60  |
| attgaagtcc | tctgctttgt  | attatttttg | ttttgctaca | ttgctatttg | gatgggaaac | 120 |
| ttactcataa | tgattttctat | cacgtgcacc | cagctcatcc | accaaccat  | gtatttcttc | 180 |

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| ctcaattacc | tctcactctc | cgacctttgc | tacacatcca | cagtgacccc | caaattaatg  | 240 |
| gttgacttac | tggcagaaag | aaagaccatt | tcctataata | actgtatgat | acaactcttt  | 300 |
| accacccatt | tttttggagg | catagagatc | ttcatttctc | cagggatggc | ctatgaccgc  | 360 |
| tatgtggcca | tttgcaagcc | cctgcactac | accattatta | tgagcaggca | aaagtgtaac  | 420 |
| acaatcatca | tagtttgttg | tactggggga | tttatacatt | ctgccagtca | gtttcttctc  | 480 |
| accatctttg | taccattttg | tggcccaa   | gagatagatc | actacttctg | tgatgtgtat  | 540 |
| cctttgctga | aattggcctg | ttctaata   | cacatgatag | gtctcttagt | cattgtctaat | 600 |
| tcaggcttaa | ttgctttggg | gacatttgtt | gtcttgttgt | tgtcttatgt | ttttatattg  | 660 |
| tatacatca  | gagcatactc | tgcagagaga | cgcagcaaag | ctcttgccac | ttgtagttct  | 720 |
| catgtaattg | ttgtggctct | gttttttgct | cctgcattgt | tcatttacat | tagaccgggc  | 780 |
| acaacattct | cagaagataa | agtgtttgcc | cttttttata | ccatcattgc | tcccattgtc  | 840 |
| aacctctca  | tatacacgct | gagaaacaca | gagatgaaga | acgccatgag | gaaagtgtgg  | 900 |
| tgttgtcaaa | tactcctgaa | aagaaatcaa | ctt        |            |             | 933 |

&lt;210&gt; 970

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g820 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 970

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| cggaacttct  | ctttcttaga  | aatctcattt | acaaccgtat | gcacccccag | atttctgggg | 60  |
| gcaattatca  | ccaggaataa  | gactattttc | tataacaact | gtgcagccca | actctttttc | 120 |
| tttatcttca  | tgggggtgac  | tgaattttac | attttaactg | ccatgtccta | tgaccgctat | 180 |
| gttgccatct  | gcaagccctc  | tcattacaca | tccatcatga | acaggaaact | ctgcactcta | 240 |
| cttggtgctgt | gtgcctggct  | aagtgggttt | cgcaccattt | tcccacccct | tatgtctctc | 300 |
| ctccagctgg  | actactgtgc  | ttccaacgct | attgatcact | ttgcatgtga | ctattttccc | 360 |
| ctcttacaac  | tatcttgttc  | agatacatgg | ctcctagaag | taattgggtt | ttactttgct | 420 |
| ttggttactt  | tgctgttcac  | tttggcatta | gtgattttat | cttacatgta | cattatcagg | 480 |
| accattttga  | gaatcccgct  | tgccagtc   | agaaaaaagg | ctttctccac | ttgttcttct | 540 |
| cacatgattg  | tcattttccat | ttcttatgga | agctgtatat | tcatgtatgc | taatccatct | 600 |
| gcaaaagaaa  | aggcatcatt  | gacaaaagga | atagctattc | tcaatacatc | tgttgcccc  | 660 |
| atgctg      |             |            |            |            |            | 666 |

&lt;210&gt; 971

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g821 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 971

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| ataattttgt  | gttttttcat  | cataggtaac  | tctcaggata  | attcccaa   | gactttgatg | 60  |
| gataacattt  | cagaagtgac  | agaattcggt  | ctcgtggggg  | taacagatgt | cctagagctt | 120 |
| cagggtccctt | tatttatcat  | ctttactgtc  | atttatctca  | ccactctggg | tgggaacttt | 180 |
| gggatgatca  | tgttgattct  | gttggaactc  | cgggtccaca  | ttcccagta  | ctttttcctt | 240 |
| ggcaaaactct | ctctgggtgga | cagtgtttgt  | cctgctagtc  | actggctcct | acatctgtgg | 300 |
| actctttcaa  | tctccatcc   | atgttgcttt  | tactttccat  | ctctccttct | gtcattctaa | 360 |
| tgtgggtta   | cacttttttt  | gtgatattcc  | accactctta  | gctctttctt | gctctgat   | 420 |
| ttacgcacat  | gagattgtgc  | tcttcatatt  | ggcagcattt  | aatatctttt | tcactctctt | 480 |
| gattatcttg  | aactcttatg  | tttttatttt  | tatttgctatc | ctgaggatgc | attcagctga | 540 |
| gggacaaaag  | aagggtctttt | ccacctgtgc  | ctatcacctc  | actactgttt | ccatcttcta | 600 |
| tgggacaate  | acctttatgt  | acttacagcc  | aagttctggg  | cattccatgg | acacagacaa | 660 |
| aatctcatct  | gtgttctaca  | ccatgggtcat | ccccatgctt  | aacctcttag | tctatagcct | 720 |
| gaggaacaaa  | gaagtccaga  | gtgcattcaa  | ggtggttatt  | ggaaaagcaa | agtcttcatt | 780 |
| gggcttagcc  | tactatttta  |             |             |            |            | 799 |

&lt;210&gt; 972

<211> 946  
 <212> DNA  
 <213> Unknown (H38g822 nucleotide)

<220>

<223> Synthetic construct

<400> 972

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tggtaacctg | tcttcaacca | gtctgcccc  | ctgagtttgt | gttccgtgtg | ttcaccacag | 60  |
| tccctgaatt | tcagggttct | ctcttccttc | tcttcctcct | cttctacttg | atgatectct | 120 |
| gtggcaacac | agccatcatc | tgggttgtgt | gcacatacag | cgttctccga | acccaatgt  | 180 |
| atttcttctt | gtccaacctg | tcctttgtag | agatctgcta | caccaccgtt | gtggtgccct | 240 |
| tgatgcttcc | caacattttt | ggggcccaga | agccatttcc | attggctgga | tgtggggccc | 300 |
| aaatgttctt | ctttctcaca | cttgggtggt | ctgactgttt | cctcttggcg | atcgtggcct | 360 |
| atgaccgcta | tgtggccatc | tgccaccctt | tgcactaccc | ctcatcatga | cctgcaatct | 420 |
| gtgcgtgcag | atgctgggcg | gcgctgtggg | cctggccctc | ttcctctccc | tgcagctcac | 480 |
| cgccttaate | ttcaccttgc | ccttctgcgg | ctaccgccag | gaaattaacc | acttctcttg | 540 |
| cgatgtacct | cccgctcctg | gcctggcctg | cgtgccatc  | cgtgttcacc | aggctgtcct | 600 |
| ctatgtcgtg | agcatcctcg | tgtgaccgt  | ccccttcttg | ctcatctgcg | tctcctacgt | 660 |
| gttcatcacc | tgtgccatcc | tgagcatccg | ttctgctgag | ggccgccacc | aggccttctc | 720 |
| cacctgctcc | tcccacctca | ccgtggctct | gctgcagtat | ggctgctgtg | ccttggcata | 780 |
| cttgcacccc | cagtccagct | cctctgcaga | tgaggatcgc | cagtttgccc | ttgtttacac | 840 |
| ctttatcaca | ccattactca | accctttgat | ttacaccctt | aggaacaagg | atgtcaaagg | 900 |
| tgcccttgaa | aaaagtgtc  | agtaccaaag | ggacacctga | gtcctt     |            | 946 |

<210> 973

<211> 936

<212> DNA

<213> Unknown (H38g823 nucleotide)

<220>

<223> Synthetic construct

<400> 973

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| atgtagaaca | gtagagaggc | gtcacagttc | atcttcctag  | gactaagcaa  | tgtcccagaa  | 60  |
| ctgcagggtc | ccttctttat | catgtttgtt | ctcatctatc  | tcataaatgt  | agttggaaac  | 120 |
| ttggggatga | tcattttgat | tctctggtac | tctcagctcc  | acaatccaat  | gtacttcttc  | 180 |
| ttcagtaate | tgtctctggt | agactttttt | tactcttcag  | ttgtcactcc  | aaaggctcatg | 240 |
| actgggctcc | ttagagaaga | caaaatcatt | tcctatactg  | tgtgggctac  | tcagacattc  | 300 |
| ttttctgatt | cctttgccag | tgtggtaaat | ttattattgg  | ccttaatggc  | ctctggccac  | 360 |
| tatgcagcag | tgtgcaaacc | cctgcattac | accaccacca  | tgatgacaag  | tgtgtgtaca  | 420 |
| tgtctggcca | taggttgata | cgttggtggt | ttcctgaatg  | cctccattca  | cactggggaa  | 480 |
| acattcagtc | tctttctgta | tgtccagtga | agtccatcac  | ttttctctgt  | aggttccagc  | 540 |
| agtcatggct | ctgtcttgct | ctgatagaca | tgtgaatgta  | gtgggttcttg | tttatgtaac  | 600 |
| cagctcaata | tctcttttgc | ccttctagtt | atcttgatat  | cctacttatt  | gatgtttatc  | 660 |
| accatcctaa | agatgcactc | aactgcagga | taccagaagg  | ctttggccat  | ttgtgcctct  | 720 |
| cacctcactg | cagttgccat | cttctatggg | actattatct  | tcatgcatat  | acagcccagc  | 780 |
| tccagtcatt | ccattgacac | agacaaaatt | gcagctgtgt  | tttatactat  | tgtcttcccc  | 840 |
| atggtgaacc | atgtggtcta | aagattgaag | aacaagggtga | agagtacatt  | caagaaaatt  | 900 |
| gttgagaagg | taaaattgtc | cctaggattg | tgagtt      |             |             | 936 |

<210> 974

<211> 954

<212> DNA

<213> Unknown (H38g824 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(954)



&lt;223&gt; n = A,T,C or G

&lt;400&gt; 974

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atggctgggg | aaaaccatac | tacactgcct  | gaattcctcc | ttctgggatt | ctctgacctc | 60  |
| aaggccctgc | agggccccct | gttctgggtg  | gtgcttctgg | tctacctggt | caccttgctg | 120 |
| ggtaactccc | tgatcatect | cctcacacag  | gtcagccctg | ccctgcactc | ccccatgtac | 180 |
| ttcttcctgc | gccaactctc | agtgggtggag | ctcttctaca | ccactgacat | cgtgcccagg | 240 |
| accctggcca | atctgggctc | cccgcatccc  | caggccatct | ctttccaggg | ctgtgcagcc | 300 |
| cagatgtacg | tcttcattgt | cctgggcata  | tcggagtgtc | gcctgctcac | ggccatggcc | 360 |
| tatgaccgat | atgttgccat | ctgccagccc  | ctacgctatt | ccacctctt  | gagcccacgg | 420 |
| gcctgcatgg | ccatgggtgg | tacctctctg  | ctcacaggca | tcatacggg  | ccaccacca  | 480 |
| tgcctccctc | atcttctctc | tacctttctg  | cagccaccgg | atcatcccg  | actttctctg | 540 |
| tgacatectg | ccagtactga | ggctggcaag  | tgctgggaag | cacaggagcg | agatctccgt | 600 |
| gatgacagcc | accatagtct | tcattatgat  | ccccctctct | ctgattgtca | cctcttacat | 660 |
| cgcacatctg | ggtgccaatc | tagcaatggg  | cctcaccacg | agccgccgca | agtcttctcc | 720 |
| acctgctcct | cccataggct | cgtggctctc  | ctcttctttg | ggacagccag | catcacnnac | 780 |
| aaccggccgc | aggcaggctc | ctctgaaacc  | acagaccgcg | tcatacgtct | cttcnacaca | 840 |
| gtcatcacac | ccatgctcaa | ccccatcata  | aacacccacg | ggaacaagga | cgtgaggagg | 900 |
| gccctgcggt | acttggtgaa | gaggcggcgc  | ccctcgccgg | gaaggggctc | gggt       | 954 |

&lt;210&gt; 975

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g825 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 975

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| atggagacaa | agaattatag | cagcagcacc | tcaggcttca | tcttcctggg  | cctctcttcc  | 60  |
| aaccctaagc | tgcagaaacc | tctcttttgc | atcttctca  | tcatagtacct | actcactgcg  | 120 |
| gtggggaatg | tgctcatcat | cctggccatc | tactctgacc | ccaggctcca  | cacccctatg  | 180 |
| tacttttttc | tcagcaactt | gtctttcatg | gatattctgt | tcacaacagt  | catagtgcct  | 240 |
| aagatgctgg | tgaattttct | atcagagaca | aagattatct | cttatgtggg  | ctgcctgatc  | 300 |
| cagatgtact | tcttcatggc | atttgggaac | actgacagct | acctgctggc  | ctctatggcc  | 360 |
| atcgaccggc | tggtggccat | ctgcaacccc | ttacactatg | atgtggttat  | gaaaccatgg  | 420 |
| cattgcctac | tcatgctatt | gggttcttgc | agcattctcc | acctacattc  | cctgttccgc  | 480 |
| gtgctactta | tgtctcgctt | gtctttctgt | gcctctcaca | tcattaagca  | ctttttctgt  | 540 |
| gacacccagc | ctgtgctaaa | gctctcctgc | tctgacacat | cctccagcca  | gatggtgggtg | 600 |
| atgactgaga | ccttagctgt | cattgtgacc | cccttctgt  | gtaccatctt  | ctcctacctg  | 660 |
| caaatcatcg | tcactgtgct | cagaatcccc | tctgcagcca | ggaagtggaa  | ggccttctct  | 720 |
| acctgtggct | cccacctcac | tgtagtggct | ctgttctatg | ggagtgtcat  | ctatgtctat  | 780 |
| tttaggcctc | tgtccatgta | ctcagtgatg | aagggcggg  | tagccacagt  | tatgtacaca  | 840 |
| gtagtgcac  | ccatgctgaa | ccctttcatc | tacagcctga | ggaacaaaga  | tatgaaaagg  | 900 |
| ggtttgaaga | aattaagaca | cagaatttac | tca        |             |             | 933 |

&lt;210&gt; 976

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g826 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 976

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atgaaaaata | aaaccgtgtt | aactgagttt  | atccttctgg | gtctaacaga | tgtccctgaa | 60  |
| ctccagggtg | cagttttcac | ctttcttttc  | cttgcgtatt | tactcagcat | ccttggaat  | 120 |
| ctgactatcc | tcacctcac  | cttgcctggac | tcccaccttc | agactcccat | gtatttcttt | 180 |
| ctccggaact | tctccttctt | ggaaatttcc  | ttcacaaaca | tcttcattcc | aagggtcctg | 240 |
| attagcatca | caacagggaa | caagagtatc  | agcttttctg | gctgcttcac | tcagtatttc | 300 |
| tttgccatgt | tccttggggc | tacagagttt  | taccttctgc | tgccattcct | atgaccgcta | 360 |

tgtgccatct gcaaactgat gactatgcac

390

&lt;210&gt; 977

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g827 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 977

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| atggagataa  | agaactacag  | cagcagcacc  | tcaggcttca | tcctcctggg  | cctctcttcc | 60  |
| aaccctcagc  | tgcagaaacc  | tctctttgcc  | atcttctcca | tcattgtacct | gctcgtgcg  | 120 |
| gtggggaatg  | tgctcatcat  | cccggccatc  | tactctgacc | ccaggctcca  | caccctatg  | 180 |
| tacttttttc  | tcagcaactt  | gtctttcatg  | gatatctgct | tcacaacagt  | catagtgcct | 240 |
| aagatgctgg  | tgaattttct  | atcagagaca  | aaggttatct | cctatgtggg  | ctgcctggcc | 300 |
| catagtgtact | tctttatggc  | atttgggaac  | actgacagct | acctgctggc  | ctctatggcc | 360 |
| atcgaccggc  | tggtggccat  | ctgcaacccc  | ttacactatg | atgtgggttat | gaaaccacgg | 420 |
| cattgcctgc  | tcattgctatt | gggttcttgc  | agcatctccc | acctacattc  | cctgttccgc | 480 |
| gtgctactta  | tgtctcgctt  | gtctttctgt  | gcctctcaca | tcattaagca  | ctttttctgt | 540 |
| gacaccacgc  | ctgtgctaaa  | gctctcctgc  | tctgacacat | cctccagcca  | gatgggtggg | 600 |
| atgactgaga  | ccttagctgt  | cattgtgacc  | cccttctctg | gtatcatctt  | ctcctacctg | 660 |
| cgaatcatgg  | tcactgtgct  | cagaatcccc  | tctgcagccg | ggaagtggaa  | ggccttctct | 720 |
| acctgtggct  | cccacctcac  | tgcagtagcc  | cttttctatg | ggagtattat  | ttatgtctat | 780 |
| tttaggcccc  | tgtccatgta  | ctcagtgggt  | agggaccggg | tagccacagt  | tatgtacaca | 840 |
| gtagtgcac   | ccatgctgaa  | ccctttcatc  | tacagcctga | ggaacaaaga  | tatgaagagg | 900 |
| ggtttgaaga  | aattacagga  | cagaattttac | cgg        |             |            | 933 |

&lt;210&gt; 978

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g828 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(939)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 978

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| atgccaataa  | agattgtggg  | gactgagttc | ttctcaciaa | ggcctgacgg  | attacaaaag | 60  |
| agcttttcagg | tggtgtttt   | tctgtccct  | gatgcttgcc | ataccttggtg | actgtctctg | 120 |
| ggaacctgaa  | tcattcatcag | ccatgacctt | gctggacacc | cgcattgcaga | catctatgta | 180 |
| cttattttctc | cagaatctgt  | cctgcttaga | aatttgttcc | agacagtcat  | cgtgcccag  | 240 |
| atgctgctca  | acattgccat  | ggggaccaag | accgttagct | ttgctgggtg  | cattaccag  | 300 |
| gactttttcc  | acattctctg  | ggggccacag | agttcttctc | cctgacagcc  | atggcctatg | 360 |
| accagtatat  | tgccatctgc  | aagccctctc | actaccccat | gctcataagt  | agtagagtct | 420 |
| gcacacagct  | catctctacc  | tgctggctac | taggtttctc | cttcatcatc  | atgcctgtca | 480 |
| tcctgaccag  | tcagcttcca  | ttctgtgata | cccacatcaa | gcatttcttc  | tgtgactaca | 540 |
| cgcctcta    | ggaggtgggtc | tgcagtgggc | caaagtgct  | ggagatgggtg | gattttaccc | 600 |
| tggccttagt  | agcactgttt  | ggcaccttgg | tactcatcac | cctgtcctat  | gtccagatca | 660 |
| tccagacaat  | tgtcagaatc  | ccgctgttcc | aggagaggaa | gaaggcttcc  | tctacctgtt | 720 |
| cctctcatgt  | cattatgggtt | accatgtgtt | atgacagctg | cttctttatg  | tatgtcaagc | 780 |
| cctctccagg  | aaagtgggtt  | gatgtcaaca | angggagtgt | ctctaataca  | tacaattatt | 840 |
| gccccactgt  | taaatccctt  | catctgtact | ctgaggaacc | aacaagttaa  | gcaggtaatg | 900 |
| aaagacctag  | tcagaaaaat  | gactttgtcc | gaaaataaa  |             |            | 939 |

&lt;210&gt; 979

&lt;211&gt; 951

&lt;212&gt; DNA

<213> Unknown (H38g829 nucleotide)

<220>

<223> Synthetic construct

<400> 979

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| atgaactcag | agaacctcac  | ccggggccgcg | gttgcccctg  | ctgaattcgt  | actcctgggc  | 60  |
| atcacaatac | gctgggacct  | gcgtgtggcc  | ctcttctga   | cctgcctgcc  | tgtctacctg  | 120 |
| gtgagcctgc | tgggaaacat  | gggcatggcg  | ctgctgatcc  | gcattggatgc | ccggctccac  | 180 |
| acacctatgt | acttcttctt  | ggccaacctc  | tccctgctgg  | atgcctgcta  | ttcctccgcc  | 240 |
| atcgccccca | agatgctagt  | ggacctgctg  | ctgccccgag  | ccaccatccc  | ttacacagcc  | 300 |
| tgtgccctcc | agatgtttgt  | ctttgcaggt  | ctggctgata  | ctgagtgttg  | cttgctggca  | 360 |
| gccatggcct | atgaccgcta  | cgtggccatc  | agaaacccac  | ttctctatac  | aacagctatg  | 420 |
| tcgcagcgtc | tatgcctggc  | cttgctggga  | gcattcaggcc | tgggtggggc  | agtgagtgcc  | 480 |
| tttgttcaca | caacctcac   | cttccgcctg  | agcttctgcc  | gctcccggaa  | gatcaatagc  | 540 |
| ttcttctgcg | atatccctcc  | actgctggcc  | atctcgtgca  | gtgacaccag  | tctcaatgaa  | 600 |
| ctccttctct | tcgccatctg  | tggcttcac   | cagacagcca  | cgggtgttagc | tatcacgggtg | 660 |
| tcttatggct | tcacgctggg  | ggctgtgate  | cacatgcgct  | cggctcgaggg | cagtcggcga  | 720 |
| gcagcctcca | ccgggtgggtc | ccacctcaca  | gccgtggcca  | tgatgtacgg  | gacactcatt  | 780 |
| ttcatgtacc | tgcccccag   | ctccagctat  | gccctggaca  | ctgacaagat  | ggcctctgtg  | 840 |
| ttctataccc | tggtcatccc  | gtctctcaac  | ccactcatct  | acagcctccg  | caataaggag  | 900 |
| gtcaaggagg | ccctcaggca  | gacctggagc  | cgattccact  | gtccagggca  | g           | 951 |

<210> 980

<211> 948

<212> DNA

<213> Unknown (H38g830 nucleotide)

<220>

<223> Synthetic construct

<400> 980

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| atggtgatcc | tgtcctggga  | aaaccaaacg | atgagagtgg  | aattcgtgct | tcaaggattc  | 60  |
| tcttccatca | gacagttaaa  | tattttcctc | tttatgataa  | ttttagtttt | ctacatctta  | 120 |
| actgtttctg | gaaacatcct  | cattgtcctt | ctagttttag  | tcagacatca | tctccacacc  | 180 |
| cctatgtact | tcctcctggg  | gaacttgtcc | tgtctggaga  | tctggtatac | ctctaaccatc | 240 |
| atccccaaaa | tgttgctgat  | tatcatagct | gaatagaaga  | ctatctctgt | ggctggctgg  | 300 |
| ctggcacaat | tctaacttct  | cggatccctg | gctgccacgg  | agtgcctctt | gctcactgtg  | 360 |
| atgtcctatg | atcgtacct   | agccatctgc | cagcctcttt  | gctaccgtgt | cctcatgact  | 420 |
| ggcccccttt | gcattcaggct | agctgctggc | tcttggttct  | gctgcttctt | ccttacagca  | 480 |
| atcaccatgg | tcttgctatg  | tagactaacc | ttctgtggac  | cctatgaaac | tgatcacttc  | 540 |
| ttttgtgact | tcacccctct  | ggttcatctc | tcctgcatgg  | atacctcagt | gactgagacc  | 600 |
| attgcctttg | ccacctcttc  | tgacagtaac | ctgatcccat  | ttctcctcat | tgtagcctcc  | 660 |
| tactcctgcg | tcctttctgc  | tatcctaaga | atcccatctt  | gcacaggcca | gaaaaaggcc  | 720 |
| ttctccacct | gctcttccca  | cctcactgtg | gtcatagtgt  | tttatgggac | actgattgcc  | 780 |
| acataccttg | tgccctcagc  | caactcatcc | caactcttgt  | gcaaagggtc | ctctctgctc  | 840 |
| tacatcatcc | tgacacccat  | gtttaacccc | atcatttata  | gcctgagaaa | tagagacatc  | 900 |
| catgaagctc | tgaagaagtg  | cttgaggaag | aagtcagggtg | tttgcctt   |             | 948 |

<210> 981

<211> 925

<212> DNA

<213> Unknown (H38g831 nucleotide)

<220>

<223> Synthetic construct

<400> 981

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| gagtaaattg | gaacaagtaa | taatgttaca  | gaatttgtcc | tcccaggcct  | ctctcaggat  | 60  |
| cctgatgtgc | aaaaagcatt | atttghtaatg | tttttactca | catacaatgt  | gactatgggtg | 120 |
| ggcaaccttc | tcattgtggg | gaccattatt  | gccatgcctt | ccttgggactc | cccagtgtcc  | 180 |

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| ttcttctctcg | catgcctgtc  | atattattgat | gctgtatatt  | ccacttcctt | ttccccctaag | 240 |
| ttgatgatag  | acttactctg  | tgataaaaaa  | gactgtttct  | ttcctggctt | gcatgggcca  | 300 |
| gctatttata  | aactacccat  | ttgggtggtat | tgaggctctt  | cttttgggtg | gtatggcctg  | 360 |
| tgatcactat  | gtggacatct  | gtaagctact  | gcactatttg  | accatcatga | actggcaggt  | 420 |
| ttgcatcctc  | ctgtttatgg  | tggtctgtgac | tgagggtttt  | tgcattctat | gtttcaaatt  | 480 |
| gttgtttgtg  | acagtctccc  | tttctgtggc  | cccaatgtca  | ttgaccattt | tgtgacatgt  | 540 |
| accattattt  | ggaaatgggtg | tgacttgaca  | cttactttat  | aggcctcact | gtgattgcca  | 600 |
| atgggtggagc | agtctgtatg  | gtcatcttca  | tccttctact  | aatctcctat | ggagtcaccc  | 660 |
| taaactccct  | taaaacttat  | agtcaggaag  | gcgggcataa  | agccctgtct | acctgcagct  | 720 |
| ccaacattac  | tggtgtgtcc  | ccttttttga  | tcctgttatt  | ttcatctatg | ttagacctga  | 780 |
| ttcaaacctt  | cctattgata  | aattcatgac  | tgtgttttat  | acaattatca | cacceatgtt  | 840 |
| gaatccatta  | atatacacac  | tgagaaattt  | agagggtgaga | attgctgtga | aaaatctctg  | 900 |
| gtgtaaaaac  | taaactatag  | taaga       |             |            |             | 925 |

&lt;210&gt; 982

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g832 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 982

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| atggatagag  | ttaaataattc | tgcggtatct | aaattttgtat | tgattggact | ttcaagctct  | 60  |
| tgaggatgac  | atccttttct  | tttttgggtc | ttctctgtgt  | tctacatggg | aattatcctg  | 120 |
| gaaaatctct  | tcattgtgtt  | cacagtaatt | attgactctc  | atttaaattc | cccagggtact | 180 |
| gcctactggc  | caacatttat  | cttcttgatc | tggtgtctct  | cctacagttc | tgactttttc  | 240 |
| actaactgca  | gcatcatttc  | ttttccaaga | tgcatgatac  | agatattttt | catttgtgtc  | 300 |
| atgctgtaaaa | attgagatgg  | tgctgctcat | aaccatggca  | tagagcaggt | acactgcca   | 360 |
| tctgtaagcc  | tccccattac  | ctgaccacaa | tgaaccccaa  | aatgtgtgtt | tactttgttg  | 420 |
| gaggcatcct  | ggatagtcag  | gataatccat | gctgtatctc  | agtttgtttt | tgccataaac  | 480 |
| ttgccttttt  | gtggccctaa  | tagagtaggt | agttttcact  | gtgattttcc | ttatgtcatg  | 540 |
| aaacttgctt  | gtgtgacac   | ttacaaacta | gagggtgtag  | tcactgctaa | cagtgggctt  | 600 |
| atatccatag  | ctacctgttt  | cttattaata | atatectata  | ttttcatttc | ggtaaccgtc  | 660 |
| tagaatcctt  | cttcaggaga  | cttatctaaa | gcatttgtgt  | catgttagat | cacatcacag  | 720 |
| tagggatttt  | gttttttatg  | ccatgtatat | ttctctatgt  | gtagcctttg | cctaaaacaa  | 780 |
| cacatgatta  | atatttgttc  | attgttcctt | ttgctatcac  | ccctgtctag | gatctacaca  | 840 |
| ttaagaaaca  | aagacatgaa  | cgtctccatg | gaaagactgg  | gaaaatggat | tgacaggtct  | 900 |
| agcaggatgt  | cataataaat  | ggtgcataac | cagagtgcac  | gatgattcag | tctacca     | 958 |

&lt;210&gt; 983

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g833 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 983

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| atggaaggaa  | taaataaaaac | tgcaaagatg  | cagtttttct  | ttcgtccatt | ctcacctgac | 60  |
| cctgagggtcc | agatgctgat  | ttttgtgggtc | ttcctgatga  | tgtatctgac | cagcctcggt | 120 |
| ggaaatgcta  | caattgcagt  | cattgttcag  | atcaatcatt  | ccctccacac | ccccatgtac | 180 |
| tttttctctg  | ctaactcttc  | agttctagaa  | atcttctata  | catcttccat | caccccatgt | 240 |
| gccttggcaa  | acctcctttc  | aatgggcaaa  | actcctgttt  | ccatcacggg | atgtggcacc | 300 |
| cagatgtttt  | tctttgtctt  | cttgggtggg  | gctgattgtg  | tcctgctggg | agtcattggc | 360 |
| tatgaccggg  | ttatagcgat  | ctgtcaccct  | ctgcgataca  | ggctcatcat | gagctggtcc | 420 |
| ttgtgtgtgg  | agctgctggg  | aggtcctttg  | gtgctggggg  | tcctgttgtc | actgccactc | 480 |
| accattttta  | tcttccatct  | cccattctgc  | cacaatgatg  | agatctacca | cttctactgt | 540 |
| gacatgcctg  | cagtcatgcg  | cctggcttgt  | gcagacacac  | gcgttcacaa | gactgctctg | 600 |
| tatatcatca  | gcttcatcgt  | ccttagcatc  | ccccctctcat | tgatctccat | ctcctatgtc | 660 |
| ttcatcgtgg  | tagccatttt  | acggatccgg  | tcagcagaag  | ggcgccagca | agcctactct | 720 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acctgctctt | ctcacatctt | agtggctctc | ctgcagtatg | gctgcaccag | ctttatatac | 780 |
| ttgtccccc  | gttccagcta | ctctcctgag | atggggcggg | tggtatctgt | ggcctacaca | 840 |
| tttatcactc | ccattttaaa | ccccttgatc | tatagtttga | ggaacaagga | actgaaagat | 900 |
| gccctaagga | aagcattgag | aaaattc    |            |            |            | 927 |

&lt;210&gt; 984

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g834 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 984

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gattcagtg  | accaagtaaa | tgactctctg | gtaacagaat | ttgtattact | tggaacttgca | 60  |
| caatccttg  | aaatgcagtt | tttccttttt | ctcttcttct | ctttattcta | tgtgggaatt  | 120 |
| atcctggga  | acctcttcat | tgtgttcaca | gtgatctttg | atcctcactt | acactcccc   | 180 |
| atgtatatc  | tgctggccaa | cctatcgctc | attgacttga | gcctttcacc | taccacagtt  | 240 |
| cctaggttg  | tctacgatct | ttttactgat | tgtaaagtta | tttccttcca | taattgtatg  | 300 |
| atacaaaagt | tctttatcca | tgttacggga | ggagttgaaa | tggtgctgct | gatagtcatg  | 360 |
| gcatatgata | ggtacactgc | gatctgcaaa | cctctccact | atccaactat | tatgaatccc  | 420 |
| aaaatgtgca | tgtttttggg | agcagcagct | tgggtcattg | gggtgattca | tgctatgtct  | 480 |
| cagtttgttt | ttgtcataaa | tttacccttc | tgtggcccta | ataatgtggg | gagcttttat  | 540 |
| tgtgattttc | ctcgggttat | taaacttgca | tgcatggaca | cttatgggct | agaatttgtg  | 600 |
| gtcactgcca | acagtggatt | catatcgatg | ggcacccttc | ttttcttaat | tgtatcatac  | 660 |
| atttttatc  | tggtcactgt | ccaacgacat | tcctcaaagt | atttatccaa | agcattcttc  | 720 |
| acttcgtagg | ctcacatcac | cgtagtggtt | ttgttttttg | ctccatgcat | gtttctctac  | 780 |
| gtgtggcctt | tcctactata | gtcattggat | aaattttttg | ccatcatgaa | ctttgttgtc  | 840 |
| acccctgtct | taaactcctg | catctatact | ttaaggaaca | aagatatgaa | gtttgcaatg  | 900 |
| agaaggctga | atcaacatat | tttaaattct | atggagatga | cataacacat | ttggttgatg  | 960 |
| agagcacagg | ataaatgcc  | tggaacca   |            |            |             | 987 |

&lt;210&gt; 985

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g835 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 985

|             |             |             |             |             |            |     |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| tccatgtact  | tcttctctgac | aaactttgca  | ggctctggaga | tcttctactt  | tttcaccatt | 60  |
| gccccctctga | ctctggccaa  | tgctctaccc  | atggggagaa  | acctcatttc  | cctgcccggc | 120 |
| tgtggaggcc  | agatgttctt  | cttcatcttc  | ctgggaaggg  | ctgactgcat  | cctgctggcc | 180 |
| gtcatggcct  | ttgactgggt  | tgtggccatc  | tgttgctctc  | tctgttacgg  | cctcatcatg | 240 |
| agctggagggt | tgtgtgtcca  | gctgaccctg  | gggtctctgc  | tgttgggggt  | cttcttagcc | 300 |
| atgcagctga  | cctgtcttat  | cttccaactc  | cctttatgca  | gcagcaaaga  | aatcagcacg | 360 |
| ttctactgtg  | atgtctctcc  | tgctcatgaga | ctggcctgtg  | cagataacctg | ggtccatgag | 420 |
| gccactatgt  | ctatgggtcag | caccaccttt  | ctcaccgtcc  | ccttctctgt  | catcactctt | 480 |
| tcctatgtct  | ccatcatggc  | cgccatcttg  | aagatttgct  | ctgcagaggg  | gaggcacaag | 540 |
| gccttctcca  | cctttctctc  | cacctgactg  | tggttctcct  | ccaggactga  | tgtacacgcc | 600 |
| tcgccttctt  | gtgtcccgag  | tctagctact  | atcctgagag  | gggccaggca  | gtgtctgtgg | 660 |
| tttacacctt  | cattaccctt  | gtgctgaacc  | ctttgatcta  | cagcatgagg  | aacacagaac | 720 |
| ttaaggatgc  | tttgaagaga  | gcaatgacga  | gggtcccgtc  | gctctaaaca  |            | 770 |

&lt;210&gt; 986

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g836 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 986

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| atggtgactg  | aattcatttt | tctgggtctc  | tctgattctc  | aggaactcca  | gaccttccta  | 60  |
| tttatgttgt  | tttttgtatt | ctatggagga  | atcgtgtttg  | gaaaccttct  | tattgtcata  | 120 |
| acagtgggat  | ctgactccca | ccttcactct  | cccatgtact  | tcctgctagc  | caacctctca  | 180 |
| ctcattgatc  | tgtctctgtc | ttcagtcaca  | gcccccaaga  | tgattactga  | ctttttcagc  | 240 |
| cagcgcaaa   | g          | tcattctctt  | caagggctgc  | cttggttcaga | tatttctcct  | 300 |
| ggtgggagt   | g          | agatgggtgat | cctcatagcc  | atgggctttg  | acagatatat  | 360 |
| aaacccctac  | actacactac | aattatgtgt  | ggcaacgcat  | gtgtcggcat  | tatggctgtc  | 420 |
| gcatggggaa  | ttggctttct | ccattcgggtg | agccagttgg  | cctttgccgt  | gcacttaccc  | 480 |
| ttctgtggtc  | ccaatgaggt | cgatagtttt  | tattgtgacc  | ttcctagggg  | aatcaaaactt | 540 |
| gcctgtacag  | atacctacag | gctagatatt  | atgggtcattg | ctaacagtgg  | tgtgctcact  | 600 |
| gtgtgttctt  | ttgttcttct | aatcatctca  | tacactatca  | tcctaattgac | catccagcat  | 660 |
| tgcccttttag | ataagtcgtc | caaagctctg  | tccactttga  | ctgctcacat  | tacagttagtt | 720 |
| cttttgttct  | ttggaccatg | tgtctttatt  | tatgcctggc  | cattccccat  | caagtcatta  | 780 |
| gataaattcc  | ttgctgtatt | ttattctgtg  | atcacccctc  | tcttgaaccc  | aattatatac  | 840 |
| acactgagga  | acaaagacat | gaagacggca  | ataagacggc  | tgagaaaatg  | ggatgcacat  | 900 |
| tctagtgtaa  | agttt      |             |             |             |             | 915 |

&lt;210&gt; 987

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g837 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 987

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| atggatagag | taaataattc | tgcggtatct  | aaatttgtat | tgattggact | ttcaagctct  | 60  |
| tgggagatgc | atctttttct | tttttgggtc  | ttctctgtgt | tctacatggg | aattatcctg  | 120 |
| gaaaatctct | tcatttgtgt | cacagtaatt  | attgactctc | atttaaattc | cccagggtact | 180 |
| gcctactggc | caacatttat | cttcttgatc  | tgggtcttct | cctacagttc | tgactttttc  | 240 |
| actaactgca | gcatcatttc | ttttccaaga  | tgcatgatac | agatattttt | catttgtgtc  | 300 |
| atgcgtaaaa | attgagatgg | tgctgctcat  | aaccatggca | tagagcaggt | acactgccaa  | 360 |
| tctgtaagcc | tccccattac | ctgaccacaa  | tgaaccccaa | aatgtgtgtt | tcctttgttg  | 420 |
| gaggcatcct | ggatagtcag | gataatccat  | gctgtatctc | agtttgtttt | tgccataaac  | 480 |
| ttgccttttt | gtggccctaa | tagagttagt  | agttttcact | gtgattttcc | ttatgtcatg  | 540 |
| aaacttgctt | gtgtagatac | ttacaaaacta | gaggttgtag | tcactgctaa | cagtgggctt  | 600 |
| atatccatag | ctacctgttt | cttattaata  | atatcctata | ttttcatttc | ggtaaccgtc  | 660 |
| tagaatcctt | cttcaggaga | cttatctaaa  | gcatttgtgt | catgttagat | cacatcacag  | 720 |
| tagggatttt | gttttttatg | ccatgtatat  | ttctctatgt | gtagcctttg | cctaaaacaa  | 780 |
| cacatgatta | atatttggtc | attgttcctt  | ttgctatcac | ccctgtctag | gatctacaca  | 840 |
| ttaagaaaca | aagacatgaa | cgtctccatg  | gaaagactgg | gaaaatggat | tgcagggttct | 900 |
| agcaggatgt | cataataaat | ggtgcatatc  | cagagtgcac | gatgattcag | tctcacca    | 958 |

&lt;210&gt; 988

&lt;211&gt; 982

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g838 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 988

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| ctttctattt | gcttctttct  | ttgcatattt  | tcagctgata | tttaatctat | gctagccatg  | 60  |
| gaacaaaata | atggcactga  | agtgcactgaa | ttcattctcc | tgggatttgc | tgggtcaacac | 120 |
| aagtcttggc | atattcctctc | catagcattt  | ctagcaatct | atgtggttac | cccagtaggt  | 180 |
| aatattggaa | tgatcctact  | tatcaaaatt  | gatgtctctc | ttcatatccc | catgtaaatt  | 240 |
| ttcctccaac | acttggcatt  | tgttgatctc  | tgttacacct | ctgctatcac | tcccaagatg  | 300 |
| ttgaaaaact | ttgtagaaac  | aaaaaaatct  | atctcatgta | taggatgtat | ggtgcaatta  | 360 |

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| ctagtttatg  | gtactttgca  | acaagtgact | gctacatcct  | ggctgctatg | gcagtagacc  | 420 |
| gttatgtggc  | cttctgtaac  | ccactccatt | atccaggggt  | tatgtcccag | agactctgca  | 480 |
| ttaaagctatt | agtttagttca | tatgtcatgg | gtttcctaaa  | tgcctctata | aacataagtt  | 540 |
| tcactttctc  | attgaacttc  | tgcaaatcca | aaacaattaa  | tcactttttc | tgtgatgaac  | 600 |
| ctccaattat  | tgccttacca  | tgtcctaata | ttgacctcaa  | catcatgtta | ttaacagtat  | 660 |
| ttgtgggatt  | aaatttgatg  | tgcactgtga | tgggtggcat  | catttcctgc | atatatgtcc  | 720 |
| tggttgccat  | cctgaggata  | tcttctgctg | caggggaagaa | aaaagtctct | ctacatgtgc  | 780 |
| ctcccacctg  | acagcagtca  | ccattttcta | tggggttctc  | tcttacatgt | atctatgccca | 840 |
| tcgtattaat  | gagtcctaaa  | aacaagaaaa | agtggcctct  | gtgttttatg | gcattattat  | 900 |
| tcccatgtta  | aaccccttga  | tttacagcca | gagaaaccaa  | gatgtgattg | aagccataaa  | 960 |
| actaacagaa  | aaaaagtatt  | tc         |             |            |             | 982 |

&lt;210&gt; 989

&lt;211&gt; 1006

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g839 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 989

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| atgatttctt  | tccttgtacc  | aggtctaattg | gaagaggaaa  | accagagggg | agtggtagac | 60   |
| ttccacttcc  | acttcttttc  | aacagacctg  | gtgggtggctt | cctttataat | tgtggccttg | 120  |
| atgttgcacc  | aagaagcctt  | gttggaact   | tcaccttttg  | gcccacagtc | tggcaagatc | 180  |
| ccttctctcca | tattccaatg  | tatttatttt  | tatttttttg  | gcattgacta | tgttggaat  | 240  |
| tggctactcc  | accaacattt  | ctcctccaac  | actggctacc  | gtcctttaca | tggggaagat | 300  |
| gcttatctcc  | ctccctggct  | atggaactca  | gatgctcttt  | gtcatccttt | tgagaggatc | 360  |
| tgagtgtgtc  | ttgcttgcctg | tcatggctta  | tgataggtat  | ataaccatct | gtcatccatt | 420  |
| caattacaat  | ctcatcatga  | gtgggtagct  | ctgtgggcag  | atgacttttg | gctctttgag | 480  |
| gctgggattc  | ctgttgtcac  | tgtttttgac  | tatgttgatc  | tgacaccctc | cattctgtgg | 540  |
| cctaattgaaa | cctaccactt  | cttctgtgac  | atgccacag   | caagtgcctg | gtctgtgcag | 600  |
| acaccacatg  | catgagtcag  | ctctctgact  | tccgtgtggc  | caccatcacc | atccccttcc | 660  |
| ttcctccttg  | tctgcctccc  | ctatggctgc  | cttgacagcca | ccatcttgag | gatgcattca | 720  |
| gctaagagaa  | agcactaggc  | cttctctacc  | agttcctccc  | acctcattgt | ggttctcctg | 780  |
| aagtattggg  | gttgcatcct  | catctgcctt  | tgccccagct  | ctagttactc | cccagaggag | 840  |
| ggctgggagg  | tatctcttgt  | tcacatgttt  | ttctcccggg  | gtggaatccc | ttgatctata | 900  |
| gcgtatggaa  | ccaagacgta  | actgatgcag  | tagagagact  | tgtggcaaga | atgtccttgt | 960  |
| tctaacagcc  | agaaatattc  | cttcttaaaa  | aatatttccc  | taacta     |            | 1006 |

&lt;210&gt; 990

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g840 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 990

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| gattcagtgg | accaagtaaa | tgactctctg | gtaacagaat  | ttgtattact  | tggacttgca | 60  |
| caatccttgg | aaatgcagtt | tttctttttt | ctcttcttct  | ctttattcta  | tgtgggaatt | 120 |
| atcctgggaa | acctcttcat | tgtgttcaca | gtgatctttg  | atcctcactt  | acactcccc  | 180 |
| atgtatatcc | tgctggccaa | cctatcgctc | attgacttga  | gcctttcacc  | taccacagtt | 240 |
| cctaggttga | tctacgatct | ttttactgat | tgtaaagtta  | tttccctcca  | taattgtatg | 300 |
| atacaaaagt | tctttatcca | tgttacagga | ggagttgaaa  | tgggtgctgct | gatagtcatg | 360 |
| gcatatgata | ggtacactgc | gatctgcaaa | cctctccact  | atccaaactat | tatgaacccc | 420 |
| aaaatgtgca | tgttttttgg | agcagcagct | tgggtcattg  | gggtgattca  | tgctatgtct | 480 |
| cagtttgttt | ttgtcataaa | tttacccttc | tgtggcccta  | ataatgtggg  | gagcttttat | 540 |
| tgtgattttt | ctcgggttat | taaacttgca | tgcattggaca | cttatgggct  | agaatttgtg | 600 |
| gtcactggca | acagtggatt | catatcgatg | ggcaccctct  | ttttcttaat  | tgtatcatac | 660 |
| atttttatcc | tggctactgt | ccaacgacat | tcctcaaatg  | atttatccaa  | agcattcttc | 720 |
| acttcgtagg | ctcacatcac | cgtagtggtt | ttgttttttg  | ctccatgcac  | gtttctctac | 780 |

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| gtgtggcctt | tccctactaa  | gtcattggat | aaatTTTTTg | ccatcatgaa | ctttgttgtc | 840 |
| acccctgtct | taaactcctgc | catctatact | ttaaggaaca | aagatatgaa | gtttgcaatg | 900 |
| agaaggctga | atcaacatat  | tttaaattct | atggagatga | cataacacat | ttggttgatg | 960 |
| agagcacagg | ataaatgccca | tggacca    |            |            |            | 987 |

&lt;210&gt; 991

&lt;211&gt; 736

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g841 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 991

|             |             |             |            |             |              |     |
|-------------|-------------|-------------|------------|-------------|--------------|-----|
| atgcaatcag  | aacaccttgc  | agaatTTTTca | gaattcctca | ttttgagcct  | ctcaggagat   | 60  |
| ccagaactgc  | agcccccttct | tgggctgttt  | ctgtccatga | acctgggtcac | agtgccttggga | 120 |
| aacctgtctca | ttatccttggc | catcagttct  | gactcccacc | tccacaagcc  | tatgtacttc   | 180 |
| ttactctcca  | aattgtccat  | ggctgccatt  | tgTTTTgtct | tcaccatgat  | ccaaaagatg   | 240 |
| atggtaaacc  | tcagggcaca  | gagcaaagac  | atctttactc | agccaagtgg  | tagtccaatt   | 300 |
| ccattctaaa  | tgtgtagtct  | tatcagattt  | cttctaattc | agcagaaatc  | tgttgtttta   | 360 |
| atcttcgaat  | actcactggg  | tctaattctc  | ctatttgaat | ctgaagatgt  | aaactaatta   | 420 |
| ttcttttTgta | tgagcctttc  | aaaataattg  | aagacagtta | tgctcttttc  | ttgataatca   | 480 |
| ccatactttc  | ttcacactaa  | ttgatacaca  | attgttaata | agtcatggat  | tttctactca   | 540 |
| aacaaccttt  | attctatcat  | cttatgtctc  | tggttatgca | acagttgact  | ctcaatgctt   | 600 |
| tatttatttt  | ttaaaccatga | tgattactat  | taacctcttt | gtaagattta  | aaaaatatctt  | 660 |
| tatgcacagt  | agtatctcaa  | taaattacaa  | ctattatttt | aaaaaataaa  | ataaagggtgg  | 720 |
| tatctatgag  | atatat      |             |            |             |              | 736 |

&lt;210&gt; 992

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g842 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 992

|             |             |             |             |             |            |     |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| atgggtgactg | aattcatttt  | tctgggtctc  | tctgattctc  | aggaactcca  | gaccttccta | 60  |
| tttatgttgt  | ttttgtatt   | ctatggagga  | atcgtgtttg  | gaaaccttct  | tattgtcata | 120 |
| acagtgggtat | ctgactccca  | ccttcactct  | cccatgtact  | tcctgctagc  | caacctctca | 180 |
| ctcattgatc  | tgtctctgtc  | ttcagtcaca  | gcccccaaga  | tgattactga  | ctttttcagc | 240 |
| cagcgcaaag  | tcattctctt  | caagggctgc  | cttgttcaga  | tatttctcct  | tcacttcttt | 300 |
| ggtgggagtg  | agatgggtgat | cctcatagcc  | atgggctttg  | acagatatat  | agcaatatgc | 360 |
| aaacccctac  | actacactac  | aattatgtgt  | ggcaacgcat  | gtgtcggcat  | tatggctgtc | 420 |
| gcatggggaa  | ttggctttct  | ccattcgggtg | agccagttgg  | cctttgccgt  | gcacttaccc | 480 |
| ttctgtgggc  | ccaatgaggt  | cgatagtttt  | tattgtgacc  | ttcctagggt  | aatcaaactt | 540 |
| gcctgtacag  | atacctacag  | gctagatatt  | atgggtcattg | ctaacagtgg  | tgtgctcact | 600 |
| gtgtgtttct  | ttgttcttct  | aatcatctca  | tacactatca  | tcctaataac  | catccagcat | 660 |
| cgcccttttag | ataagtctgc  | caaagctctg  | tccactttga  | ctgtctcacat | tacagtagtt | 720 |
| cttttgttct  | ttggaccatg  | tgtctttatt  | tatgcctggc  | cattccccat  | caagtcatta | 780 |
| gataaattcc  | ttgctgtatt  | ttattctgtg  | atcacccctc  | tcttgaaccc  | aattatatac | 840 |
| acactgagga  | acaaagacat  | gaagacggca  | ataagacggc  | tgagaaaatg  | ggatgcacat | 900 |
| tctagtgtaa  | agttt       |             |             |             |            | 915 |

&lt;210&gt; 993

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g843 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct



```

<400> 993
atggctgcag gaaatcactc tacagtgaca gagttcattc tcaagggttt aacgaagaga      60
gcagacctcc agctccccct ctttctcctc ttctctggga tctacttggg caccatcggt      120
gggaacctgg gcatgatcac tctaatttgt ctgaactctc agctgcacac ccccatgtac      180
tactttctca gcaatctgtc actcatggat ctctgctact cctccgtcat taccctaag      240
atgctgggtga actttgtgtc agagaaaaac atcatctcct acgcagggtg catgtcacag      300
ctctacttct tccttggttt tgtcattgct gagtggtaca tgctgacagt gatggcctac      360
gaccgctatg ttgccatctg ccaccctttg ctttacaaca tcattatgtc tcatcacacc      420
tgctgtctgc tgggtggctgt ggtctacgcc atcggactca ttggctccac aatagaaact      480
ggcctcatgt taaaactgcc ctattgtgag cacctcatca gtcactactt ctgtgacatc      540
ctccctctca tgaagctgtc ctgctctagc acctatgatg ttgagatgac agtcttcttt      600
tcggctggat tcaacatcat agtcacgagc ttaacagttc ttgtttctta caccctcatt      660
ctctccagca tcctcggcat cagcaccaca gaggggagat ccaaagcctt cagcacctgc      720
agctcccacc ttgcagccgt gggaaatgtt tatggatcaa ctgcattcat gtacttaaaa      780
ccctccacaa tcagttcctt gaccaggag aatgtggcct ctgtgttcta caccacggta      840
atccccatgt tgaatccctt aatctacagc ctgaggaaca aggaagtaaa ggctgccgtg      900
cagaaaacgc tgaggggtaa actgtttt                                     927

```

<210> 994

<211> 930

<212> DNA

<213> Unknown (H38g844 nucleotide)

<220>

<223> Synthetic construct

```

<400> 994
atggcagcca aaaactcttc tgtgacagag tttatcctcg aaggcttaac ccaccagccg      60
ggactgcgga tccccctctt ctctctgttt ctgggtttct acacggtcac cgtgggtggg      120
aacctgggct tgataaccct gattgggctg aactctcacc tgcacactcc catgtacttc      180
ttctttttta acctctcttt aatagatttc tgtttctcca ctaccatcac tcccaaatg      240
ctgatgagtt ttgtctcaag gaagaacatc atttcttcca cagggtgtat gactcagctc      300
ttcttcttct gcttctttgt cgtctctgag tccttcaccc tgtcagcgat ggcgtatgac      360
cgctacgtgg ccatctgtaa cccactgttg tacacagtca ccatgtcttg ccagggtgtg      420
ttgctccttt tgttgggtgc ctatgggatg ggggttgctg gggccatggc ccacacagga      480
agcataatga acctgacctt ctgtgctgac aaccttgtca atcatttcat gtgtgacatc      540
cttctctctc ttgagctctc ctgcaacagc tcttacatga atgagctggg ggtctttatt      600
gtgggtggctg ttgacgttgg aatgccatt gtcactgtct ttatttctta tgccctcatc      660
ctctccagca ttctacacaa cagttctaca gaaggcaggc ccaaagcctt tagtacttgc      720
agttcccaca taattgtagt ttctcttttc tttggttctg gtgctttcat gtatctcaaa      780
cccctttcca tcctgcccc cagagcaagg aaagtgtcct ccctgttcta taccataata      840
gtccccgtgt taaaccatt aatctatagc ttgaggaaca aggatgtcaa agttgccctg      900
aggagaactt tgggcagaaa aatcttttct                                     930

```

<210> 995

<211> 473

<212> DNA

<213> Unknown (H38g845 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(473)

<223> n = A,T,C or G

```

<400> 995
atgggagaag caaggaacag gacagtagtc caggaattta tcctggaggg atttctgtct      60
gtccagcatc tggggaatgt cttttctctg gtgcacctgc tggcatacct ggctccatc      120
atggcaaaca tgctcataat caccatcacc tgggctgacc atcacctcca gacacctatg      180

```

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tattttcttcc | tcagcagttt | ttccttctgt | gaatgctgtt | ttatcaccac | agttattcct | 240 |
| aaacttctgg  | tcatecttcc | tttcaggcag | ggcaaataat | ccccctttct | actaccttgt | 300 |
| ctcatgcagt  | ccccttttca | tttttatntt | cttgggtcaa | cagtttttct | tcccttaatg | 360 |
| gctgtgatgt  | ccccttggat | tgatacctgg | ccatttgcaa | gcctctgcat | tactccacca | 420 |
| tcatgagcct  | gaggactage | ttccacaagg | tcactgcctg | gctttgtcct | ggg        | 473 |

&lt;210&gt; 996

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g846 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 996

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| acagacccac  | agaatctaac | aacagatgtc | tcaatattcc  | tcgtcctaga  | actctcagag  | 60  |
| gatccagaac  | tacagccggg | cctcgctggg | ctgttcctgt  | ccatgtgect  | ggatcatggg  | 120 |
| ctggggaaac  | tgctcatcat | cctggccgct | agccctgact  | cccacctcca  | cacccccatg  | 180 |
| tactttcttc  | tctccaacct | gtccttgcct | gacatgggtt  | cacctccacc  | atgggtccca  | 240 |
| agatgattgt  | ggacatccaa | tctcacagca | gtcatctcct  | atgcgggctg  | cctgactcag  | 300 |
| atgtctcttt  | ttgccatttt | tggaggcatg | gaagaaagac  | atgctcctga  | gtgtgatggc  | 360 |
| cctatgaccg  | gtttgtagcc | atctgtcacc | ctctatatta  | ttcagccatc  | atgaacccat  | 420 |
| gtttctgtgg  | ctttctagtt | ctgttgtctt | gttgtctcag  | tcttttagac  | tcccagctgc  | 480 |
| acaatttgat  | tgccttgcaa | attacctgct | tcaaggatgt  | ggaaattcct  | aattttcttct | 540 |
| gtgaccttcc  | tcaactcccc | caccatgcgt | gttgtgacac  | cttcaccaat  | aacatagtca  | 600 |
| tgtatttccc  | tgctgccata | tttggttttc | ttcccacctc  | ggggatcctt  | ttctcttact  | 660 |
| ataaaaattgt | ttcctccatt | ctgagggttt | catcatcagg  | tgggaactat  | aaagccctct  | 720 |
| ctgcctgtgg  | gtctcacctg | tcagttgttt | gcttatttta  | tggaaacaggc | gttggagggt  | 780 |
| acctcagttc  | agatgtgtca | tcttccccca | gaaagggtgc  | agtggcctca  | gtgatgtaca  | 840 |
| cgggtggcac  | ccccatgctg | aaccccttca | tctacagcct  | gagaaacagg  | gatattaaaa  | 900 |
| gtgtcctgcg  | gcgcctgcac | ggcagaacag | tctaattctca | atatcttatt  | atctgttcca  | 960 |
| ttccttttgt  | agtgtgggtt | taaaaaggca | gcaagggtc   |             |             | 998 |

&lt;210&gt; 997

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g847 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 997

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| agtcaactgt | cccttatgga  | cctcatgtct  | atctgcacca | ctctacccaa  | gatgatcttc | 60  |
| agctacttgt | ctgggaagaa  | atctatctct  | ctggcagggt | gtggaactca  | gatattcttc | 120 |
| tatgtgtccc | tgcttgagc   | tgaatgtttc  | ttgttggtct | tcattggctta | tgaccgctat | 180 |
| gtggctatat | gtcacctctt  | tcagtacacc  | atcctcatga | atccggaact  | ctgtgtcttc | 240 |
| atgactgttg | cttctctggac | cttgggggtct | cttgatggga | tcatagtgtct | tgcagctgtc | 300 |
| ctgtcatttt | cttactgcag  | ctctctggaa  | attcatcatt | ttttctgtga  | tgttgctgcc | 360 |
| cttttacctc | tatcttgca   | agaaacatct  | gcatttgaaa | gactacttgt  | catttggtgt | 420 |
| gtggtaaatg | taatctttcc  | agtttcagtt  | atcatacttt | cctattccca  | tgtccttcga | 480 |
| gccgtcatcc | acatgggctc  | tggggaaagt  | cgtcgcaagg | ccttcactac  | ctgtcctctc | 540 |
| caccgctctg | tggtcggact  | ctactacggt  | gctgctatgt | tcattgtacat | gagaccagct | 600 |
| tctaaacata | cgccagacca  | ggacaagatg  | gtgtcggcct | tctacactaa  | tctcaccctc | 660 |
| atgctg     |             |             |            |             |            | 666 |

&lt;210&gt; 998

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g848 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 998

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| cttgccctgca | tagttggata | gaagtttgca | tttattattt  | ctccaaacca | tcacttcatg | 60  |
| ataatgggtca | cattcatttt | agttaacatt | taaaaacatt  | cttcaggaaa | cttatccagt | 120 |
| gctcttatca  | ttttgttcat | tttcatccct | gttggtttctc | tatttttcac | tccatgcgta | 180 |
| gttctctatg  | tttggcctac | tttgccacca | tcacttgata  | aaaatatgtt | cattgttgac | 240 |
| tttgttgta   | accctgtctt | gaagcctgcc | acctacatat  | tacagaacaa | agacataaag | 300 |
| gtagcacttt  | gaaatttgca | tgaaaagaga | acttattcca  | gc         |            | 342 |

&lt;210&gt; 999

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g849 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 999

|            |             |             |            |             |             |     |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| atggtgactg | aattcatttt  | tctgggtctc  | tctgattctc | agggactcca  | gaccttcccta | 60  |
| tttatgttgt | tttttgtatt  | ctatggagga  | atcgtgtttg | gaaaccttct  | tattgtcata  | 120 |
| acagtgggat | ctgactccca  | ccttcactct  | cccatgtact | tcctgctagc  | caacctctca  | 180 |
| ctcattgata | tgtctctgtc  | ttcagtcaca  | gcccccaaga | tgattactga  | ctttttcagc  | 240 |
| cagcgcaaag | tcattctctt  | caaaggctgc  | cttggtcaga | tatttctcct  | tcacttcttt  | 300 |
| ggtgggagtg | agatgggtgat | cctcatagcc  | atgggctttg | acagatatat  | agcaatatgc  | 360 |
| aaacccctac | actacactac  | aattatgtgt  | ggcaacgcac | gtgtcggcat  | tatggctgtc  | 420 |
| gcatggggaa | ttggttttct  | ccattcgggtg | agccagttgg | cctttgccgt  | gcacttaccc  | 480 |
| ttctgtggtc | ccaatgaggt  | cgatagtttt  | tattgtgacc | ttcctagggg  | aatcaaactt  | 540 |
| gcctgtacag | atacctacag  | gctagatatt  | atggtcattg | ctaacagtgg  | tgtgtctact  | 600 |
| gtgtgttctt | ttgttcttct  | aatcatctca  | tacactatca | tcctaattgac | catccagcat  | 660 |
| cgccttttag | ataagtctgc  | caaagctctg  | tccactttga | ctgctcacat  | tacagtattt  | 720 |
| cttttgttct | ttggaccatg  | tgtctttatt  | tatgcctggc | cattccccat  | caagtcatta  | 780 |
| gataaattcc | ttgctgtatt  | ttattctgtg  | atcacccctc | tcttgaacct  | aattatatac  | 840 |
| acactgagga | acaaagacat  | gaagacggca  | ataagacagc | tgagaaaatg  | ggatgcacat  | 900 |
| tctagtgtaa | agttt       |             |            |             |             | 915 |

&lt;210&gt; 1000

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g850 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1000

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| tccaacctgt | ccttgccctga | catcggtttc | ccctccccc  | cggtcccca  | gatgggttgtg | 60  |
| gacatccaat | ctcacagcag  | tcattctcct | atgcaggctg | cctgactcag | atgtctctct  | 120 |
| ttgccatttt | tggaggcatg  | gaagagacac | atgctcctga | atgtgatggc | ctatgtccgg  | 180 |
| ttttagtcca | tctgtcaccc  | tctatatcat | tcagccatca | tgaacctgtg | tttctgtggc  | 240 |
| ttcttacttt | tggtgtcttt  | tttttttctc | agtcttttag | acgcccagct | gcacaacttg  | 300 |
| attgccttac | aaatgacctg  | cttcaaggat | gtggaaattc | ctaatttctc | ctgtgacctt  | 360 |
| tctccactcc | cccatcttgc  | atgttgtgac | accttcacca | ataacataat | catgtatttc  | 420 |
| cctgctgcca | tatttggttt  | tcttcccatc | tcggggaccc | ttttctctta | ctataaaatt  | 480 |
| gtttcctcca | ttctgagggt  | ttcatcatca | ggtgggaagt | ataaggcctt | ctccacctgt  | 540 |
| gggtctcacc | tgctgggtgt  | ttgctgattt | tatggaacag | gcgttgaggg | gtacctcggt  | 600 |
| tcagatgtgt | catcttcccc  | gagaaagagt | gcagtggcct | cagtgatgta | cacggtgggc  | 660 |
| accccatg   |             |            |            |            |             | 669 |

&lt;210&gt; 1001

&lt;211&gt; 986

&lt;212&gt; DNA

<213> Unknown (H38g851 nucleotide)

<220>

<223> Synthetic construct

<400> 1001

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| gattcagtg  | accaagtaaa | tgactctctg | gtaacagaat | ttgtattact  | tggaacttgca | 60  |
| caatccttg  | aatgcagtt  | tttccttttt | ctcttcttct | ctttattcta  | tgtgggaatt  | 120 |
| atcctggga  | acctcttcat | tgtgttcaca | gtgatctttg | atcctcactt  | acactccccc  | 180 |
| atgtatattc | tgtggccaa  | cctatcgctc | attgacttga | gcctttcatc  | taccacagtt  | 240 |
| cctaggttga | tctacgatct | ttttactgat | tgtaaagtta | tttccttcca  | taattgtatg  | 300 |
| atacaaaagt | tctttatcca | tgttacggga | ggagttgaaa | tgggtgctgct | gatagtcag   | 360 |
| gaatatgata | ggtacactgc | gatctgcaag | cctctccact | atccaactat  | tatgaatccc  | 420 |
| aaaatgtgca | tgtttttggg | agcagcagct | tgggtcattg | gggtgattca  | tgctatgtct  | 480 |
| cagtttgttt | ttgtcataaa | ttaaccttct | gtggccctaa | taatgtgggg  | agcttttatt  | 540 |
| gtgattttcc | tcggtttatt | aaacttgcac | gcacggacac | ttacgggcta  | gaatttgtgg  | 600 |
| tcactgccaa | cagtggattc | atatcgatgg | gcaccttctt | tttcttaatt  | gtatcataca  | 660 |
| tttttattct | ggtcactgtc | caacgacatt | cctcaaatga | tttatccaaa  | gcattcttca  | 720 |
| cttcgtaggc | tcacatcacc | gtagtgggtt | tgttttttgc | tccatgcatg  | tttctctacg  | 780 |
| tgtggccttt | ccctactaag | tcattggata | aattttttgc | catcatgaac  | tttgttgtca  | 840 |
| cccctgtctt | aaatcctgcc | atctatactt | taaggaacaa | agatatgaag  | tttgcaatga  | 900 |
| gaaggctgaa | tcaacatatt | ttaaattcta | tggagacgac | ataacacatt  | tggttgatga  | 960 |
| gagcacagga | taaatgccat | ggacca     |            |             |             | 986 |

<210> 1002

<211> 659

<212> DNA

<213> Unknown (H38g852 nucleotide)

<220>

<223> Synthetic construct

<400> 1002

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| agtgtgctgt  | ctattttctga | gacctattat  | accgtggcca | tcaaccccca | aatgctgtcc | 60  |
| gggtctcctca | gtcctcaaca  | aaccatctcc  | atcccaggct | gtgccgctca | gctctttttc | 120 |
| tatctcactt  | ttgggtgcaa  | taaatgcttc  | ctgctcacag | ccatggggta | tgaccactat | 180 |
| gtggccatct  | gcaacctctc  | acagtattca  | gtcatcatgg | gcaaaaaggc | ttgtatacaa | 240 |
| ctggtcagtg  | gatcctggaa  | cattggcctg  | agcacagcta | tcattcaggt | gtcttctgta | 300 |
| ttcagccttc  | ccttctgtga  | tgctaattct  | atctcccact | tcttttgtga | tatccggccc | 360 |
| ataatgaagc  | ttgcctgtgc  | agacactact  | atcaaggagt | ttattacttt | gctcatcagt | 420 |
| ctctgtgtcc  | ttgttctgcc  | catgggtattg | atcttcatct | cctatgtcct | aattgtcacc | 480 |
| accatcctca  | agattgcac   | agctgagggc  | ggagaaaggc | ctttgctact | tgtgcctcac | 540 |
| acctcacagt  | ggtcattgtc  | cactatggcc  | gtacttcttt | catctaccta | aaacccaaat | 600 |
| cccaaaattc  | cctgcaggac  | agacttatct  | ctgtgacata | cactgttatt | actcctctg  | 659 |

<210> 1003

<211> 939

<212> DNA

<213> Unknown (H38g853 nucleotide)

<220>

<223> Synthetic construct

<400> 1003

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| atgtctacgt | ctaatacacac | ccagttccat  | ccttcttcat | tctactgct  | gggtatccca  | 60  |
| gggctagaag | atgtgcacat  | ttggattgga  | gtcccttttt | tctttgtgta | tcttgttgca  | 120 |
| ctcctgggaa | acactgctct  | cttgtttgtg  | atccagactg | agcagagtct | ccatgagcct  | 180 |
| atgtactact | tcttgcccat  | gttggtattcc | attgacctgg | gcttgtctac | agccaccatc  | 240 |
| cccaaaatgt | tgggcatctt  | ctggttcaat  | accaaagaaa | tatcttttgg | aggctgcctt  | 300 |
| tctcacatgt | tcttcatcca  | tttcttcaat  | gctatggaga | gcattgtgtt | gggtggccatg | 360 |
| gcctttgacc | gctacattgc  | catttgcaaa  | cctcttcggt | acaccatgat | cctcaccagc  | 420 |

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| aaaatcatca | gcctcattgc  | aggcattgct  | gtcctgagga | gcctgtacat | ggttggtcca | 480 |
| ctgggtgttc | tccttctgag  | gctgcccctc  | tgtgggcac  | gtatcatccc | tcatacttat | 540 |
| tgtgagcaca | tgggcattgc  | ccgtctggcc  | tgtgccagca | tcaaagtcaa | cattaggttt | 600 |
| ggccttgcca | acatatctct  | cttggttactg | gatgttatcc | ttattattct | ctcctatgtc | 660 |
| aggatcctgt | atgctgtctt  | ctgcctgccc  | tcctgggaag | ctcgactcaa | agctctcaac | 720 |
| acctgtgggt | ctcatattgg  | tgttatctta  | gcctttttta | caccagcatt | tttttcattc | 780 |
| ttgacacatc | gttttgccca  | taatatccca  | cagtatatat | atattatatt | agccaacctg | 840 |
| tatgtggttg | tcaccaccagc | cctcaatcct  | gtaatctatg | gagtcaggac | aaagcagatt | 900 |
| cgagagagag | tgctgaggat  | ttttctcaag  | accaatcac  |            |            | 939 |

&lt;210&gt; 1004

&lt;211&gt; 877

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g854 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1004

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| tacatgataa  | ccatcttatg  | ggaaatatct  | aagccagtaa | ataatatattt | tctaactctt  | 60  |
| tctgtaagat  | atcaaagtct  | aatcactact  | gtgtcataat | tgtaaagtga  | attataatat  | 120 |
| aaattttactg | agtttttctg  | agtacctaata | gagttaaaaa | atatgggagc  | atatgtagta  | 180 |
| ctgtgcttgt  | atcaatatgg  | ataaggtatc  | tggaagtctt | ttctgaacat  | ctttcggtgc  | 240 |
| tgtgagatt   | attccactga  | tgggatgggt  | ccatggctgc | tatgtgacca  | tctgcaactgc | 300 |
| atgaaaatca  | tgactcaata  | taggtgtggc  | catcttgcgt | gaatggcatg  | caactggaaga | 360 |
| tttatccagg  | cacagttag   | atcctctccc  | cagtctgact | tcctttctat  | aattccaatg  | 420 |
| tcacaatatg  | aatagcccat  | tcatatgtga  | cttaaacact | ttgttgaagc  | tcctctgcat  | 480 |
| aggtagtatg  | atacacttgg  | tctctttgtt  | gctgccaatg | atgggttcaa  | ctgcctgtta  | 540 |
| aacatcatct  | tcttgatgggt | ttcttaagtg  | gccatcctat | atactttgaa  | atcccacagc  | 600 |
| ttggaggaaa  | gatacaaagc  | tctctctacc  | tgtgtctctc | acaccaccgt  | ggccatctaa  | 660 |
| ttctttgtgt  | tctgtatact  | tgtttatctg  | tgccagtgga | cccttcccca  | gtcagtaaaag | 720 |
| cagtggctgt  | gctttacacc  | atgataacgc  | ctacattaaa | ccctttagtc  | taaccctcag  | 780 |
| aaatgcagag  | gtgaaaagtg  | ttgagaaact  | tctgggtcaa | aagatgactt  | gaagagagaa  | 840 |
| ataatccaaa  | cataagatga  | ttttactctt  | tcaatgg    |             |             | 877 |

&lt;210&gt; 1005

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g855 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1005

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| atggagaaga | aaaagaatgt | gactgaattc | attttaatag  | gtcttacaca  | gaaccccata | 60  |
| atggagaaag | tcacgtttgt | agtatttttg | gttcttttaca | tgataaacact | ttcaggcaac | 120 |
| ctgctcattg | tggttaccat | taccaccagc | caggtctctga | gtcccccat   | gtacttcttc | 180 |
| ctgacccacc | tttctttgat | agacacagtt | tattcttctt  | cttcagctcc  | taagttgatt | 240 |
| gtggattcct | ttcaagagaa | gaaaatcatc | tcctttaatg  | ggtgtatggc  | tcaagcctat | 300 |
| gcagaacaca | tttttggtgc | tactgagatc | atcctgctga  | cagtgtatggc | ctgtgactgc | 360 |
| tatgtggcca | tctgcaaac  | tctgaactac | acaaccatta  | tgagccacag  | cctgtgcatt | 420 |
| ctcctgggtg | cagtggcctg | ggtgggagga | tttcttctatg | caactattca  | gattctcttt | 480 |
| acagtattgc | tgcccttctg | tggccccaat | gtcataggcc  | acttcatgtg  | tgacttgtac | 540 |
| ccattgttaa | aacttggtt  | catagacact | catacccttg  | gtctctttgt  | tgctgtgaac | 600 |
| agtgggttta | tctgcttatt | aaacttcctt | atcttggttg  | tatcctatgt  | gatcatcttg | 660 |
| agatctttta | agaacaatag | cttggagggg | agggtgtaaag | ccctctccac  | ctgtatttct | 720 |
| cacatcatag | tagttgtctt | attctttgtg | ccctgtatat  | ttgtgtatct  | gcgctcagtg | 780 |
| accactctgc | ccattgataa | agctgttgct | gtattttata  | ctatgggtgt  | cccaatgtta | 840 |
| aatcccgtgg | tctacacact | cagaaatgct | gaggtaaaaa  | gtgcaataag  | gaagctttgg | 900 |
| agaaaaaaag | tgacttcaga | taatgat    |             |             |            | 927 |

<210> 1006  
 <211> 738  
 <212> DNA  
 <213> Unknown (H38g856 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1006  
 tgtattcaac aacattgac tccactttgt ctctgcatgt tctcctttta ttttaatttg 60  
 taccattttt ttcccaaata aaagtacttg cactcactta gagatgctga aataaattga 120  
 ttggtataaa gtaaggatc tgattaacca aatttacact aaagccaatt ggccttttca 180  
 tggattataa cactatgcac aaccactcca tactcaaaca tgcattttct tctccaatgt 240  
 tatatgatgc agcacctagc tctttacagg acattttttt cttggtgggt cacagatttt 300  
 ccttctgttg gtgatggcct aggccactat agggccatct gcaagtcctt gcagtatttg 360  
 gttgtcatga agcaatggct gtgtgttggt ctgctggtgg tgtcctgggc tggaggattt 420  
 ttgcacatag taattcaact tggacttatt tatgggctcc catcttatga cccaatgtc 480  
 attggtcatt ttatttggta catggacccc ttaatgaagc ttgtctgtga ctacacactc 540  
 aacagatttg cctattttgc aggtcatgat taaatactag gttttatgta tttcacttat 600  
 gctcagactg gactgtttcc ttttgggtgat tgcacctcat tattcttttg tcattttttc 660  
 cctagaggac ttggttctat aaatcttgct atacatagtt attatccctg tggcatctct 720  
 agagatacgg agcctacc 738

<210> 1007  
 <211> 786  
 <212> DNA  
 <213> Unknown (H38g857 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1007  
 ctaattgtag tcaccgtaac tgtcagtgag accctgggct caccaatgta cttctttctt 60  
 gctggccttat catttataga tatcatttat tcttcaccca tttccacagc attgatttca 120  
 gacttgttct ttgggaataa ttccatatcc tcccatctt gcttggccca gctctttaca 180  
 gagcaccttt ttggtgggtc agaggctctt cttctgttgg tgatggccta tgaccttgca 240  
 ttacttggtt atcatgagac aatgggtgtg tgttttgctg ctggtagcgt cctgggttgg 300  
 aggatttctg cactcagtat ttcaacttag tgttatttat gggctcccat tctgtgacct 360  
 caatgtcatt gatcattttt tctgtgatat gcaccttta ttgaaactgg tctgtactga 420  
 taccatgtt attggcctct tagtgggtggc caatggagga ctagggtgca ctattgtgtt 480  
 tctgtcttta ctcatctctt atggtgtcat ctgcactctc taaagaacct tagtcagaaa 540  
 gggagggtgaa aagccctctc aacctgcagt tccacataa ctgtgggttg tttcttcttt 600  
 gttccctgta tttttatgta tgctagacct gctaggacct tccccattga caaatcagtg 660  
 agtgtgtttt atacagtcac aactccaatg ctgaaccctt taatctacac tctgagaaat 720  
 tctgagatga caagtgtat gaagaagctc tggagaagag acttcatatc aagtagtaca 780  
 taagtg 786

<210> 1008  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g858 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1008  
 atgagacaga ataataatat tacagaattt gtccctcctgg gcttctctca ggatctggat 60  
 gtgcaaaaag cattattttg catattttta ctcacatact tggtgacagt ggtggggaac 120  
 ctgctcattg tggtgactat tattgccagc ctttccttgg gctcctcaat gtacttcttc 180  
 cttgcctgcc tgtcatttat agatgctgca tattccacta caatttctcc caaattgatt 240  
 gtagacttac tctgtgataa aaagactatt tctttccag cttgcatggg ccagttattt 300

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atagaccagc | ctggatggcg | gagctgaggt  | cgtgcttctt | gtggtgaagg | cctgtgatca | 360 |
| ccatgtggac | atctggaagc | cactgcgcta  | tctcgactat | catgaatcga | cagggctgaa | 420 |
| tgcggctgct | cgtggctgtc | gtcgcactgcg | aggtgttctg | cattcgctgt | ctcatattgt | 480 |
| gagtgtgtat | acagtctcgc | ctactgtggc  | cccaatgtca | ttgactactt | tgtctgtgac | 540 |
| atgtacccag | ttattggaac | tggtatgcac  | tgacacctac | tttattggcc | ttactgtttt | 600 |
| tgtcaatgg  | ggaacaatct | gtatagtcgt  | cttcaccctt | ctactaatct | cctatggagt | 660 |
| cacctaatac | tcccttaaaa | cttacagtca  | agaagggagg | cataaagtcc | tgtttacctg | 720 |
| cagctccac  | attatcgtct | ttgccctctt  | ttttgttccc | tgtattttca | tgtatgttag | 780 |
| acctgtttca | aacatccttt | tgataaattc  | ctgacagtgt | tttatacagt | tatcaccccc | 840 |
| atgttgaatc | ctttaatata | cacattgaga  | aattcagaga | tgagaaattc | tgtagaaaca | 900 |
| ctcttgtgta | aaaagttaac | tgtattagag  |            |            |            | 930 |

&lt;210&gt; 1009

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g859 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1009

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| atgcagagga  | gcaatcacac  | agtgactgag | tttatactgc | tgggcttcac | cacagaccca | 60  |
| gggatgcagc  | tgggcctctt  | cgtgggtgtc | ctgggcgtgt | actctctcac | tgtggtagga | 120 |
| aatagcacc   | tcatcgtgtt  | gatctgtaat | gactcccacc | tccacacacc | catgtatttt | 180 |
| gtcgttgga   | atctgtcgtt  | tctggatctc | tggtattctt | ctgtctacac | cccaaagatc | 240 |
| ctagtgatct  | gcattctctga | agacaaaagc | atctcctttg | ctggctgcct | gtgtcagttc | 300 |
| ttcttctctg  | cagggctggc  | ctatagttag | tgtctgttac | tggctgccat | ggcttatgac | 360 |
| cgctacgtgg  | ccatctccaa  | gcccctgctt | tatgcccagg | ccatgtccat | aaagctgtgt | 420 |
| gcattgtctg  | tagcagtctc  | atattgtggt | ggctttatta | actcttcaat | catcaccaag | 480 |
| aaaaacgtttt | cctttaactt  | ctgccgtgaa | aacatcattg | atgacttttt | ctgtgatttg | 540 |
| cttcccttgg  | tggagctggc  | ctgtggcgag | aaggcggtct | ataaaattat | gatgtacttc | 600 |
| ctgctggcct  | ccaatgtcat  | ctgccccgca | gtgctcatcc | tggcctccta | cctctttatc | 660 |
| atcaccagtg  | tcttgaggat  | ctcctctctc | aagggtacc  | tcaaagcctt | ctccacatgc | 720 |
| tcttcccacc  | tgacctctgt  | cactttatac | tatggctcca | ttctctacat | ctacgtctc  | 780 |
| cccagatcta  | gctattcttt  | tgatatggac | aaaatagttt | ctacatttta | cactgtggtg | 840 |
| ttccccatgt  | tgaattctcat | gatctacagc | ctaaggaata | aggatgtgaa | agaggctctg | 900 |
| aaaaaacttc  | tccca       |            |            |            |            | 915 |

&lt;210&gt; 1010

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g860 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1010

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atgatctgtg | aaaatcacac | cagagtcact | gaatttattc | ttcttggttt | tacaaacaac  | 60  |
| cccagatgc  | aagtttccct | ctttattttt | ttcctggcca | tttatacagt | cactttgttg  | 120 |
| ggcaactttc | ttattgtcac | agttaccagt | gtggatctcg | cacttcaaac | acccatgtac  | 180 |
| ttctttcttc | aaaatctgtc | acttcttgaa | gtatgtttca | ccttggttat | ggtgccaaaa  | 240 |
| atgctttag  | atctagtgtc | cccaaggaaa | attatctctt | ttgtgggctg | tggtaccacg  | 300 |
| atgtacttct | tcttcttctt | tggcagttct | gaatgtttcc | ttctctccat | gatggcttat  | 360 |
| gatcgctttg | tggccatctg | taaccctctc | cattattcag | tcataatgaa | caggctcccta | 420 |
| tgtttgtgga | tggccatagg | ctcttggatg | tccggtgttc | ctgtgtctat | gctacagaca  | 480 |
| gcttggatga | tggcccttcc | tttctgtgga | ccaaatgccg | tggaccactt | tttctgtgat  | 540 |
| ggtccccacg | tgtaaaaact | agtcacagt  | gatacaacca | tgtatgaaat | gcaagcactt  | 600 |
| gcctccacac | tcctgtttat | catgtttccc | ttttgtctca | ttttggtttc | ctacaccgcg  | 660 |
| attatcataa | caattctgag | gatgtcctct | gccactggcc | gccagaaggc | atcttctact  | 720 |
| tgttctctac | acctcattgt | ggtgtccctc | ttctacggaa | cagccagtct | gacctacctg  | 780 |
| cggcccaaat | caaaccagtc | ccctgagagc | aagaagctag | tgtcattgtc | ctacactgtc  | 840 |

atcacaccta tgctaaaccc catcatctac ggcctgagga acaatgaagt gaaaggggct 900  
gtcaagagga caatcactca aaaagtctta cagaagttag atgtgttt 948

<210> 1011

<211> 927

<212> DNA

<213> Unknown (H38g861 nucleotide)

<220>

<223> Synthetic construct

<400> 1011

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| atggcgaata | gaaacaatgt  | gacagagttt  | attctattgg | ggcttacaga | gaatccaaaa | 60  |
| atgcagaaaa | tcatatttgt  | tgtgttttct  | gtcatctaca | tcaacgccat | gataggaaat | 120 |
| gtgtcatttg | tggtcacccat | cactgccagc  | ccatcactga | gatcccccat | gtactttttc | 180 |
| ctggcctatc | tctcctttat  | tgatgcctgc  | tattcctctg | tcaatacccc | taagctgac  | 240 |
| acagattcac | tctatgaaaa  | caagactatc  | ttattcaatg | gatgtatgac | tcaagtcttt | 300 |
| ggagaacatt | ttttcagagg  | tgttgagggtc | atcctactta | ctgtaatggc | ctatgaccac | 360 |
| tatgtggcca | tctgcaagcc  | cttgcaactat | accaccatca | tgaagcagca | tgtttgtagc | 420 |
| ctgctagtgg | gagtgtcatg  | ggtaggaggc  | tttcttcctg | caaccataca | gatcctcttc | 480 |
| atctgtcaat | tacctttctg  | tggtccta    | gtcatagatc | actttatgtg | tgatctctac | 540 |
| actttgatca | atcttgccctg | cactaatacc  | cacactctag | gactcttcat | tgctgccaac | 600 |
| agtgggttca | tatgcctggt  | aaactgtctc  | ttgctcctgg | tctcctgcgt | ggtcatactg | 660 |
| tactccttaa | agaccacacag | cttagaggca  | aggcatgaag | ccctctctac | ctgtgtctcc | 720 |
| cacatcacag | ttgtcatctt  | atcctttata  | ccctgcata  | ttgtgtacat | gagacctcca | 780 |
| gctactttac | ccattgataa  | agcagttgct  | gtattctaca | ctatgataac | ttctatgtta | 840 |
| aaccctttaa | tctacacctt  | gaggaatgct  | caaataaaaa | atgccattag | gaaattgtgt | 900 |
| agtaggaaag | ctatttcaag  | tgtcaaa     |            |            |            | 927 |

<210> 1012

<211> 488

<212> DNA

<213> Unknown (H38g862 nucleotide)

<220>

<223> Synthetic construct

<400> 1012

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tggaaaaatc | atttcacctc | tgtgaattgt | ggttttgcc  | tctgcagagc | tgaatgttaa | 60  |
| ccatagccca | agatactaag | tattatagga | ttgaaatgaa | atataaatga | aactttgtaa | 120 |
| atgttaaatt | ataacacaaa | tcatatgggc | agtgtcgatg | tcctaattgt | tcctaactcc | 180 |
| tcatcacact | ctcctacttc | ttcattgtgg | ctgccatcct | gatatccgct | ctgcagaggg | 240 |
| gaggcacaag | gcttttccca | cctgtctcct | ccacctgggt | taattctcct | ccagcacaat | 300 |
| gaacaagcct | cacctatttg | tgccccagct | ccatcttctc | ttatgagagg | ggcaaggtag | 360 |
| tgtctacggg | ttacacatgc | atcactcctg | tgccaaaccc | cttgatctgc | agcatgagga | 420 |
| agaaggaact | caagcatgct | cttaaaaaaa | aagaagaaat | tgcaagggtc | ttgctgctca | 480 |
| gaacacat   |            |            |            |            |            | 488 |

<210> 1013

<211> 953

<212> DNA

<213> Unknown (H38g863 nucleotide)

<220>

<223> Synthetic construct

<400> 1013

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atgttttagct | ctgagccac  | catagatgga | aatcagtc   | tggtgtgcaa | attcacattt | 60  |
| gtggcttttt  | cttctataga | agaattacag | cttgactct  | tcattgtgtt | cttaatcatc | 120 |
| acttatgcac  | tataggagga | aatatcatca | tcactctcct | gatctggatc | acccctgccc | 180 |
| tgcacactcc  | aatgtatttc | ttcctggtga | acctctcatt | tctggagatg | tgctatacca | 240 |



|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| ccagtgtggt | gcctcatgct | ggtgcacctg | ctgggtggaga | ccaaaaccat | aagtgtgggt  | 300 |
| ggctgtgcaa | cccagatgta | catatttgcc | atcttgggac  | tgacagaatg | ctgcttgcta  | 360 |
| gcagctatgg | cttacgatcg | ctttgtagct | atctgttacc  | cactgcatta | cactctcttc  | 420 |
| atgggccctc | gtgtttgttt | gaaattggct | gcagcatctt  | ggttcactgg | agtgggtggtg | 480 |
| gagtcagccc | agatcaccct | gatcttcact | ttgcctttct  | gtggaacagg | aaagattcaa  | 540 |
| cacttttttg | tgacataatg | cctgtactga | aactggcttg  | tattgatacc | tcccaaattg  | 600 |
| aaattgtgat | gttttctctc | tccgtgctat | ttattgtgag  | tccttgtttc | ctcattctgt  | 660 |
| gctcccacat | gcacatccct | gtgaccatct | tgagaatccc  | ttcagcagct | ggaagacaca  | 720 |
| aagctttctc | cacttggtct | tctcatatct | tggttgtttc  | tctgttctat | ggcactgcct  | 780 |
| tgttcactta | tctgcaacct | aagactgcac | acactccaga  | aacagacaaa | gcaactgcac  | 840 |
| tcatgtacac | aatggtcaca | cctgctttga | atcctgttat  | ctataccttg | aggaacaagg  | 900 |
| aagtaaagga | agcctttcaa | aggataaccc | aaaggaactc  | tcttagacaa | acg         | 953 |

&lt;210&gt; 1014

&lt;211&gt; 873

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g864 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1014

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| tccatgtacc | tggtcacgat | gctgaggaac  | ctgttcatca  | tcttggtggtg | cagctctgac | 60  |
| ccccacttcc | acacccccat | gtacttcttc  | ctctccaacc  | tgctctgggc  | tgacattggt | 120 |
| ttcacctcgg | ccacagttcc | caagatgatt  | gtggacatgc  | agtcgcatag  | cagagtcac  | 180 |
| tcttatgcgg | gctgcctgac | acagatgtct  | ttctttgtcc  | tttttgcatg  | tatagaagac | 240 |
| atgctcctga | ctctgatggc | ctatgaccga  | tttggtggcca | tctgcccac   | tgccaccccc | 300 |
| tgcaactacc | agtcacatcg | aatcctcacc  | tctgtgtctt  | cttagttttg  | gtgtcctttt | 360 |
| tccttagcct | gttggtattc | cagctgcaca  | gctggattgt  | gttacacaa   | tcaccttctt | 420 |
| caagaatgtg | gaaatctata | atttttttct  | tgtagcccat  | ctcaacttct  | caaccttgcc | 480 |
| tgttctgaca | gcacatcaaa | taacatatta  | tgtatttttag | atatccctat  | atttggtttt | 540 |
| cttcccattt | cagggatcct | tttgtcttac  | tataaaattg  | tctcctccat  | tccaagaatt | 600 |
| ccatcgtcag | atgggaagta | taaagccttc  | tccacctgtg  | gctctcacct  | ggcagttggt | 660 |
| tgcttatttt | atgaaacagg | cattggcggtg | tacctgactt  | cagctgtgtc  | atcatctccc | 720 |
| aggaatggag | tggtggcatc | agtgatgtac  | gctgtgggtc  | tccccatgct  | gaaccttttc | 780 |
| atctacagcc | tgagaaacag | ggacattcat  | agtgccctgt  | ggaggctgcg  | cagcagaaca | 840 |
| gtcaaatctc | atgatctggt | ccatccttct  | tct         |             |            | 873 |

&lt;210&gt; 1015

&lt;211&gt; 981

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g865 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1015

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atggatgtct  | ctatatctct | cctcctagaa | ccacagagga | tccagaacgg | cagccggtcc | 60  |
| tcactgggct  | gttcctgtcc | atgtgcctgg | tcacagtgtc | ggggaagctg | ctcatcatgt | 120 |
| tgcccttcag  | ccctgactcc | cacctccaca | cccacatgta | cttcttcttc | tccaacctgt | 180 |
| ccttgccctga | catcggtttc | acctccacca | ttgtccccaa | gatgattgcg | gacatccagt | 240 |
| ctcacagcag  | agtgatctcc | tatgcaggcc | gcctgactca | gatgtctctc | tttgccattt | 300 |
| ttggaggcat  | ggaagacaga | catgtcctcg | agtgtgatgg | cctatgaccg | gtttgtagcc | 360 |
| atctgtcacc  | ctctatatca | ttcagccatc | atgaatccgt | gtttctgtgg | cttctacttt | 420 |
| ttgttgtctt  | tttttttttc | tcagtctttt | agacacccag | ctgcacaact | tgattgcttt | 480 |
| acaaatgacc  | tgcttcaagg | atgtggaaat | tcctaatttc | ttctgtgacc | cttctcaact | 540 |
| cccccatctt  | gcatgttggt | acaccttcac | caataacatc | atcgtgtatt | tccctgctgt | 600 |
| catattttgt  | ttccttccca | tctcggggac | ccttttctct | ttaaaactgt | tctctccatt | 660 |
| ctgagggttt  | catcatcagg | cgggaagtat | aaaaccttct | ccacctgtgg | gtctcacctg | 720 |
| tcagttattt  | gctgatttta | tggaacaggt | gttgagggtg | acctcagttc | agatgtgtca | 780 |
| tcttccctga  | gaaaggctgc | agtggcctca | gtgatgtaca | agatgggtc  | ccccatgctg | 840 |

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aaccccttca | tctacagcct  | gagaaacagg | gatatgaaaa | gtgtcctgcg | gcggccgcac | 900 |
| ggcagcacgg | tctaattctca | atatcttctt | atctgttcca | ttccttttgt | aggggtgggt | 960 |
| aaaaaaggca | gcaaggtcaa  | a          |            |            |            | 981 |

&lt;210&gt; 1016

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g866 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1016

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| atgggtgaca  | agggaaacagg | caaccattca | gatgtaactg | atttcattct | tgaaggcttc | 60  |
| aggggtccgcc | cagagttcta  | cattctcctc | ttcttctcgt | tcctgctgat | ctatagcatg | 120 |
| gttctttttgg | ggaacattag  | tgtgatgaca | atcattgtaa | ctgattccca | gctgaacaca | 180 |
| ccaatgtatt  | tttttctagg  | caacctctcc | ttcattgacg | tctcctactc | cactgttatt | 240 |
| gctcctaag   | ccatggcccc  | cttctgtctc | gaaaaaaaga | cagtctcttt | tgcaggttgt | 300 |
| gttgcccag   | tattcctttt  | tgccctgttc | attgtaacag | aggggtttgt | cctggcagcc | 360 |
| atggcctatg  | accgcttcag  | tgccatctgc | aatcctcttc | ttcatagtgt | tcacatgtca | 420 |
| agacgcctct  | gcactcagtt  | ggttgctggg | tcttatttct | gtggctgggc | cagttccatc | 480 |
| ctccaagtca  | gtgtaacatt  | ctcagtgctc | ttctgtgctt | ccagagtcac | tgctcacttc | 540 |
| tactgtgatt  | cttatcaaat  | tgaaaagatt | tcctgttcta | atctctttgt | caataagatg | 600 |
| gtatctctga  | gtttgagtg   | catcattatt | ttgcctacaa | ttgttggtat | tatagtatct | 660 |
| tacctgtata  | ttgtatcctc  | agtcttgaag | atccccctca | gtgaaggag  | aaagaaagac | 720 |
| ttttccactt  | gcagctccca  | tcggggtgtt | gtaagtttgc | tc         |            | 762 |

&lt;210&gt; 1017

&lt;211&gt; 1008

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g867 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1017

|             |            |             |            |            |             |      |
|-------------|------------|-------------|------------|------------|-------------|------|
| tatacagacc  | cacagaatct | aacagatgct  | tcaaaatacc | tcctcctaga | actctcagag  | 60   |
| gatccaaaac  | tgcagctggc | cctcgagtgg  | gcgtgaaccg | tgtacatgta | cctagtcatt  | 120  |
| gggtctggag  | aatctgctca | ttatcctggc  | cgctcagctc | gacttccacc | tcacaccccc  | 180  |
| catgtacttc  | ttcctctcca | acctgtcctt  | ggctgacatc | ggtttcacct | ccaacacggt  | 240  |
| ccccaaagatg | attgtggaca | tccaatctca  | cagcagagtc | atctcctatg | caggctgcct  | 300  |
| gactcagatg  | tctctctttg | ctgttttttg  | aggcatggaa | gaaagacatg | ctcctgagtg  | 360  |
| tgagggccta  | tgaccgggtt | gtagccatct  | gtcacccctc | atattattca | gccatcatga  | 420  |
| acccatgttt  | ctgtggcttc | ctagttttgt  | gttttttttt | ttctcagctc | tttagactcc  | 480  |
| cagctgcaca  | atttgattgc | cttaciaaatg | acctgcatca | aggatgtgga | aattcctaata | 540  |
| ttcttctgtg  | acccttctca | actcccacac  | cttgctgtgt | gtgacacctt | caccaataac  | 600  |
| atagtcatgt  | atttccttgc | tgccatattt  | ggttttcttc | ctatctcacg | gatcattttc  | 660  |
| tcttactata  | aaattgtttc | ctccatgctg  | agtgtttcat | catcagggtg | gaagtataaa  | 720  |
| gccttctcca  | cctgtgggtc | tcccctgtca  | gttgtttget | tattttatgg | aaaagtcggt  | 780  |
| gggggggtacc | tgagttcaga | tgtgtcatct  | tccccagaa  | aggggtgcag | ggcctcaatg  | 840  |
| atgtacacgg  | tgatcacccc | catgctgaac  | cccttcatct | acagactgag | aaacagggac  | 900  |
| atcaaaaagg  | tcctgtgggt | gttgcagggc  | agaacagttt | aatctcatta | ttttattatc  | 960  |
| tgttccattc  | cttttgtagt | gtgggttaaa  | aaaggcagca | aggtcaaa   |             | 1008 |

&lt;210&gt; 1018

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g868 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1018

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| acaggtgtct  | gagaattcct  | cctcctggga | ctctcagagg | atccagaact  | gcagccggcc  | 60  |
| ctcgttttgc  | tgteectgtc  | cctgtccatg | tatctggtea | cgggtgctgag | gaacctgttc  | 120 |
| agcatcctgg  | ctgtcagctc  | tgactgcccc | ctccacaccc | ccatgtactt  | cttccctctcc | 180 |
| aacctgtgct  | ggcctgacat  | cggtttcacc | tcggccatgg | ttcccaagat  | gattgtggac  | 240 |
| acgcagtcgc  | atagcagagt  | catctctcat | gcgggctgcc | tgacacagat  | gtctttcctg  | 300 |
| ctccttggtg  | catgtataga  | aggcatgctc | ctgactgtga | tggcctatga  | ctgctttgtg  | 360 |
| gccatctgtc  | gcccctctga  | ctaccagtc  | atcgtgaate | ctcacctctg  | tgtcttcttc  | 420 |
| gttttggtgt  | cctttttcct  | tagcctggtg | gattcccagc | tgacacagttg | gattgtgtta  | 480 |
| caattaacca  | tcatcaagaa  | tgtggaaatc | tctaatttgg | tctgtgaccc  | ctctcaactt  | 540 |
| ctcaaaacttg | cctgtttctga | cagcgtcatc | aataacatat | tcatatattt  | cgatagtact  | 600 |
| atgtttgggt  | ttcttcccat  | ttcagggatc | tttttgtctt | actataaaat  | tgtcccctcc  | 660 |
| attctaagga  | tttcatcgtc  | agatgggaag | tataaagcct | tctccacctg  | tggctgtcat  | 720 |
| ctagcagttg  | tttgctgggt  | ttatggaaca | ggcattggca | tgtacctgac  | ttcagctgtg  | 780 |
| tcaccacccc  | ccaggaatgg  | tgtgggtggc | tcagtgatgt | acgctgtggt  | caccccatgc  | 840 |
| tgaacctttt  | catctgcagc  | ctgagaaaac | gggacataca | aagtgccctg  | cggaggctgg  | 900 |
| gcagcagagc  | attcgaatct  | catgatctgt | tccatccttt | ttcttgtgt   |             | 949 |

&lt;210&gt; 1019

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g869 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1019

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| atgggtgaca | ggggaacaag  | caatcactca  | gaaatgactg | acttcattct  | tgcaggcttc | 60  |
| agggtacgcc | cagagctcca  | cattctcctc  | ttcctgctat | ttttgtttgt  | ttatgccatg | 120 |
| atccttctag | ggaatgttgg  | gatgatgacc  | attattatga | ctgatcctcg  | gctgaacaca | 180 |
| ccaatgtatt | ttttcctagg  | caatctctcc  | ttcattgatc | ttttctatcc  | atctgttatt | 240 |
| gaacccaagg | ctatgatcaa  | cttctgggtc  | gaaaacaagt | ctatctcctt  | tgcaggctgt | 300 |
| gtggcccagc | tctttctctt  | tgccctcctc  | attgtgactg | agggatttct  | cctggcggcc | 360 |
| atggccttat | accgctttat  | tgccatctgc  | aaccctctgc | tctactctgt  | tcaaagtgtc | 420 |
| acacgtctgt | gtactcagtt  | ggtggctggt  | tcctattttt | gtggctgcat  | tagctcagtt | 480 |
| attcagacta | gcatgacatt  | tactttatct  | ttttgocgtt | ctcgggctgt  | tgaccacttt | 540 |
| tactgtgatt | ctcgcccaact | tcagagactg  | tcttgttctg | atctctttat  | ccatagaatg | 600 |
| atatcttttt | ccttatcatg  | tattattatc  | ttgcctacta | tcatagtcat  | tatagtatct | 660 |
| tacatgtata | ttgtgtccac  | agttctaaag  | atacattcta | ctgagggaca  | taagaaggcc | 720 |
| ttctccacct | gcagctctca  | cctggggagt  | gtgagtgtgc | tgtatggtgc  | tgtctttttt | 780 |
| atgtatctca | ctcctgacag  | atttccctgag | ctgagtaaag | tggcatcctt  | atgttactcc | 840 |
| ctagtcactc | ccatgttgaa  | tccttttgatt | tactctctga | ggaacaaaaga | tgtccaagag | 900 |
| gctctaaaaa | aatttctaga  | gaagaaaaat  | attattctt  |             |            | 939 |

&lt;210&gt; 1020

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g870 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1020

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| cattctttttc | tcagatatat  | tttcgctaag | ttgacagggtg | agccagagct | tcaaccctct  | 60  |
| ctctactctg  | tgttttgggtc | accctaactg | ggatgaccac  | accacacctc | catgtaccca  | 120 |
| ctgcccacac  | tccatgtacc  | tttatatctt | tagcttttcc  | ttcatagggt | tctttctatcc | 180 |
| ctctgtcatt  | tctcccaaaa  | tgacaataag | ctttgtgaca  | gaaaagaaca | tcatcacata  | 240 |
| tgtgacatca  | aacactcagc  | cttttctctc | ggcttctttg  | tcattagtga | ttactccata  | 300 |
| tttatcccac  | tggccttggg  | tcactatgag | gccatgaccc  | tgccggtctc | tttcataagt  | 360 |
| ttcattttctg | tagatgggtc  | ataagttata | gaatttgctg  | atgctgtggt | ccatcaaggg  | 420 |

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| acatggacca | attcctgttt | tgtgatcaca  | gttgcacgag | ccttaacttg | tgtaacatag  | 480 |
| gcccgcctca | ggctgcctga | atcagtacct  | atgtcagaag | caggtggatt | tgtattcatg  | 540 |
| agaaccagca | gtgtaccatg | ctgtgttatc  | attttcatat | tttgttttca | ttcttttcaa  | 600 |
| catttttcat | taaccacagt | gtccaaatct  | tcagccagat | tccataaatc | tgttttatttc | 660 |
| tttttttggg | ttagggacat | tcagtgtacct | cagatctcca | gaagctatgg | gttagtgtaa  | 720 |
| attacagtgt | ccttcaccaa | gatggggcca  | gtgatgaacg | gtctgttcaa | caccttgagg  | 780 |
| aacaagacta | tctaacttgc | tgcaatgaaa  | cctttgtcat | tttcttct   |             | 828 |

&lt;210&gt; 1021

&lt;211&gt; 1001

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g871 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1021

|             |            |             |             |            |             |      |
|-------------|------------|-------------|-------------|------------|-------------|------|
| gatacagacc  | cacagagtct | aacagatgtc  | tctatatctc  | ttctcctcga | actctcagag  | 60   |
| gaccagaaac  | tgcagccggt | cgctcgctggg | ctgttctctgt | ccatgtgcct | ggtcacgggtg | 120  |
| ctgggagaacc | tgctcatcat | cctggccgctc | agccctgact  | cccacctcca | caccccatgt  | 180  |
| acttcttctc  | ctccaacctg | tccttgccctg | acatcggttt  | cacctccaca | cgggtcccca  | 240  |
| gatgattgtg  | gacatccagt | ctcacagcag  | agtcacatctc | tatgcaggct | gcctgactca  | 300  |
| gatgtctctc  | tttgccattt | ttggaggcag  | ggaagagaga  | catgtctctg | agtgtgatgg  | 360  |
| cctacgacca  | gtttgtagcc | atctgtcacc  | ctccatatcg  | ttcagccatc | ttgaaccctg  | 420  |
| gtttctgtgg  | cttcctagat | ttgttgctct  | tggttttttt  | tttttttttt | ttttttccct  | 480  |
| cagtctttta  | gactctcagc | tgcaacaact  | gattgcctta  | caaataacac | gcttcaagga  | 540  |
| tggtgaaatt  | cctaatttct | tctgggaacc  | ttctgtgaca  | ccttcaccag | gaacatcaac  | 600  |
| atgtatttcc  | ctgctgccgt | atttggtttt  | cttcccatct  | cggggaccct | tttctcttac  | 660  |
| tgtaaaattg  | tttctcccat | tctgagggtt  | tcacatcatg  | gtgggaagta | taaaccttca  | 720  |
| ccacctgtgg  | gtctcacctg | tcagttgttt  | gctgatttta  | tggaacaggc | gttgagggtg  | 780  |
| acctcggttc  | agatgtgtca | tcttccccga  | gaaagcgtgc  | agtggcctca | gtgatgtaca  | 840  |
| cgggtggtcac | ccccatgctg | aaccccttca  | tctacagcct  | gagaaacagg | gatatgaaaa  | 900  |
| gtgtcctgcg  | gcggccgcac | agcagcgcag  | tctaattctca | atatcttctt | atctgttcca  | 960  |
| ttccttttgt  | aggatgggtt | aaaaaaggca  | gcaagggtcaa | a          |             | 1001 |

&lt;210&gt; 1022

&lt;211&gt; 1025

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g872 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1022

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| gatacagacc  | cacagagtct  | aacagatgtc  | tctatatctc  | ttctcctcga | actctcagag  | 60   |
| gatccagaaac | tgcagccggt  | cgctcgctggg | ctgttctctgt | ccatgtgcct | ggtcacgggtg | 120  |
| ctggggaacc  | tgctcatcat  | cctggccgctc | agccctgact  | cccacctccc | cacccccatg  | 180  |
| tacttcttcc  | tctccaacct  | gtccttgccct | gacatcggtt  | tcacctccac | cacgggtcccc | 240  |
| aagatgagcg  | tggaacatcca | gtctcacagc  | agagtcacat  | cctatgcagg | ctgcctgact  | 300  |
| caaattgtctc | tctttgccat  | ttttggaggc  | atggaaaaaa  | gacatgtctc | tgagggtgatg | 360  |
| gcctatgacc  | tggttggtacc | catctgtcac  | cttctatctc  | gttcaaccat | cttgaaccctg | 420  |
| tttgtccgtg  | gcttctctaaa | tttgttgtct  | tttgttgtgg  | tttttttttt | ttttctctca  | 480  |
| gtctttttaga | ctcccagctg  | cacaacttga  | ttgccttaca  | aatgacctac | ttcaaggatg  | 540  |
| tggaatttcc  | taattttctc  | tggaacacct  | ctcaactccc  | ccatcttgca | tggtgtgaca  | 600  |
| ccttcaccag  | gaacaacaac  | atgtatttcc  | ctgctgccgt  | atttggtttt | cttcccatct  | 660  |
| cggggaccct  | tttctcttac  | tgtaaaattg  | tttctcccat  | tctgagggtt | tcacatcatg  | 720  |
| gtgggaagta  | caaaccttct  | ccacctgtgg  | gtctcacctg  | tcagttgttt | gctgatttta  | 780  |
| tggaagcctc  | gttgagggtg  | accttggttc  | agatgtgtca  | tcttccccga | gaaagggtgc  | 840  |
| agtggcctca  | gtgacgtacg  | tacacgggtg  | tcaccccatc  | gctgaactcc | ttcatctaca  | 900  |
| gcctgagaaa  | cggggatatt  | aaaagtgtcc  | tacggcgccc  | gcatggcagc | acagtctaat  | 960  |
| ctcaatacgt  | tcttatctgt  | tccattcctt  | ttgtagggtg  | ggttaacaaa | gacagcaagg  | 1020 |

tcaaaa

1025

&lt;210&gt; 1023

&lt;211&gt; 1044

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g873 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1023

|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| atggatctgg | ggaactcagg | gaatgattca  | gttgtgacca  | agtttgtcct | gctgggacctc | 60   |
| acagagactg | cagctctaca | gcccatactc  | tttgtcatct  | tccttcttgc | ttacgtcact  | 120  |
| accattggag | gcaccctcag | catectggcg  | gccatcctta  | tggaaaccaa | actccacagc  | 180  |
| cccattgact | tcttcctggg | gaacttgtcc  | ctgccagatg  | tggggtgtgt | cagtgtcact  | 240  |
| gtccctgcca | tgtctagcca | tttcatatcc  | aacgacagaa  | gcattcccta | taaggacctgc | 300  |
| ctctccgagc | tcttcttctt | ccacctcctg  | gctggggcag  | actgcttctt | gctgaccatc  | 360  |
| atggcctatg | accgctatct | ggccatctgc  | cagtccctca  | cctacagcag | ccgcatgagc  | 420  |
| tggggaatcc | agcaagccct | ggtgggcatg  | tcattgtgtct | tttccctcac | caatgcactg  | 480  |
| acccaaactg | ttgccctgtc | tcctcttaac  | ttctgtggcc  | ccaatgtgat | caatcacttc  | 540  |
| tactgtgacc | tcacacagcc | cttcacagctc | tcctgcgcca  | gtgttcatct | caatgggcag  | 600  |
| ttgctgtttg | tagcagcagc | tttcatgggt  | gtggccccct  | tggctctcat | cactgtgtcc  | 660  |
| tatgcccatg | tggcagctgc | agtcctgcga  | atccgctctg  | cagagggcaa | aaagaaagcc  | 720  |
| ttctccacgt | gtagttccca | cctcactgtg  | gtgggcatct  | tctatgggac | gggcgtcttc  | 780  |
| agctacacaa | ggctgggttc | agtggagtct  | tcggacaagg  | acaagggcat | tggcaccctc  | 840  |
| aacactgtca | tcagcccat  | gctgaaccca  | ctcatctact  | ggacatctct | gctggacgtc  | 900  |
| gggtgcatca | gtcactgttc | ctccgatgct  | ggcgtgtctc  | caggcccacc | agtgcagagt  | 960  |
| tccttatgct | gcctgcagtt | cacagctctt  | ctttcccccac | ctcctggctg | gggtggactg  | 1020 |
| tcacctctta | atagccatgg | ccta        |             |            |             | 1044 |

&lt;210&gt; 1024

&lt;211&gt; 688

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g874 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1024

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atgctcatatc | ctagctccac | caggaaaatg | gcagcagaaa | gtcactctac | ggtgacagag | 60  |
| ttcattctca  | ggaaaaagcc | agcaagggct | ccagctcccc | ctcttctagg | gatctgtttg | 120 |
| aaaaccgtag  | tggggggcct | catcttgatc | actctagttt | tccttaattc | tcagcttcac | 180 |
| cttcccattg  | actacgtcat | cagaaattta | tcatttatgg | atcactgcaa | ttgctctatt | 240 |
| agtaccctta  | aaatactggg | gaagtttggg | ttagagaaga | ccatcatctc | ctatgaggac | 300 |
| ggcatgtcac  | agctttgtag | tgtttcgtgt | ttatattgtc | atggccaagc | gtaacatgag | 360 |
| gaccagcaac  | tgtgtgcatc | acatttcac  | aagtcagctc | cctgctggta | gttgtagtat | 420 |
| ttatatggag  | ttgactggta | caacaataga | tattttgcct | tgtattaaaa | tagtactagt | 480 |
| gtgagttatt  | catcagtcac | acttctctca | tgcactagca | tctatgatat | tgataggaca | 540 |
| attttctttt  | ttacttgatg | caatattgta | gtcactagat | taacagttgt | ttcctactcc | 600 |
| ttttctctcc  | agcatcctcc | acatcagctt | tacaaagggc | aagctctggg | tttttcccg  | 660 |
| aggtctgacg  | cattcatgct | gttgccct   |            |            |            | 688 |

&lt;210&gt; 1025

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g875 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1025

```

cacacagagc cacggaatct cacaagtgtc tgagaattcc tcctcctggg actctcagag      60
gatccagaac tgcagccgct cctcgctttg ctgtccctgt ccctgtccat gcatctggtc      120
atggtgctga ggaacctgct caacatcctg gctgtcagct ctgactcccc cctccacacc      180
cccacgtact tcttcctctc caacctgtgc tgggctgaca tcggtttcac ctgggccacg      240
gttcccaata tgattgtgga catgcagtcg catagcagag tcatctctca tgcggactgc      300
ctgacacaga tttccttctt gtcctttttt gcatgtatag aaggcatgct cctgactgtg      360
atgacctatg actgctttgt agccatctgt tgccctctgc actaccagc catcgtgaat      420
cctcacctct gtgtcttctt cgttttggtg tcctttttcc ttagcctggt ggattcccag      480
ctgcacagtt ggattgtggt acaattcacc atcatcaaga atgtggaaat ctctaattct      540
gtctgtgacc cctctcaact tctcaaactt gcttgttctg acagcgcat caatagcata      600
ttcatgcatt tccataatac tatgtttggt tttcttccca tttcagggat ccttgtgtct      660
tactataaaa tcgtcccttc cattcttagg atttcatcgt cagatgggaa gtataaagcc      720
ttctccacct gtggctctca cctagcagtt gtttgctgat tttatggaac aggcatggc      780
gtgtacttga cttcagctct gtcaccaccc ccaggaatg gtgtggtggc gtcagtgatg      840
tacgctgtgg tcacccccat gctgaacctt tcatctaca gcctgagaaa caggacata      900
caaagtgcc tgtggaggct gctcagcaga acagtccaat ctcgatctct gttccatcct      960
ttttcttggt tgggtaaggg caaccacatt aaa

```

&lt;210&gt; 1026

&lt;211&gt; 965

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g876 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1026

```

cacagagagc cacggaatct cacaggtgtc tgagaattcc tcctcctggg actctcagag      60
gatccagaac tgcagccgct ctcgctttgc tgtccctgtc cctgtccatg tatctgggtca      120
cgggtgctgag gaacctgtct agcatcctgg ctgtccgctc tgactcccc ctccacaccc      180
ccatatactt cttcctctcc aacctgtgct gggctgacat cggtttcacc tcggccacag      240
ttcccaagat gattgtggac atgcagtcgc atagcagagt catctctcat gcaggctgcc      300
tgacgcagat gtctttcttg gtcttttttg catgtataga aggcagctc ctgactgtga      360
tggcctatga ctgctttgta gccatctgtc accctctgca ctaccagtc atcgtgaatc      420
ctcacctctg tgtcttcttc gttttggtgt cttttttcct tagcctgttg gattcccagc      480
tgcacagttg gattgtgtta caattcacca tcatcaagaa tgtggaaatc tctaattttg      540
tctgtgacct ctctcaactt ctcaaatttg cctgttctga cagcatcatc aatagcatat      600
tcataatatt ccatagtact atgtttggtt tttcttccat ttcagggatc cttttgtctt      660
actataaaat catccctctc attctaagga tttcatcatc agatgggaag tataaagcct      720
tctccacctg tggctctcac ctagcagttg tttgctgatt ttatggaaca gacattggca      780
tgtacctgac ttcagctgtg tcaccacccc ccaggaatgg tgtggtggca tcagtgatgt      840
acgctgtggt caccctcatg ttgaaccttt tcatctacag cctgagaaac agggacatac      900
aaagtgcctt gtgggggctg cacagcagaa cagtcgaatc tcatgatctg ttccatcctt      960
tttct

```

&lt;210&gt; 1027

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g877 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1027

```

atgcagccag aatctggggc caatggaaca gtcattgctg agttcatcct gctgggcttg      60
ctggaggcgc cagggtgca gccagttgtc tttgtgctct tcctctttgc ctacctggtc      120
acggtcaggg gcaacctcag catcctggca gctgtccttg tggagcccaa actccacacc      180
cccattgact tcttctctgg gaacctatca gtgctggatg ttgggtgcat cagcgtcact      240
gttccatcaa tgttgagtcg tctcctgtcc cgcaagcgtg cagttccctg tggggcctgc      300
cttaccagc cttcttctt ccactctgtt gttggagtgg actgcttctt gctgaccgcc      360
atggcctatg accaattcct ggccatctgc cggccctca cctacagcac ccgcatgagt      420

```

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cagacagtcc | agaggatggt | ggtggctgcg | tcctgggctt | gtgctttcac | caacgcactg | 480 |
| accacactg  | tggccatgct | cacgctcaac | ttctgtggcc | ccaatgtgat | caatcacttc | 540 |
| tactgtgacc | tcccacagct | cttccagctc | tcctgtccca | gcacccaact | caatgagctg | 600 |
| ctgctttttg | ctgtgggttt | tataatggca | ggtaccccca | tggctctcat | tgtcatctcc | 660 |
| tatatccacg | tggcagctgc | agtcctgcca | attcgctctg | tagagggcag | gaagaaagcc | 720 |
| ttctccacat | gtggctccca | cctcactgtg | gttgccatat | tctatggttc | aggtatcttt | 780 |
| aactatatgc | gactgggttc | aaccaagctt | tcagacaagg | ataaagctgt | tggaattttc | 840 |
| aacactgtca | tcaatcccat | gctgaacca  | atcatctaca | gcttcagaaa | ccctgatgtg | 900 |
| cagagtgcc  | tctggaggat | gctcacaggg | aggcggtcac | tggct      |            | 945 |

&lt;210&gt; 1028

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g878 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1028

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| atgacagatt  | acaatgaacc | aatggaacca | atggaagata | agaaccagac  | agtagtgact  | 60  |
| gaattttctct | tattgggctt | cacagatcat | ccctatcaga | agattgttct  | cttcttcatg  | 120 |
| tttctctttg  | tttatcttat | cacctggga  | ggtaacttgg | ggatgatcac  | tctcatatgg  | 180 |
| attgatccca  | gactccacac | tcctatgtac | ttttttctta | ggcacttgct  | ctttgtagat  | 240 |
| atttgttctt  | cttcttctgt | tgtgcctaag | atgctgtgta | atatctttgc  | agagaaaaaa  | 300 |
| gacatcactt  | ttctgggttg | tgtgtcacag | atgtggttct | ttggctctct  | tgaggcagct  | 360 |
| gagtgttttc  | tcctggctgc | catggcatat | gaccggtatg | tggccatctg  | caagcccttg  | 420 |
| ttgtatacgc  | tcattatgtc | tcagcaggtc | tgtatgcagc | tgggtggtagg | gccttatgcc  | 480 |
| atggctctta  | taagcaccat | gactcataca | attttcaact | tttgcctacc  | cttttgtggg  | 540 |
| tcaaatatta  | tcaatcactt | tttctgtgat | atttttccac | tgtcttccct  | agcatgtgca  | 600 |
| gacacctggg  | tgaataaatt | tgtgtctgtt | gtcttggctg | gagctatagg  | agtactcagt  | 660 |
| ggctctgatca | tcattgtctc | ctatatctgc | atcctgatga | ccatcttgaa  | gatccagact  | 720 |
| gctgatggga  | agcaaaaagc | tttcttcacc | tgtttttctc | accttgcggc  | tgtctccatc  | 780 |
| ctgtatggga  | ctcttttctt | gatttatgtt | cggccaagtt | caagttcctc  | cctgggtatc  | 840 |
| tataaagtga  | tttctctatt | ttatactgtg | gtaatcccca | tgggttaacc  | ccttattttac | 900 |
| agcttgagga  | ataaggaggt | gaaagatgca | ttcagaagaa | aaattgagag  | gaaaaaattt  | 960 |
| attataggt   |            |            |            |             |             | 969 |

&lt;210&gt; 1029

&lt;211&gt; 687

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g879 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1029

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| ttcttttctt | tagacctcat | tagaagccaa  | gcaaatacaa | tgtcaaagaa  | acactggaca | 60  |
| gccatagctg | agtttattcc | cctgggaccg  | acagatcaag | ccgagttgca  | gcttgtcctt | 120 |
| tttttctgtc | acgttcctgg | tcattttacct | tattatggta | atgggcaatt  | tgagcatgat | 180 |
| tttgatcatt | agaagtgact | gaaaacttca  | cattccaatg | tacttcttcc  | tcagtcacct | 240 |
| ctccttttga | gttctctgtt | atactctcaa  | tgtcactcct | cagatattgg  | ttaatttctt | 300 |
| atccaagaga | aaaaccattt | tcttcattgg  | ttgtgtaagt | gttttataat  | tctacttttt | 360 |
| cattgtcctg | ataatcagag | attatcatat  | gcttacagtg | atggctaattg | actgctacat | 420 |
| ggccatttgc | aagcccttgt | tatatggtag  | taaaatgtcc | agatttgtct  | gcctctctct | 480 |
| ggcttctgtt | tcttaaatat | atggctttgc  | aaactatctg | gcacagacca  | tccggatgct | 540 |
| tcttctgtcc | ttctgaggat | ccaatgagat  | caaccacttt | gactgtgcgg  | acccccctct | 600 |
| gttagtcctc | ccttgccgag | gtacctgtgt  | caaataaatc | atcatgttga  | tggagccaca | 660 |
| ctgtcttttg | aaacctggat | atattttt    |            |             |            | 687 |

&lt;210&gt; 1030

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g880 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1030

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| atgtatctgg | tcacgggtgct | gaggaacctg  | ctcagcatcc | tggctgtcag | ctctgactcc | 60  |
| cacccccaca | cacccatgta  | cttcttccctc | tccaacctgt | gctgggctga | catcggtttc | 120 |
| accttggcca | cggttcccaa  | gatgattgtg  | gacatggggg | cgcatagcag | agtcattctt | 180 |
| tatgggggct | gcctgacaca  | gatgtcttct  | ttgggtactt | ttgcatgtat | agtagacatg | 240 |
| ttcctgactg | tgatggctta  | tgactgcttt  | gtagccatct | gtcgcctct  | gcactaccca | 300 |
| gtcatcgtga | atcctcacct  | ctgtgtcttc  | ttcgttttgg | tgctcttttt | ccttagcctg | 360 |
| ttggattccc | agctgcacag  | ttggattgtg  | ttacaattca | ccttcttcaa | gaatgtggaa | 420 |
| atctctaat  | ttgtctgtga  | gccatctcaa  | cttctcaagc | ttgcctctta | tgacagcgtc | 480 |
| atcaatagca | tattcatata  | ttttgataat  | actatgtttg | gttttcttcc | catttcaggg | 540 |
| atccttttgt | cttactataa  | aattgtcccc  | tccattctaa | ggatttcatc | atcagatggg | 600 |
| aagtacaaag | ccttctcagc  | ctgtggctgt  | cacctggcag | ttgtttgctt | attttatgga | 660 |
| acaggcattg | gctgtgtacc  | tgacttcagc  | tgtggcacca | cccctcagga | atggtatggg | 720 |
| ggcgtcagtg | atgtacgctg  | tggtcacccc  | catgctgaac | cctttcatct | acagcctgag | 780 |
| aaacagggac | attcaaagtg  | ccctgtggag  | ggtgtgcaac | aaaacagtcg | aatctcatga | 840 |
| tctgttccat | cctttttct   |             |            |            |            | 859 |

&lt;210&gt; 1031

&lt;211&gt; 975

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g881 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1031

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| atggctaagt | aaaactacac | aaagggtcacc | taattcattt | tcacaggctt  | gaattacaat | 60  |
| cctcagttgc | gggtcttcc  | tttcttactc  | tttctgacaa | ctttctatgt  | catcaatgta | 120 |
| actggaaact | tgggaatgat | tgtcctcatc  | cgaattgatt | cccgccttca  | cacacccatg | 180 |
| tactttttcc | tcagccacct | gtcctttgtg  | gacacctgct | tctcctcagt  | tgtgagcccc | 240 |
| aagatgctca | ctgacttctt | tgtgaagagg  | aaagccattt | ctttccttgg  | ctgtgctttg | 300 |
| cagcagtggg | tctttggggt | ctttgtggca  | gcagactggt | tctctttgga  | gtccatggcc | 360 |
| tatgactgct | atgtggccat | ctgtaaccca  | ttgttatact | cagttgctat  | gtcccagagg | 420 |
| ctctgcatec | agctagtggg | gggtccctat  | gtcattggac | tcatgaatac  | catgactcac | 480 |
| acaacaaatg | cattttgtct | ccctttttgt  | ggccctaatt | tcatcaatcc  | tttcttctgt | 540 |
| gatatgtccc | ccttactttc | ccttgatagt  | gctgatacca | ggctcaataa  | gttggcagtt | 600 |
| ttcatcgtgg | ctggagctgt | gggagtcttc  | agtggctctg | ctatcctgat  | ttcctacatt | 660 |
| tacatectca | tggccatcct | gaggatccgc  | tctgctgatg | ggagggtgcaa | aaccttttct | 720 |
| acttgctctt | ctcacctgac | agctgttttc  | atctcgtatg | gtaccctttt  | ctttatttat | 780 |
| gtacatccca | gtgcaacctt | ctccctggat  | ctcaataaag | tagtgtctgt  | gttttacaca | 840 |
| gcagtgattc | ctatgttgaa | cccacttatc  | tacagcttga | gaaacaagga  | agtcaaagat | 900 |
| gccatccaca | ggactgtcac | tcagaggaag  | ttttgcaagg | cctaaattct  | tatccagaag | 960 |
| gaattagggg | ggaaa      |             |            |             |            | 975 |

&lt;210&gt; 1032

&lt;211&gt; 941

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g882 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1032

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggagactg | aaaacaatac | aacagtgaca | gagttcatta | ttttgggatt | aacagacaat | 60  |
| cctatgctat | gtgccatttt | cttcgtgttt | tttctagcag | tttatatagt | tactataccg | 120 |



|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| ggaaatatta  | gcataatcct  | cttaatccaa | agcagccac   | agcttcacac  | gctaattgtac | 180 |
| ctttttctca  | gccatttggc  | ttctgtggac | attgggtatt  | ccatatcagt  | tacgccaatc  | 240 |
| attctcatca  | atttcttaag  | agagaaaacg | actattcctg  | tcacaggctg  | tatagcacag  | 300 |
| cttggctctg  | atgtcatgtt  | tggaaccaca | gagtgtcttc  | tgtgtgtcac  | tatgtggcta  | 360 |
| tctgtctctc  | cctgtcttac  | tccatccaaa | tgtgtgtctc  | cgtctgtctc  | ctctactggt  | 420 |
| gagcctccta  | cctgggtgga  | tgcctgaacg | cttcgtcttt  | tacaggctgt  | ttgatgaacc  | 480 |
| tgtccttctg  | cgggtccaaat | aaaatcaacc | actttttctg  | tgacctcttc  | ccactcttga  | 540 |
| agctttcttg  | tggccatgtt  | tacattgctg | aaatatcccc  | tgccatctcc  | tctgcatctg  | 600 |
| tccttatcag  | cacgtgtgtt  | accataatcg | tgtcctacat  | ctacatcctt  | cactccatcc  | 660 |
| tgaagggtgtg | ctctactgag  | ggaaggaaga | aggctttctc  | cacctgctgt  | tcccacctca  | 720 |
| ctgcagtcac  | tttgttctat  | gggaccattt | tgtttgttta  | tgtgatgccc  | aagtcaagct  | 780 |
| attcagcgga  | tcaggtaacg  | gtggcatttg | tgatctacac  | ggtgggtgatt | cccatgctga  | 840 |
| acccctcat   | ctacagtctc  | aggaataagg | agggtgaaaga | ggccatgaga  | aaattgatgg  | 900 |
| caagaacaca  | ttgggttttc  | tgaattaaat | cagtataatc  | c           |             | 941 |

&lt;210&gt; 1033

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g883 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1033

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| atctttgcca | tcttgaccac  | cattgactgc | tgtgtatttg | tctgggaatt  | cctggagtgc | 60  |
| acagtctttg | tgaataagag  | ggcatgtgac | cagctggcgt | gtgggtgcctt | ttgcattggc | 120 |
| ctgatcatga | cagtgggtcta | aataaccaca | gtgtcacaga | ggtacaaaag  | gagcacatat | 180 |
| gctatattga | ctgtctcttg  | tttgacaccc | ttcttgtcat | gaaactctcc  | tgcattgaca | 240 |
| atactatcta | tgaataaaac  | agtattttat | tcaccacaca | tgtgtgcagg  | tgtccatggg | 300 |
| tttggtttgc | atttcttata  | ttgacatccc | tgttacctcc | atcgtgtcta  | gaatttctta | 360 |
| atctgaggtc | tttgccacct  | gtgtccccc  | acccccacct | catcatgggc  | attgtctata | 420 |
| tgtctgtgct | tgtactgctt  | acctcaagca | caagccaatg | aattcaatag  | aaaacaggtc | 480 |
| ttctataaga | gacctacatt  | atcatcattc | attctgcctc | tggacactgt  | tgtttacact | 540 |
| ctgaggtaca | tggaggccaa  | ggataccatg | tacagagctg | tggacagaaa  | tatttcttaa | 600 |
| cagatt     |             |            |            |             |            | 606 |

&lt;210&gt; 1034

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g884 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1034

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| atggagccag  | aagctgggac | caataggacc | gctgttctgt  | agttcattct | actgggccta | 60  |
| gtgcaaacag  | aagagatgca | gccagttgtc | tttgtgtctc  | tcctctttgc | ctatctgggc | 120 |
| acaactgggg  | gcaacctcag | catcctggca | gccgtcttgg  | tggagcccaa | actccacgcc | 180 |
| cccattgact  | tcttcttggg | gaacctgtca | gtgtgtggatg | tcggatgtat | cactgtcact | 240 |
| gttcttgcaa  | tgttgggtcg | tctcttgtcc | cacaagtcca  | caatttctta | tgacgcctgc | 300 |
| ctctcccagc  | tcttcttctt | ccacctctct | gctgggatgg  | actgcttctt | gctgaccgcc | 360 |
| atggcctatg  | accgactcct | ggccatctgc | cagcccccca  | cctacagcac | ccgcatgagt | 420 |
| cagacagtcc  | agaggatgtt | ggtgggtgcg | tccttggctt  | gtgccttcac | caacgcactg | 480 |
| acccacactg  | tggccatgtc | cacgtctaac | ttctgtggcc  | ccaatgaggt | caatcacttc | 540 |
| tactgtgacc  | tcccacagct | cttccagctc | tcctgtctca  | gcacccaact | caatgagctg | 600 |
| ctgctctttg  | ctgtgggttt | catcatggca | ggcacacctt  | tggttctcat | catcactgcc | 660 |
| tacagccacg  | tggcagctgc | agttctacga | atccgttcag  | tggagggccg | aaagaaggcc | 720 |
| ttctccacgt  | gtggctccca | cctcaccgtc | gtttgtcttt  | tctttggaag | aggtatcttc | 780 |
| aactacatga  | gactgggttc | agaggaggtc | tcagagcaag  | ataaaggggt | tggagttttc | 840 |
| aacactgtta  | tcaaccctat | gctgaacctt | cttatctaca  | gcctcagaaa | ccctgatgtt | 900 |
| caggggtgctc | tgtggcaaat | atttttgggg | aggagatcac  | tgacc      |            | 945 |

<210> 1035  
 <211> 927  
 <212> DNA  
 <213> Unknown (H38g885 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1035  
 atgaagagaa agaacttcac agaagtgtca gaattcattt tcttgggatt ttctagcttt 60  
 ggaaagcatc agataaccct ctttgtgggt ttcctaactg tctacatttt aactctgggt 120  
 gctaacatca tcattgtgac tatcatctgc attgaccatc atctccacac tcccatgtat 180  
 ttcttcctaa gcatgctggc tagttcagag acggtgtaca cactgggtcat tgtgccacga 240  
 atgcttttga gcctcatttt tcataaccaa cctatctcct tggcaggctg tgctacacaa 300  
 atgttctttt ttgttatctt ggccactaat aattgcttcc tgcttactgc aatgggggat 360  
 gaccgctatg tggccatctg cagacccttg agatacactg tcacatgag caagggacta 420  
 tgtgcccagc tgggtgtgtg gtcctttggc attgggtctga ctatggcagt tctccatgtg 480  
 acagccatgt tcaatttgcc gttctgtggc acagtggtag accacttctt ttgtgacatt 540  
 taccagtcga tgaactttc ttgcattgat accactatca atgagataat aaattatggt 600  
 gtaagtcat ttgtgatttt tgtgcccata ggctgatata ttatctccta tgtccttgtc 660  
 atctcttcca tcttcaaat tgcctcagct gagggccgga agaagacctt tgccacctgt 720  
 gtctcccacc tcaactgtgt tattgtccac tgtggctgtg cctccattgc ctacctcaag 780  
 ccgaagtcag aaagttcaat agaaaaagac cttgttctct cagtgcagta caccatcatc 840  
 actcccttgc tgaaccctgt tgtttacagt ctgagaaaca aggaggtaaa ggatgcccta 900  
 tgcagagttg tgggcagaaa tatttct 927

<210> 1036  
 <211> 958  
 <212> DNA  
 <213> Unknown (H38g886 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1036  
 atgttgcaga gagttgggga aatgggatgga ggcaaccaga gtgaagggtc agagttcctt 60  
 ctcttgggga tctcagagag tcttgagcag cagcagatgc tgttttggat gttcctgggtc 120  
 aggtacctgg tcacgggtgct gggaaatgtg ctcacatcc tggccatcag ctctgattcc 180  
 cgctgcaca ccccatgta cttcttctct gccaacctct ccttcaactga cctcttctt 240  
 gtcaccaaca caatcccaa gatgctgggt aacctccagt cccagaacaa agccatctcc 300  
 tacacagggt gtctgacaca gctctacttc ctggtctcct tgggtggcct ggacaacctc 360  
 aacctggcgg tgatggcgta tgatcgctat gtggccatct gccgtcccct ccactatgtc 420  
 acagccatga tccctgggct ctgtatcttg ctctctcct tgtgttgggt gttctctgcc 480  
 ctctatggcc tcatccatat cctctcatg accaggtgac cttctgtggg tctcaaaaga 540  
 tccactacct cttctgtgag atgtacttcc tgctaaggct ggcattgtcc aacatccacg 600  
 tcaaccacac agtactgggt gccacgggct gcttcatctt cctcatcccc ttaggtttca 660  
 tgatcacatc ctacgcccgc attgtcagag ccatcctcca aataccctca gccactggga 720  
 agtacaaagc cttctccacc tgtgcttccc atttggctgt ggtctccctc ttctatggga 780  
 ctctgggtat ggtgtacctg cagccctctc aaacctactc catgaaggac tcagtagcca 840  
 cagtgatgta tgcggtgggt acgccatgat taacctttc atctacagcc tgaggaacaa 900  
 ggacatgcat ggggctctgg gaagacttgc ccaaggaaaa gccttccaga agttgaca 958

<210> 1037  
 <211> 828  
 <212> DNA  
 <213> Unknown (H38g887 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1037

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| atgcgaagaa  | agaacctcac | agaggtaaca  | gagtttggtt  | tcctgggatt | ctccagattc  | 60  |
| cacaaacatc  | acatcactct | ctttgtgggt  | tttctcatcc  | tgtacacatt | aactgtggct  | 120 |
| ggcaatgcc   | tcacatgac  | catcatctgc  | attgaccgtc  | acctccacac | tcccatgtac  | 180 |
| ttcttcctga  | gcacgtctgg | tagctcaaag  | acagtgtaca  | cactgttcat | cattccacag  | 240 |
| atgctctcca  | gcttcgtaac | ccagacccag  | ccaatctccc  | tagccgggtg | taccacccaa  | 300 |
| acgtttctct  | ttgttacett | ggccatcaac  | aattgcttct  | tgctcacagt | gatgggctat  | 360 |
| gaccactata  | tggccatctg | caatcccttg  | agatacaggg  | tcattacgag | caagaagggtg | 420 |
| tgtgtccagc  | tgggtgtgtg | agccttttagc | attggcctgg  | ccatggcagc | tgtccaggta  | 480 |
| acatccatat  | ttaccttacc | tttttgtcac  | acgggtgggtg | gtcatttctt | ctgtgacatc  | 540 |
| ctccctgtca  | tgaactctc  | ctgtattaat  | accactatca  | atgagataat | caatttttgtt | 600 |
| gtcagggttat | ttgtcatcct | ggcccccatg  | ggctctggct  | tcctctccta | tgtcctcatc  | 660 |
| atctccactg  | tcctcaagat | tgcctcagct  | gaggggttgg  | agaagacctt | tgccacctgt  | 720 |
| gccttccacc  | tcactgtgtg | cattgtccat  | tatggctgtg  | cttccattgc | ctacctcatg  | 780 |
| cccaagtcag  | aaaactctat | agaacaagac  | ctccttctct  | cagtgacc   |             | 828 |

&lt;210&gt; 1038

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g888 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1038

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| atggatggag  | ataaccagag  | tgagaactca  | cagttccttc | tcctggggat  | ctcagagagt  | 60  |
| cctgagcagc  | agcagatcct  | gttttggtatg | ttcctgtcca | tgtacctggt  | cacgggtgctg | 120 |
| ggaaatgtgc  | tcacatcctt  | ggccatcagc  | tctgattccc | acctgcacac  | ccccatgtac  | 180 |
| ttcttctctg  | ccaacctctc  | cttcaactgac | ctcttctttg | tcaccaacac  | aatccccaaag | 240 |
| atgctgggtga | acttccagtc  | ccagaacaaa  | gccatctcct | atgcaggggtg | tctgacacag  | 300 |
| ctctacttcc  | tgggtctcct  | ggtgacctg   | gacaacctca | tcctggccgt  | gatggcgat   | 360 |
| gatcgctatg  | tggccatctg  | ctgccccctc  | cactatgtca | cagccatgag  | ccctgggctc  | 420 |
| tgtgtcttgc  | tcctctcctt  | gtgttggggg  | ctgtctgttc | tctatggcct  | cctcctcacc  | 480 |
| ttcctcctga  | ccaggggtgac | cttctgtggg  | cctcgagaga | tcactacct   | cttctgtgac  | 540 |
| atgtacatcc  | tgtgtgtggt  | ggcatgttcc  | aacaccacac | tcattcacac  | agcattgatt  | 600 |
| gccactgggt  | gcttcatctt  | cctcaccctc  | ttagggttca | tgaccacatc  | ctatgtacgt  | 660 |
| attgtcagaa  | ccatccttca  | aatgccctcg  | gcctctaaga | aatacaaaac  | tttctctacc  | 720 |
| tgtgcctcgc  | atttgggtgt  | ggtctccctc  | ttttatggga | cgcttgctat  | ggtgtacctg  | 780 |
| cagccccctc  | atacctactc  | catgaaggac  | tcagtagcca | cagtgtatga  | tgtgtgtctg  | 840 |
| acacctatga  | tgaacccttt  | catctacagc  | ctgaggaaca | aagacatgca  | tggggctccg  | 900 |
| ggaagagtcc  | tatggagagc  | ctttcagagg  | cctaaa     |             |             | 936 |

&lt;210&gt; 1039

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g889 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1039

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggctgatg | gaaatataaa | aggatcacag | aattcatttt | tgtaggctta | aggtatcatc | 60  |
| ttcagctgca | agtcttctct | ttcttaccat | ttctaccttt | tttacctcat | tactatgaca | 120 |
| gaaaacttgg | gcacatggtg | tcgcatctgg | ctcgattcct | gctttcacac | acctatgtac | 180 |
| tttgtctcca | gctacctgtc | ctttgtggac | atctgcttct | catccgttgt | gggccacaag | 240 |
| ttgtcactg  | acttatttgc | tgtaaagaaa | gccatctctt | tcctgggctg | tccttgcag  | 300 |
| cagtgggtct | ttgggttctt | cgtagtcat  | gagtatcttc | tcttggcttc | catggcctat | 360 |
| gacaattatg | tggccatctg | taaccattg  | ttgtactcag | tggccatgta | atagagactg | 420 |
| tgcacccagc | tgggtgtgtg | acgttatgca | gctgatttct | tcaacaccat | aactcacaca | 480 |
| acggctgctt | ttcattttcc | cttttttcc  | tccaacatta | tcaatcattt | cttctgtgac | 540 |
| atgtctctcc | ttctttctct | cgtgtgtgct | gacgcccggg | tcaataaatt | gttagttttc | 600 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| attgtggctg | gagctgtact | agttgtcagt | agcctgacca | ttataatctc | ctatTTTTac | 660 |
| atccttactg | acattctgag | gatctgctct | gctaattggg | aagaacaaaa | ctTTTTccac | 720 |
| ctgtctttca | cacttaacag | ctgtttccat | cttttatggg | tctctcttct | ttagctacgt | 780 |
| ttcgaccagg | tgcaactttt | tacccggaac | tcaataaaat | agtgttggtg | ttctgtacat | 840 |
| ccccatgttg | aaacctctca | tctacagctt | gataaataaa | gaagtatcct | agccacta   | 898 |

&lt;210&gt; 1040

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g890 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1040

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| atggaaaaaa  | taaacaacgt  | aactgaattc  | atTTTTctggg | gtctttctca | gagcccagag | 60  |
| attgagaaag  | tttgTTTTgt  | ggtgTTTTct  | ttcttctaca  | taatcattct | tctgggaaat | 120 |
| ctctcatca   | tgctgacagt  | ttgcctgagc  | aacctgttta  | agtcacccat | gtatttcttt | 180 |
| ctcagcttct  | tgtctTTTTgt | ggacatttgt  | tactcttcag  | tcacagctcc | caagatgatt | 240 |
| gttgacctgt  | tagcaaagga  | caaaaccatc  | tcctatgtgg  | ggtgcatgtt | gcaactgctt | 300 |
| ggagtacatt  | tctttgggtg  | cactgagatc  | ttcatcctta  | ctgtaatggc | ctatgatcgt | 360 |
| tatgtggcta  | tctgtaaacc  | cctacattat  | atgaccatca  | tgaaccggga | gacatgcaat | 420 |
| aaaatgttat  | taggggacgtg | ggtagggtggg | ttcttacact  | ccattatcca | agtggctctg | 480 |
| gtagtccaac  | taccctTTTTg | tggacccaat  | gagatagatc  | actacttttg | tgatgttcac | 540 |
| cctgtgttga  | aacttgccctg | cacagaaaca  | tacattgttg  | gtgttggtgt | gacagccaac | 600 |
| agtgggtacca | ttgctctggg  | gagttttgtt  | atcttgctaa  | tctcctacag | catcatccta | 660 |
| gtttccctga  | gaaagcagtc  | agcagaaggc  | aggcgcaaa   | ccctctccac | ctgtggctcc | 720 |
| cacattgcca  | tggtcggttat | ctttttcgag  | cccctgtact  | tttatgtaca | tgcgccctga | 780 |
| tacgaccttt  | tcagaggata  | agatgggtggc | tgtattttac  | accattatca | ctcccatggt | 840 |
| aaatcctctg  | atttatacac  | tgagaaatgc  | agaagtaaag  | aatgcaatga | agaaactgtg | 900 |
| gggcagaaat  | gttttcttgg  | aggctaaagg  | gaaa        |            |            | 934 |

&lt;210&gt; 1041

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g891 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1041

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| atggactata  | gaaatcaaac | tttggttact  | gaattttttt | ccgtgggatt | aacaaatctc  | 60  |
| tttcagcaca  | agattgctct | ctttctggta  | tttctcttgg | tttatcttgt | cactgttccg  | 120 |
| ggaaacttgg  | gaatgatcac | tcttatttgg  | atggattctc | gactccagac | ccccaaagtac | 180 |
| ttttctctct  | gccacttgte | ctttgtggat  | gtctgtcctt | cttctgccat | cggteccaaag | 240 |
| atgttgactg  | atatcttcgt | ggagaaaaaa  | gtaatctctt | tggttggtgt | gcccagttat  | 300 |
| ggttttttgg  | ccatttttga | gtaactgaat  | gtttctctct | ggctgccatg | gcatatgacc  | 360 |
| ggtataggct  | atctataagc | ctttgttgta  | tacactcatt | atgtcccaac | aggtctgtgt  | 420 |
| gcagctgggtg | gtgggcctta | tgctgtgggc  | cttataagca | ccatgaccca | tatgactttc  | 480 |
| acctttcgcc  | tactctactg | tggtccaaac  | atcatcaatc | acttcttctg | tgaccttctc  | 540 |
| cctgtcctct  | ccctggcata | tgcagatacc  | catattaata | aatgtttact | ttttatcttg  | 600 |
| gtgggtgccc  | tgggagtact | cagtgggtgtg | atcatcttgg | tctcctacat | ttacattgtc  | 660 |
| attgccatcc  | tgagaattcg | ctctgtgcag  | gcgagacgca | aagacttctc | cacttgctct  | 720 |
| tcacacctga  | tggctgtctc | catcctgtat  | gggacactct | tctttatctg | tgtatgtcca  | 780 |
| agctctagtt  | tctctatcaa | catcaataaa  | gtggtttccc | tgttctacac | agcagtgatc  | 840 |
| cccatgttga  | atccccttat | ctacagcctg  | agaacaagg  | aggtaaaaga | ttcattcagc  | 900 |
| aagaagtttg  | aaagaaagaa | gtttcttata  | ggtaggtgaa | ctagaatacc | a           | 951 |

&lt;210&gt; 1042

&lt;211&gt; 930

&lt;212&gt; DNA

<213> Unknown (H38g892 nucleotide)

<220>

<223> Synthetic construct

<400> 1042

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| atggtgaatt  | ttacacatgt | ctcagaattt | gttctacttg | ggttccaagg | gggtcccggg  | 60  |
| atgcaggcta  | tgctatttct | gatttttctg | atcctgtatg | gcatagctgt | gggtgggaaac | 120 |
| cttggcatga  | ttgtaattat | ctgggtagat | gcacacctcc | acacccaat  | gtatgccttc  | 180 |
| ctgcaaagcc  | tttcattgtt | ggacatctgc | tattcctcca | caattgcacc | cagggtctctg | 240 |
| gcgaactcca  | tgcaagagga | ccacacaatt | tcctttggcg | gatgtgctgc | tcagtctctt  | 300 |
| ttcttgtctc  | tctttgggat | cacagaggct | ttcctcctgg | ctgccatggc | ctatgaccgc  | 360 |
| ttcatcgcca  | tctgcaaccc | tcttctgtac | tctgtgagca | tgtctcacca | ggctctgtgtg | 420 |
| ctgttaatat  | caggatccta | cttgtggggt | gtagtcaatg | ccattgctca | aacaaccatg  | 480 |
| accttcagggt | tgcttttctg | tgggtccaat | gagatcaacg | actttttctg | tgatgttccc  | 540 |
| ccactcttgt  | ccctctcatg | ttcagatacc | tttataaacc | aactgggtct | tcttgggtta  | 600 |
| tgtggctcca  | ttattgtcag | tacctttttg | attgtcctgg | tctcatacat | ttacatcatc  | 660 |
| tcaacaattc  | tgaggatccc | gaccatgcag | ggacgctaga | aagccttctc | cacgtgcgct  | 720 |
| tcccacctaa  | caggagtgtg | cttgtttttt | ggtactgttt | tcttcatgta | tgcacaaccc  | 780 |
| agtgccatct  | tcttcatgga | gcaaagtaaa | atagtgtcca | tattctacac | tatgggtcatc | 840 |
| cccattgctga | atcccctgat | atacagcctg | aggaacaaag | aggccaagca | ggctctgaga  | 900 |
| cggagcatgc  | agaagctgtc | tttgtgatca |            |            |             | 930 |

<210> 1043

<211> 927

<212> DNA

<213> Unknown (H38g893 nucleotide)

<220>

<223> Synthetic construct

<400> 1043

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| atgagggaaa  | ataaccagtc  | ctctacactg | gaattcatcc | tcttgggagt | tactgggtcag | 60  |
| caggaacagg  | aagatttctt  | ctacatcctc | ttcctgttca | tttaccat   | cacattgatt  | 120 |
| ggaaacctgc  | tcattgtcct  | agccatttgc | tctgatgttc | gccttcacaa | ccccatgtat  | 180 |
| tttctccttg  | ccaacctctc  | cttgggtgac | atcttctctt | catcggtaac | catccctaag  | 240 |
| atgctggcca  | accatctctt  | gggcagcaaa | tccatctctt | ttgggggatg | cctaacgcag  | 300 |
| atgtatttca  | tgatagcctt  | gggtaacaca | gacagctata | ttttggctgc | aatggcatat  | 360 |
| gatcgagctg  | tggccatcag  | ccaccactt  | cactacacaa | caattatgag | tccacgggtct | 420 |
| tgtatctggc  | ttattgtctg  | gtcttgggtg | attggaaatg | ccaatgccct | ccccacact   | 480 |
| ctgctcacag  | ctagtctgtc  | cttctgtggc | aaccaggaag | tggccaactt | ctactgtgac  | 540 |
| attacccccct | tgttgaagtt  | atcctgttct | gacatccact | ttcatgtgaa | gatgatgtac  | 600 |
| ctaggggttg  | gcattttctc  | tgtgccatta | ctatgcatca | ttgtctccta | tattcgagtc  | 660 |
| ttctccacag  | tcttccagggt | tccttcacc  | aaggcgctgc | tcaaggcctt | ctccacctgt  | 720 |
| ggttccacc   | tcacggttgt  | ctctttgtat | tatggtacag | tcatgggcac | gtatttccgc  | 780 |
| cctttgacca  | attatagcct  | aaaagacgca | gtgatcactg | taatgtacac | ggcagtgacc  | 840 |
| ccaatgttaa  | atcctttcat  | ctacagtctg | agaaatcggg | acatgaaggc | tgccctgcgg  | 900 |
| aaactcttca  | acaagagaat  | ctcctcg    |            |            |             | 927 |

<210> 1044

<211> 927

<212> DNA

<213> Unknown (H38g894 nucleotide)

<220>

<223> Synthetic construct

<400> 1044

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgaagaaag | aaaatcaatc | ctttaacctg | gattttattc | tcttgggagt | tactagtcag | 60  |
| caagaacaga | ataatgtctt | ctttgtgatt | ttttgtgca  | tttaccat   | cacactgact | 120 |
| ggaaatctgc | tcatcatctt | ggccatctgt | gctgacattc | gccttcacaa | ccccatgtat | 180 |

|             |            |            |            |            |              |     |
|-------------|------------|------------|------------|------------|--------------|-----|
| tttctccttg  | ccaacctctc | cttggttgac | atcatcttct | catccgtaac | catccctaag   | 240 |
| gtgctggcca  | accatctctt | gggcagcaag | ttcatctcct | ttgggggatg | cctaatagcag  | 300 |
| atgtattttca | tgatagcctt | ggccaaggca | gacagctata | ccttggctgc | aatggcatac   | 360 |
| gatcgagctg  | tggccatcag | ctgcccactt | cattacacaa | caattatgag | tccacgggtct  | 420 |
| tgtatcctgc  | ttattgctgg | gtcttgggtg | attggaaaca | ccagtgtctt | ccccacact    | 480 |
| ctgctcacag  | ctagtttgtc | cttctgtggc | aaccaggaag | tagccaattt | ctactgtgac   | 540 |
| attatgcctt  | tgetgaagtt | gtcctgttct | gacgtccact | ttaatgtgaa | gatgatgtac   | 600 |
| ctaggggtcg  | gcgttttctc | tttgccatta | ctatgcatca | ttgtctccta | tggttcagggtc | 660 |
| ttttccacag  | tcttccaagt | tccatctacc | aagagtctat | tcaaagcctt | ctgcacctgt   | 720 |
| ggctcccacc  | tcacagttgt | ttttttatat | tatggtacaa | cgatgggcat | gtatttccgc   | 780 |
| cctctgacca  | gttacagccc | caaagatgca | gtgataactg | tgatgtatgt | ggcagtgacc   | 840 |
| ccagcattaa  | atcctttcat | ctatagtctg | agaaattggg | atatgaaggc | agccctacag   | 900 |
| aaactcttca  | gcaagagaat | ctcctca    |            |            |              | 927 |

&lt;210&gt; 1045

&lt;211&gt; 990

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g895 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1045

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| gctcttcttt  | tccattccta  | caaacatccc  | accagagga  | gaatgactgt | caaaagtcac  | 60  |
| tctatagtga  | cagagttcag  | tctcagggga  | ttaacgaagc | agccagatct | ccagctcttt  | 120 |
| cacttcctca  | ttttccttga  | tatccatatg  | gtcacatgg  | tggggaactt | gggcatgac   | 180 |
| actctaattt  | gtcttaactc  | tcagcttcac  | accccatgt  | actacttctt | cagcaatctg  | 240 |
| tcactcttgg  | atctctgcta  | ttcctccatt  | actaaccta  | agatgctggg | gaactttgtg  | 300 |
| ttaaagaaga  | gcattatctc  | ttatgcaggg  | tacatgtcat | agttctactt | tttcttggtt  | 360 |
| tttgtcatag  | ctaggtgtta  | catgctgatg  | gtgaaggcct | gtgaccacta | tggtgccatc  | 420 |
| tgctgccctt  | tgctttgcaa  | cgctcatctc  | tctcatgtca | cctgctccct | gatgggtggct | 480 |
| gtgggtctaca | ccatgggact  | cgttgtctcc  | acaatagaga | ctggggtcat | attaaaactg  | 540 |
| ccctattgtg  | aactcctcac  | cagtcgctgc  | ttctgtgaca | tcctccctct | catgaaactc  | 600 |
| tcctgatcta  | gtgccttatg  | atgttgagat  | ggcagttctc | ttttttgcta | gattgcaacc  | 660 |
| tgagaatcat  | gatcttaaca  | gttcttgttt  | tcttacacct | tcattctctt | cagcatectg  | 720 |
| cacatcagca  | ccactgaggg  | cagggtccaaa | gtcttcagca | cctgcagctt | ccaccttgca  | 780 |
| gctatagggg  | tgttccatgg  | atagactgca  | ttcaggtact | taaaaccgcg | cataaccagt  | 840 |
| tccttgcccc  | aagagaatgt  | ggcctctgtg  | ttctacacta | cagtaatcta | cgtgccgaat  | 900 |
| cccctaattg  | acagcctgaa  | aaacaaggat  | gtaaaagctg | ccatgcagaa | aacactaagg  | 960 |
| agtaagtttt  | gttgccagatg | taattatctt  |            |            |             | 990 |

&lt;210&gt; 1046

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g896 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1046

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| ctcctggaag | gagggaaatca | gactagcacc  | tttgagttcc | tcctctgggg  | actctcagac | 60  |
| cagccacagc | agcaacacat  | cttcttctctg | ctgtttctgt | ggatgtacgt  | ggtcactgtg | 120 |
| gctgggaacc | tgctcattgt  | cctggccatt  | ggcactgaca | cacacctcca  | caccctatg  | 180 |
| tacttcttcc | ttgccagctt  | gtcgtgtgca  | gatatctttt | ccacctccac  | cactgtgccc | 240 |
| aaggccctgg | tgaatatcca  | gacccagagc  | aggtccattt | cctacgcagg  | gtgtttggca | 300 |
| cagctctact | tcttcttgac  | ttttggggac  | atggacatct | ttctcccggc  | tacaatggcc | 360 |
| tatgaccgct | atgtggccat  | ttgccacctg  | ctccactata | tgatgatcat  | gagcctccac | 420 |
| cgctgtgcct | tcctgggtgac | agcctgctgg  | accctcacaa | gtcttctcgc  | catgactcgc | 480 |
| accttctcta | tattccggct  | ttccttgtgc  | tcttagatcc | ttcctggctt  | cttctgtgat | 540 |
| ttgggaccgc | tgatgaaggt  | gtcttgctct  | gacgcccagg | tcaatgagct  | tgtgctcctc | 600 |
| ttcctagggg | gagcagtcac  | tttaatccct  | tttatgtcca | tcctgggtctc | ttatatccgc | 660 |

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| attgtttcag  | ccatcctcag | ggccccctct | gcccaggga  | ggcgcaaggc | cttctctacc | 720 |
| tgcgactctc  | acctcgttgt | tgttgctttg | ttctttggga | cagtgatcag | ggcttatctg | 780 |
| tgcccccat   | cctcttcttc | caactcagta | aaggaggata | cagcggtgc  | tgtcatgtac | 840 |
| acagtgggtga | ctccccgtct | gaaccccttt | atttacagca | tgcggaacaa | ggacatgaag | 900 |
| gcggcggttg  | ttagacttct | caagggcagg | gtctccttct | cacagggc   |            | 948 |

&lt;210&gt; 1047

&lt;211&gt; 1007

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g897 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1047

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| gatacagacc | cacagagtct  | aacagatgtc | tctatatctc | tcctcctcaa | actctcagag | 60   |
| gatccagaac | tgcagcaggt  | cgtcgctggg | ctgttcctgt | ccatgtgcct | ggtcacggtg | 120  |
| ctggggaacc | tactcatcat  | cctggccgtc | agccctgact | cccacctcca | cacccccatg | 180  |
| tacttggtcc | tctccaacct  | gtcccttgcc | tgacatcggt | ttcacctcca | ccacggtccc | 240  |
| caagatgatt | gtggacatcc  | agtctcacag | cagagtcate | tcctatgcag | gctgcctgac | 300  |
| tcagatgtct | ctctttgcca  | tttttgagg  | tatggaagag | agacatgctc | ctgagtgtga | 360  |
| tggcctatga | cgggtttgta  | gccatctgtc | accctctata | ttgttcagcc | atctttaacc | 420  |
| cgtgtttctg | tggcttctca  | gatttggtgt | cttttttttt | ttttttctca | gtctttcaga | 480  |
| ctcccagctg | cacaacttga  | ttgccttaca | aatgacctgc | ttcaaggatg | tggaaattcc | 540  |
| taattttctt | tgggaacctt  | ctcaactctc | ccatcttgca | tgttgtagca | ccttcaccag | 600  |
| gaacatcagt | atttccctgc  | tgccatattt | ggttttcttc | ccatcttggg | gacctttttc | 660  |
| tcttactgta | aaattgtttc  | ctccattctg | aggggttcat | catcaggtgg | gaagtataaa | 720  |
| ccttctccac | ctgtgggtct  | cacctgtcag | ttgtttgctg | attttatgga | acaggcattg | 780  |
| gagggtagct | cgggttcagat | gtgtcatctt | ccccgagaaa | gggtgcagtg | gcctcagtg  | 840  |
| tgtacatggt | ggtcaccccc  | atgctgaacc | ccttcactca | cagcctgaga | aacagggata | 900  |
| tgaaaagtgt | cctgcggcgg  | cgcgatggca | gcacagtcta | atctcaacat | cttcttatct | 960  |
| gttccattcc | ttttgtagg   | tggtttaaaa | aaggcgccaa | ggtcaaaa   |            | 1007 |

&lt;210&gt; 1048

&lt;211&gt; 926

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g898 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1048

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| atgagacaga  | ataataatat | tacagaattt | gtcctcctgg | gcttctctca | ggatctggat  | 60  |
| gtgcaaaaag  | cattatttgt | catattttta | ctcacatact | tggtgacagt | gggtggggaac | 120 |
| ctgctcattg  | tggtgactat | tattaccagc | ccttccttgg | gtccccaat  | gtacttcttc  | 180 |
| cttgccctgc  | tgtcatttat | agatgctgca | tattccacta | caatttctcc | caaattgatt  | 240 |
| gtagacttac  | tctgtgataa | aaagactatt | tctttcccag | cttgcatggg | ccagttattt  | 300 |
| atataccact  | tgtttgggtg | ttctgaggtc | ttccttcttg | tggtgatggc | ctgtgatcac  | 360 |
| tatgtggcca  | tctgtaagcc | actgcactat | ttgaccatca | tgaatcgaca | ggtttgaatc  | 420 |
| cttctgttgg  | tggtggctgt | gactggaggt | tttctgcatt | ctgtgtttca | aattgttgtt  | 480 |
| gtatacagtc  | tcgctttctg | tggccccaat | gtcattgact | actttgtctg | tgacatgtac  | 540 |
| ccattattgg  | aactggatg  | cactgacacc | tactttattg | gccttactgt | ttttgtcaat  | 600 |
| gggtggaacaa | tctgtatagt | cgtcttcacc | cttctactaa | tctcctatgg | agtcaccta   | 660 |
| aactccctta  | aaacttacag | tcaagaagg  | aggcataaag | tcctgtttac | ctgcagctcc  | 720 |
| cacattatcg  | tctttgccct | cttttttgtt | ccctgtattt | tcatgtatgt | tagacctgtt  | 780 |
| tcaaacatcc  | ttttgataaa | ttcctgacag | tgttttatac | agttatcaca | cccatgttga  | 840 |
| atcctttaat  | atacacattg | agaaattcag | agatgagaaa | ttctgtagaa | acactcttgt  | 900 |
| gtaaaagtta  | actgtattag | agtaag     |            |            |             | 926 |

&lt;210&gt; 1049

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g899 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1049

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atggaaagaa | tcaacagcac | actgttgact | gcgtttatcc | tgacaggaat | tccgtatcca  | 60  |
| ctcaggctaa | ggacactcct | ttttgtgttc | ttttttctaa | tctacatect | gactcagctg  | 120 |
| ggaaacctgc | ttattttaat | cactgtctgg | gcagacccaa | ggctccatgc | ccgccccatg  | 180 |
| tacatctttc | ttggtgttct | ctcagtcatt | gatatgagca | tctcctccat | cattgtccct  | 240 |
| cgctcatga  | tgaacttcac | tttaggtgtc | aaacccatcc | catttggtgg | ctgtgttgct  | 300 |
| caactctatt | tctatcactt | cctgggcagc | acccagtgtc | tcctctacac | cctaattggcc | 360 |
| tatgacaggt | acctggcaat | atgtcagccc | ctgcgctacc | ctgtgctcat | gactgctaag  | 420 |
| ctgagcgcct | tgtttgtggc | tggagcctgg | atggcaggat | ccatccatgg | ggctctccag  | 480 |
| gccatcctaa | ccttccgcct | gccctactgt | gggcccacac | aggtggatta | cttcttctgt  | 540 |
| gacatccctg | cagtgttgag | actggcctgt | gctgacacaa | cagtcaacga | gctggtgacg  | 600 |
| ttttagacaa | ttgggggtgg | gggtgccagt | tgcttctccc | tgatcctcct | ctcctacata  | 660 |
| cagatcattc | aggccatcct | gagaatccac | acagctgatg | ggcggcgccg | ggctttttca  | 720 |
| acttgtggag | cccatgtaac | cgtggtcacc | gtgtactatg | tgccctgtgc | cttcatctac  | 780 |
| ctgaggcctg | aaaccaacag | ccccctggat | ggggcagctg | ccctagtccc | cacggccatc  | 840 |
| actcctttcc | tcaacccctt | tatctacact | ctgcggaacc | aagaggtgaa | gctggccctg  | 900 |
| aaaagaatgc | tcagaagccc | aagaactccg | agtgaagtt  |            |             | 939 |

&lt;210&gt; 1050

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g900 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1050

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atgggaaaga | ccaaaaacac | atcgctggac  | actgtggtga | gagatttcat | tcttctgggt | 60  |
| ttgtctcacc | ccccgaatat | aagaagcctc  | ctcttcctgg | tcttcttcgt | catttacatc | 120 |
| ctcactcagc | tggggaacct | gctcattctg  | ctcaccgtgt | gggctgaccc | gaagctccgt | 180 |
| gctcgcccca | tgtacattct | tctgggagtg  | ctctcattcc | tggacatgtg | gctctcctca | 240 |
| gtcatcgttc | cttgaattat | tttaaaacttc | actcctgcca | acaaggctat | cccgtttggt | 300 |
| ggctgtgtgg | ctcaactgta | tttctttcac  | ttcctgggca | gcacccagtg | cttctcttac | 360 |
| accttgatgg | cctatgacag | gtacctggca  | atatgtcagc | ccctgcgcta | cccagtgtct | 420 |
| atgaatggga | ggttatgcac | agtccttgtg  | gctggagctt | gggtcgccgg | ctccatgcat | 480 |
| gggtctatcc | aggccaccct | gaccttcgcg  | ctgccctact | gtgggcccac | tcaggtagat | 540 |
| tactttatct | gtgacatccc | cgcagtattg  | agactggcct | gtgctgacac | aactgtcaat | 600 |
| gagcttgtga | cctttgtgga | catcggggta  | gtggccgcca | gttgcttcat | gttaattctg | 660 |
| ctctcgtagt | ccaacatagt | aaatgccatc  | ctgaagatac | gcaccactga | tgggaggcgc | 720 |
| cgggccttct | ccacctgtgg | ctcccaccta  | atcggtgtca | cagtctacta | tgtcccctgt | 780 |
| attttcatct | accttagggc | tggctccaaa  | ggccccctgg | atggggcagc | ggctgtgttt | 840 |
| tacactgttg | tactccatt  | actgaacccc  | ctcatctata | cactgaggaa | ccaggaagtg | 900 |
| aagtctgccc | tgaagaggat | aacagcaggt  | caagggactg | aatgaaaata | agta       | 954 |

&lt;210&gt; 1051

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g901 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1051

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgggaaaga | ccaaaaacac | atcgctggat | gccgtggtga | cagatttcat | tcttctgggt | 60  |
| ttgtctcacc | ccccaaatct | aagaagcctc | ctcttcctgg | tcttcttcat | catttacatc | 120 |



|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctcactcagc | tggggaacct | gctcattctg | ctcaccatgt | gggctgaccc | gaagctctgt | 180 |
| gctcgcccca | tgtacattct | tctgggagtg | ctctcattcc | tggacatgtg | getctctca  | 240 |
| gtcaccgttc | ctcggcttat | tttggatttt | actccttcca | tcaaggctat | ccggtttggt | 300 |
| ggctgtgtgg | ctcaactgta | tttctttcac | ttcctgggca | gcacccagtg | cttctctac  | 360 |
| accttgatgg | cctatgacag | gtacctagca | atatgtcagc | ccctgcacta | cccagtgtct | 420 |
| atgaatggga | ggttatgcac | agtccttgtg | gctggagctt | gggtcgccgg | ctccatgcat | 480 |
| gggtctatcc | aggccacctt | gaccttcgcg | ctgcccact  | gtgggcccga | tcaggtggat | 540 |
| tactttatct | gtgacatccg | cgcagtattg | agactggcct | gtgctgacac | aactgtcaat | 600 |
| gagcttgtga | cctttgtgga | cgtcagggtg | gtggccgcca | gttgcttcat | gttaattctg | 660 |
| ctctcctatg | ccaacatagt | ccatgccatc | ctgaagatac | gcaccgctga | tgggaggcgc | 720 |
| cgggccttct | ccacctgtgg | ctcccaccta | atcgtggtea | cagtctacta | tgtceectgt | 780 |
| attttcatct | accttagggc | tggctccaaa | gacccctgg  | atggggcagc | ggctgtgttt | 840 |
| tacactgttg | tcactccatt | actgaacccc | ctcatctata | cactgaggaa | ccaggaagtg | 900 |
| aagtctgccc | tgaagaggat | aacagcaggt |            |            |            | 930 |

&lt;210&gt; 1052

&lt;211&gt; 900

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g902 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1052

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| atgtttatat | tgacaggctt | cacagatgat  | tttgagctgc | aagtcttcct | atttttacta  | 60  |
| ttttttgcaa | tctatctctt | taccttgata  | ggcaatttag | ggctggttgt | gttggtcatt  | 120 |
| gaggattcct | ggctccacaa | ccccatgtat  | tattttctta | gtgttttatc | attcttggat  | 180 |
| gcttgctatt | ctacagttgt | caactccaaa  | atgttggtea | atttcctggc | aaaaaataaa  | 240 |
| tccatttcat | ttatcggatg | tgcaacacag  | atgcttcttt | ttgttacttt | tggaaactaca | 300 |
| gaatgttttc | tcttggtgcg | aattggcttat | gatcactatg | tagccatcta | caacctctc   | 360 |
| ctgtattcag | tgagcatgtc | accagagatc  | tatgtgccac | tcatactgc  | ttcctacggt  | 420 |
| gctggcattt | tacatgctac | tatacatata  | gtggctacat | ttagcctgtc | cttctgtgga  | 480 |
| tccaatgaaa | ttaggcatgt | cttttgtgat  | atgcctctc  | tccttgctat | ttcttgttct  | 540 |
| gacactcaca | caaaccagct | tctactcttc  | tactttgtgg | gttctattga | gatagtcact  | 600 |
| atcctgattg | tcctcatttc | ctgtgatttc  | attctgttgt | ccattctgaa | gatgcattct  | 660 |
| gctaaggga  | ggcaaaaggc | cttctctaca  | tgtggctctc | acctaactgg | agtgacaatt  | 720 |
| tatcatggaa | caattctcgt | cagttatatg  | agaccaagtt | ccagctatgc | ttcagaccat  | 780 |
| gacatcatag | tgtcaatatt | ttacacaatt  | gtgattccca | agttgaatcc | catcatctat  | 840 |
| agtttgagga | acaaagaagt | aaaaaaggca  | gtgaagaaaa | tgttgaaatt | ggtttacaaa  | 900 |

&lt;210&gt; 1053

&lt;211&gt; 974

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g903 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1053

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| cacacagagc  | cacggaatct | cacagggtgc | tgagaattcc | tcctcctggg  | actctcagag | 60  |
| gatccagaac  | tgcagccagt | cctcgctttg | ctgtccctgt | ccctgtccat  | gtatctggtc | 120 |
| acgggtgctga | ggaacttget | gagcatcctg | gctgtccgct | ctgagtcctc  | gctccacaca | 180 |
| accatgtact  | tcttctctc  | catcctgtgc | tgggctgaca | tcggtttcac  | ctcagccaca | 240 |
| gttcccaaga  | tgattgtgga | catgcagtg  | tatagcaaag | tcatactctca | tgcgggctgc | 300 |
| ctgacacaga  | tgtctttctt | ggtccttttt | gcatgtatag | aaggcatgct  | cctgactgtg | 360 |
| atggcctatg  | actgctttgt | aggcatctgt | cgcctctctc | actaccagct  | catcgtgaat | 420 |
| cctcatctct  | gtgtcttctt | tgttttgggt | tcctttttcc | ttagcctgtt  | ggattcccag | 480 |
| ctgcacagtt  | ggattgtgtt | acaattcacc | atcatcaaga | atgtggaaat  | ctctaatttt | 540 |
| gtctgtgacc  | cctctcaact | tctcaaaact | gcctgttctg | acagcgtcat  | caatagcatc | 600 |
| ttcatatatt  | ttggtagtac | tatgtttggt | tttcttccca | tttcagggat  | ccttttgtct | 660 |
| tactataaaa  | tcgtccctc  | cattctaagg | atttcatcgt | cagatgggaa  | gtataaagcc | 720 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttctccacct | atggetctca | cctagcagtt | ttttgctgat | ttgatggaac | aggcattggc | 780 |
| gtgtacctga | cttcagctgt | ggcaccaccc | ctcaaggaat | ggtgtggtgg | tgctcagtga | 840 |
| gtaagctgtg | gtcacccccc | atgccgaacc | ttttcatcta | cagcctggag | aaacagggac | 900 |
| atacaaagtg | ccctgcgagg | gctgcccac  | aaaacagtcg | aatctcatga | tctgttccat | 960 |
| cctttttctg | gtgt       |            |            |            |            | 974 |

&lt;210&gt; 1054

&lt;211&gt; 1006

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g904 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1054

|             |            |            |              |            |            |      |
|-------------|------------|------------|--------------|------------|------------|------|
| gatacagacc  | cacagagtat | aacagatgtc | tctatatattcc | tcctcctcga | actctcagag | 60   |
| gatacagaac  | tgcaaccggg | cgtcgctggg | ctgttcctgt   | ccatgtgcct | cgatcatggg | 120  |
| ctgggggaacc | tgctcatcat | cctggacgtc | agccctgact   | cccacctccc | cacccccatg | 180  |
| tactttcttcc | tctccaacct | gtccttgcc  | gacatcgggt   | tcacctccac | cacgggtccc | 240  |
| aagatgattg  | tggacatcca | gtctcacagc | aaagtcattc   | atgcaggctg | cctgactgtg | 300  |
| atgtctctct  | ttgccatttt | tggaggcatg | gaaaaaagac   | atgctcctga | gtgtgatggc | 360  |
| ctatgaccgg  | tttgtaccca | tctgtcaccc | tctatatcgc   | tcagccatct | tgaacccgtg | 420  |
| tttctgtggc  | ttcctaaatt | tgttgtcttt | tttttttttc   | cctcagtctt | ttagactccc | 480  |
| agctgcacaa  | cttgattgcc | ttacaaatga | cctgcttcaa   | ggatgtggaa | attcctaatt | 540  |
| tcttctggga  | accttctcaa | ctccccatc  | ttgcatgttg   | tgacaccttc | accaggaaca | 600  |
| tcagcatgta  | tttccctgct | gccgtatttg | gttttctttc   | catctcgggg | acccttttct | 660  |
| cttactgtaa  | aatggtttcc | tccattctga | gggtttcatc   | atcagggtgg | aagtataaac | 720  |
| cttctccacc  | tgagggtccc | acctgtcagt | tgtttgctga   | ttttatggaa | caggcgttgg | 780  |
| agagtacctc  | ggttcagatg | tgctcatctc | cccagaaag    | ggtgcagtgg | cctcagtgat | 840  |
| gtacacgggtg | gtcaccacca | tgctgaaccc | cttcatctac   | agcctgagaa | acggggatat | 900  |
| taaaagtgtc  | ctgcggcggc | cgcaaggcag | cacagtctca   | tctcaatacc | ttcttatctg | 960  |
| ttccattcct  | tttgtagggt | gggttaacaa | agacagcaag   | gtcaaa     |            | 1006 |

&lt;210&gt; 1055

&lt;211&gt; 929

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g905 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1055

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| atggaaaaata | ggaaaaattg | acttaattca | tcctcttggg  | gctcacacag | aaccctgagg  | 60  |
| gccaaaaagt  | tttatttgtc | acattcttac | tcattctacat | tgtgacgata | atgggcaacc  | 120 |
| tccttatcat  | ggtgaccatc | atggccagcc | agtccttggg  | ttcccccatg | tacttttttc  | 180 |
| tggtcttctt  | atcatttata | cataccgtct | attatactgc  | cattgtctcc | aaaatgattg  | 240 |
| ttgacctgct  | ctctgagaaa | aagaccattt | cttttcaggg  | ttgtatggct | caacttttta  | 300 |
| tggatcattt  | atttgctggg | gctgaagtea | ttcttctggg  | ggtaaatggc | tatgatcaat  | 360 |
| atgtggccat  | ctgtaagcct | cttcattatt | tgatcatcat  | gaatcgtcga | gtctgtgttc  | 420 |
| tcattgctgt  | ggtggcctgg | attggaggct | ttcttcactc  | attggttcaa | tttctcttta  | 480 |
| tttatcagct  | ccctttctgt | ggacccaatg | tcattgacaa  | cttcctgtgt | gatttgtatc  | 540 |
| ccttattgaa  | acttgcttgc | accaataacc | atgtcactgg  | gctttctatg | atagctaattg | 600 |
| gtggagcgat  | ttgtactgtc | accttcttcc | ctctcctgct  | ttcctatggg | gtcatattac  | 660 |
| cctctcttaa  | gactcagagt | ttggaaggga | aatgcaaagc  | tttctacacc | tgtgcattcc  | 720 |
| acatcactgt  | gatcacttta | ttctttgtcc | cctgcatctt  | cctgttagca | aggcccaact  | 780 |
| ccacctttcc  | cattgataaa | tccatgactg | tggttttaac  | ttgtataact | cccatgctga  | 840 |
| aaccactaat  | ctatgccctg | aggaatgcag | aaatgaaaag  | tgccatgagg | aaacttttga  | 900 |
| gtgaaaaagt  | aagcttagct | ggaaaaggg  |             |            |             | 929 |

&lt;210&gt; 1056

&lt;211&gt; 925

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g906 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1056

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| cacatgcctc  | ccaacaatgt | gactgaattc  | attctcttgg | ggctcacaca | gaatccacac  | 60  |
| ttgcagaaaa  | tactctttat | tgtattttta  | tttatttttc | tatttaccat | gctggccaat  | 120 |
| ctgttcattg  | tcacacccat | ctcctgtagc  | cccacacttt | catcacccat | gtacttcttt  | 180 |
| ctcacttact  | tatcctttat | agatgcctcc  | tacacctctg | tcacaacccc | caaaatgatc  | 240 |
| accgacctgc  | tctaccagag | gagaactatt  | tccttggtg  | gctgcctgac | tcagctcttt  | 300 |
| gtggagcact  | tgtctgggag | ctcagagatc  | atcctcctta | ttgtcatggc | ctatgaccgc  | 360 |
| tacgtggcca  | tctgcaagcc | cctgcactac  | acaaccatta | tgcaacaagg | gatctgccac  | 420 |
| cttctgtgtg  | tgtatgcctg | gattggaggc  | atcctgcatg | ccactgtgca | gattcttttc  | 480 |
| atgaccgact  | tgcccttctg | tggtcccca   | tgctattgac | cactttatgt | gtgatctctt  | 540 |
| cccattgttg  | aaacttgctt | gcagagacac  | ctacagactt | gggatgctgg | tggcagccaa  | 600 |
| cagtggagcc  | atgtgcttgc | tcactctttc  | cctgctcgtc | atctcttaca | tagtcatcct  | 660 |
| gagctccctg  | aaatcctata | gctctgaagg  | acagcacaaa | gccctctcca | cctgtggctc  | 720 |
| ccactttact  | gtcgttgtac | tcttttttgt  | gccttgcata | ttcacctaca | tgcactcctgt | 780 |
| ggtcacctac  | tctgtggaca | agttgggtgac | tgtgttcttt | gcaatcctca | ctcccatggt  | 840 |
| aaatccctata | atttacactg | tgagaaacac  | agaggtaaaa | aatgccgtga | ggagtttggt  | 900 |
| gaggaaaaga  | gtaacagttt | atgca       |            |            |             | 925 |

&lt;210&gt; 1057

&lt;211&gt; 499

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g907 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1057

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atgtacacga | ctttactcat | ggcccagggt | gtgtctctgt | gcagacaatg | gatccacac   | 60  |
| tctttctgtg | atatgtctgc | tctgctgaag | ctggccctct | ctgacactcg | agttaatgaa  | 120 |
| tgagtgatat | ttatcatggg | agggctcatt | cttgtcatcc | catccatact | catccttggg  | 180 |
| tcctatgcaa | gaattgtctc | ctccatcctc | aaggctcctt | cttctaagtg | tatctgcaag  | 240 |
| gccttctcta | cttgtggctc | ccaccctgtc | tgtgggtgtc | ctgttctatg | gaaccgttat  | 300 |
| tggtctctac | ttatgtctat | cagctaatag | ttctactcta | aaggacactg | tcattggctat | 360 |
| gatgtacact | gtggtgaccc | ccatgctgaa | ccccttcctc | tacagcctga | ggaacagaga  | 420 |
| catgaaggga | gccctgagca | gagtcattca | tcagaagaaa | actttcttct | ctctctgatg  | 480 |
| ataacacttg | gagctatta  |            |            |            |             | 499 |

&lt;210&gt; 1058

&lt;211&gt; 996

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g908 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1058

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgggacca  | agaatcta   | tcgtgttttg | gaattcttcc | tcctccactt | cttagatgac | 60  |
| ttggaactgc | agcctttcct | cttcaggctg | tccctgaacc | atgcacctag | tcacagtgt  | 120 |
| tgcgaacttg | ctcacatcct | tctgactgtc | agctttgccc | tcacctccac | aaccccatga | 180 |
| acttcaacct | gtccttagct | gacattgggt | tcacctctgc | cacaatttca | aagataactg | 240 |
| tagacctcca | aactcacagc | agaatcattt | tatacatgag | ctgcctgaaa | tagatgtctt | 300 |
| ttaaaattat | ttttggatgt | ttgcacaatc | tactcatgac | tgtgatggcc | tatgacccat | 360 |
| ttgtggcgac | ctgtcatctc | ttgtactaca | cagtcatcag | gaatccccac | ctctgtggcc | 420 |
| tcttgcttct | gggtctctct | tctctctctc | tttttttttt | ttgatcagtc | ttttggaaac | 480 |
| ccagctgtac | agtttgatgg | tgtcacaagt | tctctcatgc | aatgtagac  | attcctcatt | 540 |

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| tcttctgtga | cccttctcag | tttctccacc  | tttctgttc   | tgacactgcc | accaataaca | 600 |
| cattaatgca | ttttattggt | gccatctctg  | tgggtccattc | tcagggatcc | tttactgtta | 660 |
| tactcaaatt | atgttctcca | tactcataaac | cctataaaat  | gtgggaagta | taaagcaaac | 720 |
| cttctccacc | catcgctctc | acctgtcagt  | tgtttgctta  | ttttatggaa | caggccttgg | 780 |
| agtatacctt | agtttggctg | gctcaccttc  | cccaagaaca  | ggtgtggtgg | cctcaatggt | 840 |
| atataccaca | gtcacctca  | tgttgaaccc  | tgcattcaca  | gcctgaggaa | cagagacatc | 900 |
| aagaatacct | ggtggtggct | cctcagcata  | actgcctggt  | atcaatacct | gtgctatcct | 960 |
| ttatggagtg | tggttagaaa | aaacagcaaa  | ctcaaa      |            |            | 996 |

&lt;210&gt; 1059

&lt;211&gt; 923

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g909 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1059

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| atggggactt  | caaataatga  | gactgaattc  | attcttttgg | gcattacaaa | aaatccagaa | 60  |
| ctaaggaaaa  | tattctctgc  | tttgtttcta  | gccatgtatg | tgaccacagt | gttgggaaat | 120 |
| ctattcattg  | tggtgactct  | ggctgcaagt  | tggagtctga | gatcacctat | gtacttttcc | 180 |
| cttacttctt  | tgtctctcat  | gggtgccacc  | tactcttcca | tcactgcccc | taagatgact | 240 |
| gtggactctt  | tgagaacact  | accatttccc  | ttgaaggctg | catgaccag  | ctctttgcag | 300 |
| agcatttctc  | tgatggtgta  | gcgatcatcc  | ttctcactgt | gatggtctgt | gactgctatg | 360 |
| aggccatcag  | taagccccctg | catgacacaa  | ccatcatgag | tccacgggtg | tgctgctgtt | 420 |
| ggtggttagaa | gcttgggtgg  | ggggattaac  | acatgccaca | atacagcttt | ttttttttca | 480 |
| tatatcaaat  | acccttctgt  | ggtcccaata  | ttattgacca | ttttatatgt | gatttgtttc | 540 |
| cattgttaaa  | acttgcttac  | atggacaccc  | acatgctggg | tctcttagtc | atcctcaaca | 600 |
| gtggggatgat | gtgtatggcc  | atcttccctta | tcctaattgc | atcctacatt | gtcacctgt  | 660 |
| actctctgaa  | gtcttgcagc  | tcggtaggtc  | gacgcaacac | actttccacc | tgtggctccc | 720 |
| accacacagt  | ggtcattctg  | ttcttcgtgg  | agtgtatttt | cttgtagata | agacctgtgg | 780 |
| tcacttaccc  | catagacaag  | gatatggcta  | tttcctttac | tattgttgca | cccatgttaa | 840 |
| atcctctgat  | ctataccctg  | aggggcatca  | aggtaaaaaa | tgccataaga | aaaatgtgga | 900 |
| tgaaacaggg  | gaccctaggt  | ggt         |            |            |            | 923 |

&lt;210&gt; 1060

&lt;211&gt; 950

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g910 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1060

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| atggctccga | ccaacctcac  | atctgcccc   | gctgttcttc  | ctcctcggcc  | tggtggacgg  | 60  |
| aacagacgcc | caccgcgtgc  | tgttctctgt  | ctgccttggg  | tctatctgct  | caacgccctg  | 120 |
| agcaacctga | gcattggtggc | gctggtgaga  | tccgacgggg  | ccctccgctc  | ccccatgtat  | 180 |
| tacttcttgg | gtcactgagc  | ctcgtggacg  | tctgctttac  | caccgtcacg  | gtccccaggc  | 240 |
| tgctggccgg | cctgctccac  | ccgggcccagg | ccatatacctt | ccaggcgtgt  | ctgccgagat  | 300 |
| gtactttctt | gtgactctgg  | catcacccag  | agctacctca  | tggcggccat  | gtcctagcga  | 360 |
| gccccagcgc | gcgtgccggc  | acctctgtac  | ggcgcgctgg  | tgacgccatc  | ggcgtgcgcc  | 420 |
| tgcgtggtgc | tgcgtcgtgg  | gccgtgacgc  | acctgcactc  | gctgctgcac  | acgctgctcc  | 480 |
| tctccgcgct | ctcctacccc  | tacccacccc  | ccgtgcgccc  | cttcttttgc  | gacatgacgg  | 540 |
| tgatgctgag | cttggcgacc  | tcggacacgt  | ccgccgcgga  | gacggccatc  | ttctccgagg  | 600 |
| gcctggccgt | ggtgttggcc  | ccgctgtccc  | tcgtgttccc  | tttccctacgc | gcgcactcctg | 660 |
| gtcgcggtgc | tcggcttggc  | cggccgcgcc  | gcgccttctc  | cacctgcggg  | gcccacctag  | 720 |
| tggcggtggc | ggtggcgctt  | ttctttggct  | ctgtcctctc  | cgtgtatttc  | ccgccgtcgt  | 780 |
| ctgcctactc | agcccgtac   | gaccgcctgg  | ccagcgtggt  | ctacgctgtc  | atcacgccga  | 840 |
| ccttgaaccc | tttcatcaac  | agccttcgca  | acaaagaggt  | caagggcgcc  | ctgaaaaggg  | 900 |
| ggctcagcat | ggagggctgc  | accccaagag  | gcgtgagggc  | aaatctggct  |             | 950 |

<210> 1061  
 <211> 933  
 <212> DNA  
 <213> Unknown (H38g911 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1061  
 atgaaagggg caaacctgag ccaaggggatg gagtttgagc tcttgggcct caccactgac 60  
 cccagctcc agaggctgct cttcgtgggtg ttctgggca tgtacacagc cactcfigctg 120  
 gggaacctgg tcatgttctt cctgatccat gtgagtggca cctgcacac acccatgtac 180  
 tccctcctga agagcctctc cttcttggat ttctgtact cctccacggg tgtgccccag 240  
 accctgggtga acttcttggc caagaggaaa gtgatctctt attttggctg catgactcag 300  
 atgttcttct atgcggtgtt tgccaccagt gagtgctatc tcatcgctgc catggcctat 360  
 gaccgctatg ccgctatttg taacccctg ctctactcaa ccatcatgtc tcctgaggtc 420  
 tgtgcctcgc tgattgtggg ctctacagt gcaggattcc tcaattctct tatccacact 480  
 ggctgtatct ttagtctgaa attctgcggg gctcatgtcg tcaactcactt cttctgtgat 540  
 gggccacca tctgtcctt gtcttgtgta gacacctcac tgtgtgagat cctgctcttc 600  
 attttggctg gtttcaacct tttagctgc accctcacca tcttgatctc ctacttctta 660  
 attctcaaca ccatcctgaa aatgagctcg gccagggca ggtttaaggc attttccacc 720  
 tgtgcatccc acctactgc catctgcctc ttcttggca caacactttt tatgtacctg 780  
 cgccccaggc ccagctactc cttgacccag gaccgcacag ttgctgtcat ctacacagtg 840  
 gtgatccag tgctgaacc cctcatgtac tctttgagaa acaaggatgt gaagaaagct 900  
 ttaataaagg tttggggtag gaaaacaatg gaa 933

<210> 1062  
 <211> 948  
 <212> DNA  
 <213> Unknown (H38g912 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1062  
 atgcaaaacc aaagctttgt aactgagttt gtccctcctgg gactttcaca gaatccaaat 60  
 gttcaggaaa tagtatttgt tgtatttttg tttgtctaca ttgcaactgt tgggggcaac 120  
 atgctaattg tagtaaccat tctcagcagc cctgctcttc tggtgtctcc tatgtacttc 180  
 ttcttgggct tctgtcctt cctggatgag tgcttctcat ctgtcatcac cccaaagatg 240  
 attgtagact ccctctatgt gacaaaaacc atctcttttg aaggctgcat gatgcagctc 300  
 tttgctgaac acttctttgc tggggtggag gtgattgtcc tcacagccat ggcctatgat 360  
 cgttatgtgg ccatttgcaa gcccttgcat tactcttcta tcatgaacag gaggtctgtg 420  
 ggcattctga tgggggtgag ctggacaggg ggcctcttgc attccatgat acaaattctt 480  
 tttactttcc agcttccctt ttgtggcccc aatgtcatca atcactttat gtgtgacttg 540  
 taccggttac tggagcttgc ctgcactgat actcacatct ttggcctcat ggtggtcatc 600  
 aacagtgggt ttatctgcat cataaacttc tccttgttgc ttgtctccta tgctgtcatc 660  
 ttgctctctc tgagaacaca cagttctgaa gggcgctgga aagctctctc cacctgtgga 720  
 tctcacattg ctggttgat tttgttctt gtcccatgca tatttgtata tacacgacct 780  
 ccattctgctt tttcccttga caaatggcg gcaatatctt atatcatctt aaatcccttg 840  
 ctcaatcctt tgatttacac tttcaggaat aaggaagtaa aacaggccat gaggagaata 900  
 tggaacagac tgatggtggt ttctgatgag aaagaaaata ttaaactt 948

<210> 1063  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g913 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1063

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| atgcaactga  | ataataatgt | gactgagttc | attctgcttg  | gattgacaca | ggatcctttt | 60  |
| tggaagaaaa  | tagtggttgt | tatttttttg | cgtctctact  | tgggaacact | gttgggtaat | 120 |
| ttgctaataca | ttattagtgt | caaggccagc | caggcactta  | agaaccaaat | gttcttcttc | 180 |
| cttttctact  | tatecttata | tgataacttg | ctctctactt  | ccatagcccc | tagaatgatt | 240 |
| gtggatgccc  | ttttgaagaa | gacaactatc | tccttcagcg  | agtgcacgat | ccaagtcttt | 300 |
| tcatcccatg  | tctttggctg | cctggagatc | ttcatcctca  | tcctcacggc | tggtgaccgc | 360 |
| tatgtggaca  | tctgtaagcc | cctgcactac | atgaccatca  | taagccagtg | ggtctgtggt | 420 |
| gttttgatgg  | ctgtggcctg | ggtgggatcc | tgtgtgcatt  | ctttagtcca | gatttttctt | 480 |
| gccctgagtt  | tgccattctg | tggccccaat | gtgatcaatc  | actgtttctg | tgacttgacg | 540 |
| cccttggtga  | aacaagcctg | ttcagaaacc | tatgtgggta  | acctactcct | ggtttccaat | 600 |
| agtggggcca  | tttgtgcagt | gagttatgtc | atgtaataat  | tctcctatgt | catcttcttg | 660 |
| cattctctga  | gaaaccacag | tgctgaagtg | ataaagaaaag | cactttccac | atgtgtctcc | 720 |
| cacatcattg  | tggtcatctt | gttctttgga | ccttgcataat | ttatgtacac | atgccctgca | 780 |
| accgtattcc  | ccatggataa | gatgatagct | gtattttata  | cagttggaac | atcttttctc | 840 |
| aaccctgtga  | tttacacgct | gaagaataca | gaagtgaaaa  | gtgccatgag | gaagctttgg | 900 |
| agcaagaaat  | tgatcacaga | tgacaaaaga |             |            |            | 930 |

&lt;210&gt; 1064

&lt;211&gt; 964

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g914 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1064

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| atggagacaa  | caaatcactc | tgccgtgact  | gaattctttc  | tggtggggct | ttcccaatat  | 60  |
| ccagagctcc  | agctttttct | gttctctgct  | tgccctcatca | tgtacatgat | aatcctcctg  | 120 |
| ggaaatagct  | tcctcattat | catcaccatc  | ttggattctc  | gcctccatac | ccccatgtat  | 180 |
| ttctttcttg  | gaaacctctc | attcttgggc  | atctgttaca  | catcatcatc | cattcctcca  | 240 |
| atgcttatta  | tatttgtatc | tgagagaaaa  | tccatctcct  | tcattggctg | tgctctgcag  | 300 |
| atgggtgtgt  | cccttggtct | gggtctccatt | gagtgatccc  | tcctggctgt | gatggcctat  | 360 |
| gaccgctatg  | tggccatctg | caaccacactg | aggtaactcca | tcatcatgaa | cagagtgtctg | 420 |
| tatgtgcaaa  | tggctgcatg | gtcctggatc  | ataggctgtc  | tgacctccct | attgcgaaca  | 480 |
| gttctgacaa  | tgatgttgcc | tttctgtggg  | aataatatca  | ttgatcatct | tacctgtgag  | 540 |
| atcctggctc  | ttcttaaagt | catatgctca  | gatctctcca  | taaatgtgtt | tataatgaca  | 600 |
| gtgtcaagta  | ttgttttatt | ggtgattcct  | cttaattttt  | atctcctatg | tgttttattct | 660 |
| ctcttccatc  | ttgagaatta | attctgctga  | gggaagaaag  | aaagcctttt | ttacctgttc  | 720 |
| agcgcaactg  | actgtggcca | tcttattctg  | tggttcagtt  | cttttcacgc | acatgaagcc  | 780 |
| caaatcaaaag | ttcacaacag | catctgatga  | aatcattgga  | ttgtcttatg | aagtgtacac  | 840 |
| cccaatgaac  | cccatcatct | acagcctgag  | gaataaggag  | ataaaagaag | ctgtgaagaa  | 900 |
| aatcctcagc  | agacacgtgc | atctatggaa  | aatatgaaag  | gccttgaggc | atgtgacgtt  | 960 |
| ctca        |            |             |             |            |             | 964 |

&lt;210&gt; 1065

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g915 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(620)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1065

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| gatgcatgct  | cgagcgccccg | cagtgtgatg | gatatctgca  | gaattcgccc | ttccaatgta | 60  |
| ctttttcctg  | aagaacctct  | ctgttttgga | tctgtgtctac | atctcagtea | ctgtgcctaa | 120 |
| atccaatccgt | aactccctga  | ctgcagaag  | ctccatctct  | tatcttggct | gtgtggctca | 180 |
| agcctatttt  | ttctctgcct  | ttgcatctgc | tgagctggcc  | ttccttactg | tcatgtctta | 240 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tgaccgctat | gttgccattt | gccaccccct | ccaatacaga | gccgtgatga | catcaggagg | 300 |
| gtgctatcag | atggcagtc  | ccacctggct | aagctgcttt | tcctacgcag | ccgtccacac | 360 |
| tggaacatg  | tttcgggagc | acgtttgcag | atccaatgtg | atccaccagt | tcttcctgta | 420 |
| catccctcag | gtgttgccc  | tggtttcctg | ngagggtttt | ttttagagac | tttgacceng | 480 |
| ccctgagcct | caatgcttgg | ntctgggatg | ctttattccc | atgatgatct | ccnattttcc | 540 |
| anatcttctn | aanggggctc | nagaatccct | tnaggaccag | antcnagcta | aaagcctttn | 600 |
| ccnnctgct  | tccccccacg |            |            |            |            | 620 |

&lt;210&gt; 1066

&lt;211&gt; 611

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g916 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(611)

&lt;223&gt; n = A,T,C or G

|            |  |
|------------|--|
| <400> 1066 |  |
| gatgcatgct | cgagcggccg ccagtgatgat ggatatctgc agaattcgcc cttccaatgt 60 |
| atattttct  | ctctgacctc tccttcttgg acctctgctt taccacaagt tgtgtccccc 120 |
| agatgctggg | caacctctgg ggcccaaaga agaccatcag cttcctggga tgctctgtcc 180 |
| agctcttcat | cttctgtgcc ctggggacca ctgagtgcac cctcctgaca gtgatggcct 240 |
| ttgaccgata | cgtggctgtc tgccagcccc tccactatgc caccatcatc ccccccgcc 300  |
| tgtgctggca | gctggcatct gtggcctggg ttatgagtct ggttcaatcg atagtccaga 360 |
| catcatccac | cctccacttg ccttctgtc cccaccagca gatagatgac tttttatgtg 420  |
| aggteccatc | tctgattcga ctctcctgng gagatacctc ctacaatgaa atccagttgn 480 |
| ctgtgtccag | tgtcatcttt ggtggntgtg cctctcagcc tcatccttgc ctcttatgga 540 |
| gccactgccc | aggcnggggc tgaggattaa ctttgccnna gccatggaag aaaggctctt 600 |
| nggacctngn | n  |
|            | 611  |

&lt;210&gt; 1067

&lt;211&gt; 619

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g917 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(619)

&lt;223&gt; n = A,T,C or G

|             |   |
|-------------|---|
| <400> 1067  |   |
| gatgcatgct  | cgagcggccg ccagtgatgat ggatatctgc agaattcgcc ctttctttat 60  |
| ttcgaagagt  | atacactagt ggattgaaga gaaacaaata cataggaagg gcgaattcca 120  |
| gcacactggc  | ggcgttact agtggatccg agctcggtag caagcttgat gcatagcttg 180   |
| agtattctaa  | cgcgtcacct aaatagcttg gcgtaatcat ggtcatagct gtttctgtg 240   |
| tgaaattgtt  | atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa 300  |
| gcctgggggtg | cctaattgagt gagctaactc acattaattg cgttgcgctc actgtccgct 360 |
| ttccagtcgg  | gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcgngnaga 420  |
| ggccggnttg  | cgtattgggc gctcttccgc ttctcgtcga ctgactcgtc gcgctcggga 480  |
| cgtccggctg  | cggcgagcgg taccagctta ctcaanggcc gtantacggt tattcncagg 540  |
| aatnnggggt  | taacgcncng naaagaacat tgtgngccan angncaagcn taatgcccag 600  |
| gaaccgntan  | aacgntccc   |
|             | 619   |

&lt;210&gt; 1068

&lt;211&gt; 621

&lt;212&gt; DNA

<213> Unknown (H38g918 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(621)

<223> n = A,T,C or G

<400> 1068

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| gnnnnntntt  | cantccattg | ggccctctag  | atgcatgctc | gagcggccgc  | eagtgtgatg | 60  |
| gatatctgca  | gaattcgccc | ttattccgga  | gggtatacat | gaagggattg  | gtaactagac | 120 |
| gtaaactcga  | agccaagaac | agaatttctc  | ttagaaaaga | gaattgaaac  | taaagagaaa | 180 |
| gaactagcaa  | agaaggaaat | attgaatata  | caagagagag | gagacagatg  | atggaacaag | 240 |
| actctgaaag  | aggtggaagg | gattgaatac  | aatcaaaagt | atgggtgactg | ctagttccaa | 300 |
| gatgggtggcg | taggggcaag | ctggctttgc  | ttacccccct | ggcagaaaac  | caaaaacaaa | 360 |
| tagcaccaag  | attatcacta | gcaatatccc  | agaactcaca | tataaggatg  | agacagttcc | 420 |
| cagggcccgag | agaagatcag | aagcacaaagt | gggagaagtc | agctttggat  | gctactttgt | 480 |
| tctaagggag  | acaagttggg | aggatgattg  | cagatgtata | ttcaatgtta  | taaaacagcc | 540 |
| cataaaacaa  | agattggaaa | atgttgaatt  | ttgcaaccag | gagcaaatac  | tgggaaaggc | 600 |
| gaattccagc  | cacttgcngc | c           |            |             |            | 621 |

<210> 1069

<211> 615

<212> DNA

<213> Unknown (H38g919 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1069

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| gnnnnntnna | tcantgccct | ngggccctct  | agatgcatgc | tcgagcggcc | gccagtgtga  | 60  |
| tggatatctg | cagaattcgc | ccttggttgcg | caaggtgtaa | atgaaagggg | ttgcgcagga  | 120 |
| gtaaatgaag | ggattacgca | ggagtaaatg  | aagggattac | gcaggagtaa | atgaagggat  | 180 |
| tacgcaggag | taaatgaagg | gattacgcag  | gagtaaatga | agggattacg | caggagtaaa  | 240 |
| tgaagggatt | acgcaggagt | aaatgaaggg  | attacgcagg | agtaaatgaa | gggattacgc  | 300 |
| aggagtaaat | gaagggatta | cgcaggagta  | aatgaaggga | ttacgcagga | gtaaatgaag  | 360 |
| ggattacgca | ggagcaaata | cataggaagg  | gcgaattcca | gcacactggc | ggccggtact  | 420 |
| agtggatccg | agctcggtag | caagcttgat  | gcatagcttg | agtattctaa | cgcgtcacct  | 480 |
| aaatagcttg | gcgtaatcat | ggtcatagct  | gtttcctgtg | tgaaattgtt | atccgctcac  | 540 |
| aattccacac | aacatacgag | cccgggaagca | taaagtgtaa | agnctggggg | gcctaattgag | 600 |
| tgacttactc | catta      |             |            |            |             | 615 |

<210> 1070

<211> 614

<212> DNA

<213> Unknown (H38g920 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(614)

<223> n = A,T,C or G

<400> 1070

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| ggnnttnant | cattgccccg | ctngatgcat | gctcgagcgg | ccgccagtgt | gatggatatc | 60 |
|------------|------------|------------|------------|------------|------------|----|



```

tgcagaattc gcccttccga tgtattttct tctacgttaa ggtatttttaa attgttacta 120
atgcataagg gcaacacatt ctgtaatgct gacaagatga aagagccaaa agtaattaat 180
gatgctgtta cctcacaaat atgtatgtgt ggatgtatat atatctattc aatataatgta 240
actatacata tgtctgtttc taattgaaaa caccaggtaa ttatcatctg tagaaaccct 300
agtgtctcag ataagttggc tagttttttg tttcacataa aggaacaaac atttatagat 360
ttatatgtat attaaaaatg gtaaaaaattg gctgggtgca gtgggttcag cctataatac 420
cagcactttg ggaagccgag gtgggaggat tacttgaggt aaggagccca gcctgaccaa 480
caagggtgaaa ccccatccct actaaaaata caagaattag cccgggggatg gtgggtggcca 540
cctgtaatcc cagctacttg ggagactgaa gccaggaaaa tcacttgacc caggaagcng 600
aggttgcagg ngag 614

```

&lt;210&gt; 1071

&lt;211&gt; 857

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g921 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(857)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1071

```

atggnnnnnn nntttnnnaa anttttnccc antttgggcc gneccccct tctttaaggn 60
aatgggcccc ttgggccctt cccggaaggc ccggggggcnc ccggccccaagggtttgggt 120
tgggaaatgg ggggaattta aattcctttg ggccaaggna aaaattttcc ngccccctt 180
tttttccctt ttgggttttt anccggggga anggggggggt tgattaatta atcggaagn 240
tnggggggaa nttttttaa aaaaaccttg ggggaagggt ccaaccacac aaggttggtt 300
ttccanggga ccgttgggac caggcttttn gaatcaagaa tcccaaaggg cattcttttg 360
gattaaggaa nggtgccggg accggtgaaa gggaaaaaac tgggtggacc catacaaaa 420
tgagaaccac ggtgagatgc cgaggagcac gtggagaaag gctttgcttc cggccactgg 480
cagaggggat cctgaggatg gtgcttgatg atgtacacat agggagacaa ggggtgatgag 540
gcatgaactc aggataacca caacagcnat cacaaggcc acaaagctct actgcctgtg 600
tgttgggtgc aggccagggc aatccagggg tgcaatgtca caagaaagaa agtgggtgat 660
ggcacgggng ggccacagaa ggacaggcca ctgtgatgaag ggcttgtggg cactgcaatg 720
gccacgaaac caccagacc aggaaccan ggccaagctt gcgcctgaag agcaaggcta 780
ctcatgaatg gcttccgtag tngtaaagga tagcaagatg gcaaaggcaa gccggtcatn 840
aagccatggc ttgccng 857

```

&lt;210&gt; 1072

&lt;211&gt; 593

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g922 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(593)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1072

```

aacgcagagt accgcccact acgtaatctg tacatgaaag ggtttaaaag agactgggaa 60
gagaggaatt ggcaagatca agcagaggca actccttcta gtccttctag taccgcaagg 120
ggcagataaa tggaatgggt aacacctaga ggaaagtata cttgccaaaa gcaaatncat 180
aggggggagt acattatcgg gttgaaaaaa gtattccatg cagataaaaa ccaaaagcaa 240
atacatcggg ggcgtacttc tgcgtcttt gagcgtagt atggtaccca gcttttgnct 300
ctttagtgag ggttaattgc gcgcttgccg taatcatggt catagctggt ttctgtgtga 360
aattgttatc ccgctcacia ttcacacaac atacgagccc gggagcataa agtgtaaagc 420
ctgggggtgcc taatgagtgg agcttactta cattaaattg cgttgcgctc actggccgct 480

```

tttccaagtc gggaaacctg tctgtncagc ttcantaatg aatcggccaa cgccgcgggg 540  
agaggcgggt tgcgtattgg gcgctcttcc gcttcttngt tnactgactt cgg 593

<210> 1073

<211> 624

<212> DNA

<213> Unknown (H38g923 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(624)

<223> n = A,T,C or G

<400> 1073

gnnntttaac nccggngctn cnagcagtggt aacaacgcag agtacgcccc cgatgtactt 60  
tctttttcag tctcaagtct tctctttctc caaagatttt gtcttttcta ctacctgagc 120  
taccaaatcc cttgtcatca atttcaataa ctgtattctc ttcattcattt caacttcaaa 180  
cgtgtcatct cagaacaagc ttcattgttac ttccaatttt atccttcttg tttgtgtatt 240  
ccaagaattc cagtcccatc taggcccgcga atgcattggt cctgccaccc ttttcataatc 300  
ctcaattccc ttgtatcatc actttccttt tatatagcac agattccatg attcataaca 360  
ataattatgt ttttttttgc atgtgtctctt aatttccttt cttgtctcta ttatcttcta 420  
tcatactttt ctggaaacac taattctggt gaaatatact ctttgtggac tttgcactta 480  
tgctcagtcg gctgaagatg atggctagac aaatactcac aatcatgctg actggcccaa 540  
tttatagtcg tgaccaccga ttacaaaccc cttcatttat tctccgcaac aggggcgtct 600  
tctgcgcttg agcgtccggt gggg 624

<210> 1074

<211> 637

<212> DNA

<213> Unknown (H38g924 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(637)

<223> n = A,T,C or G

<400> 1074

ttatnnccat tggagctcca aagcagtggt aacaaccgca gagtacgccc cccatgtatt 60  
ttctttttct tggggnagct gnatgcttcc tncgtgctac catggnatat gaccggctat 120  
gnggncatct gcagtccttt gnnctcccag tcattatgaa ccaaaggaca cgggccaaac 180  
tggtctggtgn ttcttgggtc ccaagctttc ctgnagctac tngcaagac cacaatggct 240  
cttnagnntt ccattctgng gcaccaacaa ggtgaaccac ttntttctgn gacagccggc 300  
tgtgtgaaa gctggtctgn tgcaagacac agcactgttt gagatctacg ccatcgctcg 360  
aaccattctg gtggtcaatg aacccttctg tgctgatctt gngttcctat actcgnattg 420  
gtgctgctat cctcaagaa cccatcaagc taaangggaa gcaataaagn ccttttctcta 480  
cgtgtctctt aacacctccc ttggtggcct ctcttttcta atataatcnt ctaagcctca 540  
acctacttct tgggcctnaa ntcaaataaa ttcttctgga gaggcaagaa ggtggtattc 600  
atztatncta cactggtngn gactccatgn tggaaact 637

<210> 1075

<211> 621

<212> DNA

<213> Unknown (H38g925 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(621)  
 <223> n = A,T,C or G

<400> 1075  
 gtnatnccnt ttaatnccnt tggagctcca agcagtggta acaacgcaga gtacgcccgt 60  
 tcctcagaca gtatatgaat ggggttaaaaa tgggccagag cagatgcagg aagatcaaat 120  
 agggaggctac tgcagtagag tcaaactctag ggctgatggg ttcttgggat gcatagtaat 180  
 aggtagatag agaaagtctt taggaggtag aatggacagg acttcacaat gcattaaatg 240  
 tagggagaaa aaaaatgatt cctgggtttc tagcttgagc tagtagggat agtggtagaa 300  
 tttactgata tggaaaactg gaggaaaaag agtttgggaag agaaagatgg caagttaaat 360  
 acctgtggga aatataatca cagacactaa ataggcagct gtgtgggtgg caaaggagag 420  
 ccatgggcta ggaacatata gtgggattcc ctggcatgtc attggttact gaagtcagag 480  
 tgtatgagac agcctaagga gagaatncac acaggagaag aaagaactaa acattcagtg 540  
 gctggccaga ggatgagaaa cccaagagat tggactgttt aggagcaaca gtgttgngaa 600  
 aaggagaaa nggttgaaat t 621

<210> 1076  
 <211> 631  
 <212> DNA  
 <213> Unknown (H38g926 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(631)  
 <223> n = A,T,C or G

<400> 1076  
 ggntttannc nctggagctc caaagcagng gtaacaacgc agagtacgcc cattgcgtag 60  
 cgtgtacata aaggggttgg agctgaagga ggagataaag aagaagacag ccagaacctt 120  
 gtcctctgtc ggagatcgca gggatcttgg gccgtagata ggtataagca aaggggtgcat 180  
 agtagaaaagt cactacagtg aggtgggtgc tgcaggtcga ataggccttc ttctccctt 240  
 ctgcagagtg catgtggtag acagcaagga gaatccggcc ataggaacat gcaatacaaa 300  
 tgaagggaaa cacaagaaaa atgggtggtgc tcaaaaacac cgtgcactca tagaccagg 360  
 tatccgtgca ggctagggtc aacatagctg gaacatcaca gaaaaaatga ttgatggctc 420  
 tggacttgca atatgggata cggagtgcac ataccgtgtg agcacaagag ttgatggagc 480  
 ctatcatcca agatcctgtt atcatcagt cacaactct ttttctcata cggatgagat 540  
 agtggagagg aaagcaata gccacataac gatcataggc cattgatgtc aggagcagcg 600  
 ctctgcacc tgctaaagtc aggaagaaga t 631

<210> 1077  
 <211> 620  
 <212> DNA  
 <213> Unknown (H38g927 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(620)  
 <223> n = A,T,C or G

<400> 1077  
 tgttantecn ntttntncc attggagctc ccaagcagtg gtaacaacgc agagtacgcc 60  
 ctcttgttt ctgagagtgt agatgaagg gttataggag ataaagatca gggcaatatg 120  
 taggacaagg acacagacac tgacaacaaa gttgattatc tcattgacag tgggtgtctgt 180  
 gcaggccagc ttcagcagg gtctcacatc acagaagaag tgggagatga caaagtcac 240  
 acaaaagggc aggccaaaca tagatgttac ttggacaata gccatgcccc ggccaatcct 300  
 cagtgaccca gatccagtc agacacaagc cctcttacct atgaataccg taaggggttg 360

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| cagaagacca | catagcaatc | atatcccatg | gctatgagaa | gaaagcagtt  | gttgatgcca | 420 |
| aaagtcacat | agaagagctg | agtgacacag | ccttgcatga | caataagcta  | gtgaggattc | 480 |
| aagaggcgag | aaagcatatg | gggagtaatg | gccaccatgt | agcagggtctc | agagatagac | 540 |
| agcaatgctt | aggaaaaagt | acatgggccc | tacttctgtc | gtccttgagcg | tactgatggt | 600 |
| accagctttt | tgttcccttt |            |            |             |            | 620 |

&lt;210&gt; 1078

&lt;211&gt; 627

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g928 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(627)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1078

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| tgtagctcca | aagcagtggg | aacaacgcag | agtacgcctt | cttggttacg | taagggaata  | 60  |
| gatgatgggg | ttcagcatgg | gggtgactac | agtgtacatg | acagtggcca | cacgggtccca | 120 |
| ctctgctcgc | gtcgggacgt | ggcctggaag | tagactgcaa | tgactgtcct | atagaaagag  | 180 |
| gtccaccaca | nccagggtgg | agccacaggt | gggncacaag | tcccggagcc | tcccagaggc  | 240 |
| ttgagggcag | ctggagcacg | ggnaagcttg | ntatggncct | acaaggaggc | gaggatgagc  | 300 |
| agnaagggag | tgaccaccac | ttgcngcgcc | ctnggtgaag | atgagcagct | tggatgtggt  | 360 |
| ggntgtcaga | gcacgagagc | ctttaagaga | ggcttggtgg | gtcacagaag | aagtgggngc  | 420 |
| actttgtggg | aaagcacaga | aaggacaagc | gagccatgag | caggatatac | aggagggagt  | 480 |
| tgtccgtggg | acaccagcca | tgccattcca | accagggctg | cgcacatngc | cggggacatt  | 540 |
| ctcgtgggat | aagggaaggg | gtgccggatn | ggcacgtatc | agtcataggc | cttggnccgc  | 600 |
| agaagacagc | tttnaattta | ccccagg    |            |            |             | 627 |

&lt;210&gt; 1079

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g929 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1079

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| gcagtggtaa  | caacgcagag | taccgcccc  | tatgtacttt | ttcttgggaa  | acttgtctgt  | 60  |
| gtttgacatg  | ggtttctcct | cagtgacttg | tcccaaaatg | ctgctctacc  | ttatggggct  | 120 |
| gggccgactc  | atctcctaca | aagactgtgt | ctgccagctt | ttcttcttcc  | atttccctcg  | 180 |
| gagcattgag  | tgtctcttgt | ttacggtgat | ggcctatgac | cgcttccactg | ccatctgtta  | 240 |
| tcctctgcga  | tacacagtca | tcatgaaccc | aaggatctgt | gtggccctgg  | ctgtggggcac | 300 |
| atggctgtta  | gggtgcattc | attccagtat | cttgacctcc | ctcaccttca  | ccttgccaca  | 360 |
| ctgtgggtccc | aatgaagtgg | atcacttctt | ctgtgacatt | ccagcactgt  | tgcccttggc  | 420 |
| ctgtgctgac  | acatccttag | cccagagggt | gagcttcacc | aacgttggcc  | tcatatctct  | 480 |
| ggctgctttc  | tgctaaatct | tttatcctac | actagaatca | caaatatcta  | tcttaagcat  | 540 |
| tcgtacaac   |            |            |            |             |             | 549 |

&lt;210&gt; 1080

&lt;211&gt; 616

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g930 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(616)

<223> n = A,T,C or G

<400> 1080

```

gnnnnnnnnt tcatnccatt gggccctcta gatgcatgct cgagcggccg ccagtgtgat      60
ggatatctgc agaattcgcc cttgttgctt agagtgtaaa taaaagggtt aacattggct      120
tagagggtgaa gagtaaatac ataggaaggg cgaattccag cactctggcg gccgttacta      180
gtggatccga gctcgggtacc aagcttgatg catagcttga gtattctaac gcgtcaccta      240
aatagcttgg cgtaatcatg gtcatactgt tttcctgtgt gaaattgtta tccgctcaca      300
attccacaca acatacgagc cggaagcata aagtgtaaaag cctgggggtgc ctaatgagtg      360
agctaaactca cattaattgc gttgcgctca ctgcccgcct tccagtcggg aaacctgtcg      420
tgccagctgc attaatgaat cggccaacgc gcggggagag gcggtttgcg tattgggagc      480
tcttccgctt cctcgtctac tgactcgtg cgctcggctg ntcggctgcg gcgagcggta      540
tcaagctcac tcaaaggcgg taatacgtt atccacagaa tcagggggat acgcangaaa      600
gaacatgtga gcaaat
                                                                                   616

```

<210> 1081

<211> 615

<212> DNA

<213> Unknown (H38g931 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1081

```

ngnnnnnttna ntcnangccn ngngccctct agatgcatgc tcgagcggcc gccagtgtga      60
tggatatctg cagaattcgc ccttccaatg tatttacttc tcagccagct ctcccttatg      120
gacctgatgt acatctccac caccgtcccc aagatggcgt acaacttcct gtccggccag      180
aaaggcatct ccttctctgg atgtgggtgtg caaagcttct tcttcttgac catggcgtgt      240
tctgaaggct tactctgac ctccatggcc tacgaccgtt atttgccat ctgccactct      300
ctctattatc ctatccgcat gagtaaaatg atgtgtgtga agatgattgg aggctcttgg      360
acactggggg ccatcaactc cttggcacac acagtctttg cccttcatat tccctactgc      420
aggtctaggg ctattgacca tttcttctgc gatgtcccag ccattgttgc tcttgctgta      480
cagatacttg ggtctatgaa tatatggttt ttgtaaggac aaagcctctt tcttcttttn      540
cctttcattg gcatcacttc ttctgngggc cgagtectaa ttgctgggta tataatgcac      600
tcaaaggagg ggagg
                                                                                   615

```

<210> 1082

<211> 628

<212> DNA

<213> Unknown (H38g932 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(628)

<223> n = A,T,C or G

<400> 1082

```

gnnnnnnnnat ttnatgcct tnttgattcc cnttnnnnnn ncaagcagng gtaacaacgc      60
agagtacgcc ccctatgtat ttcttcttaa gatccaaata ttaaaataaa agacagtcac      120
cccaccacta actaaagtag tgtttccac acttctctat taagaagcat gtgagatact      180
tggtacaac ataacatcct ggtcccaccc caaagccact caatcaaata ctccagggaa      240
gggatctagg aattcgtagg tttaacgagt gcccacaaat gattattacc tgttgagaa      300
tctaggcaac aatgaattaa ggaaagctct ctaccatttg gtactggtag cagggtttgag      360
gatcacaggg aagagggtaa gcatatcaga ctagcagagc tgccagaact cgggctttca      420
aaagagaggt gccaccctct ccatgtcca tgtaagtagc aaacaaccct ctcatgtaca      480

```

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| ctctgaggaa | caagggggcg | tacttctgtc | gtcttgagcg | tactgatggt  | acccagcttt | 540 |
| tgtcccttta | gtgagggtta | attgcgcgct | tggcgtaatc | atgggtcatag | ctgtttcctg | 600 |
| tgtgaaattg | ttatccgctc | acaattct   |            |             |            | 628 |

&lt;210&gt; 1083

&lt;211&gt; 613

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g933 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(613)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1083

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| annncntng   | gagctccaaa | gcagtggtaa | caacgcagag  | tacgccccct  | atgtacttac  | 60  |
| ttttgttaag  | tccaacctcc | atcctccttg | gccttttgat  | tcaattgac   | actccttcct  | 120 |
| cctcaaaaaca | ccttggtcac | tcatectttc | tcagtctcct  | ttgtggattc  | ttcctcattt  | 180 |
| atttgacctc  | ttgctggtga | accctttcat | atacactctc  | cgtaacaaag  | agggcggtact | 240 |
| tctgtcgtct  | tgagcgnact | gatggnaccc | agcttttggt  | cccttttagtg | agggntaatt  | 300 |
| gcgcgcttgg  | cgnaatcatg | gncatagctg | nttctgngn   | gaaantgnta  | tttcgntnac  | 360 |
| aattncacac  | aacatacnag | ccgggagcat | aaaggggnnaa | gncctggggg  | gcctaattgag | 420 |
| ggagcttact  | cacaataatt | ggggtgngcc | cactggcccc  | ttttcaggcg  | ggaaaacctn  | 480 |
| gcggggccag  | ctggaataaa | tgaatcgggc | cacgcgccgg  | ggaggagggc  | gggttnngga  | 540 |
| attgggcgct  | ttttccnttt | ctnggttaat | ggactnggtn  | ggcnnngtcc  | gttcggttgg  | 600 |
| ggggancggn  | nnt        |            |             |             |             | 613 |

&lt;210&gt; 1084

&lt;211&gt; 886

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g934 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(886)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1084

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggtcccntcg | ngtatncntt | naccctctga | tgctgctcga | gcggccggca | gggtgatgga | 60  |
| tatctgcaga | attcgccctt | ctgttacgca | ggaatatata | aaggggttac | tgaggaataa | 120 |
| ataaatgggt | tactgaggaa | taaataaatg | ggttactgag | gaacaaatac | ataggggtga | 180 |
| aagaactgta | aaatagaaaa | aggaccttnt | gctgctctc  | aggatggcgg | nacttagggg | 240 |
| ccatgtacat | gacgatgng  | ctgccnntna | agagtccac  | tnctcancng | cctcagcccc | 300 |
| nccttttnt  | caennncnt  | ntttntctnc | cctcttnnnc | tctttntctc | ctattcccc  | 360 |
| cccttcnct  | cctccctttt | gcntnaccat | tgncctnat  | ccctttaatt | cnntcnntcn | 420 |
| tctccctct  | attccttcnn | tnctcgnttt | cantctctnc | ctctttctcc | cccnctttct | 480 |
| ctentctnet | cttctctng  | tcatectngt | tcnttctctt | ncctantcc  | ctctancctt | 540 |
| ntcttattnc | tcctctatnc | cctctcatct | caentctent | cctctentcn | tacttnnctc | 600 |
| nnctctecn  | ctcctctnc  | cnctttctct | tcntnacgcc | acccctcnnn | cntnctctct | 660 |
| ntctentct  | cactctctcc | tctccctncn | cntcactntt | ctcncctct  | acntcctatn | 720 |
| ctcnctttct | nncttnactt | tgtaacgctc | tcctctctct | ctctaacgac | nttttatctc | 780 |
| ttatctcnen | catncctctc | nnctctncac | netattnact | cttttctcnc | atactntatn | 840 |
| ctcctntcnn | cttanatcnc | ctcccttctn | tnancnntc  | actgcn     |            | 886 |

&lt;210&gt; 1085

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g1 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1085

```

Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Pro Asp
 1           5           10           15
Val Gly Leu Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr
          20           25           30
Thr Arg Ile Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg
          35           40           45
Arg Arg Ala Phe Ser Thr Cys Ser Ala His Leu Ile Ala Ile Leu Cys
          50           55           60
Ala Tyr Gly Pro Ile Ile Thr Val Tyr Leu Gln Pro Thr Pro Asn Pro
65           70           75           80
Met Leu Gly Thr Val Val Gln Ile Leu Met Asn Leu Val Gly Pro Met
          85           90           95
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Thr Ala
          100          105          110
Leu Lys Thr Ile Leu His Arg Thr Gly His Val Pro Glu
          115          120          125

```

&lt;210&gt; 1086

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g2 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1086

```

His Thr Glu Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Met Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Thr Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
          50           55           60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65           70           75           80
Val Pro Thr Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro
          85           90           95
His Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Val Phe Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Phe Asp Ser Thr Met

```

```
<210> 1087
<211> 312
<212> PRT
<213> Unknown (H38a3 protein)
```

|       |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> | 1087 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met   | Asp  | Gly | Asp | Asn | Gln | Ser | Glu | Asn | Ser | Gln | Phe | Leu | Leu | Leu | Gly |
| 1     |      |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile   | Ser  | Glu | Ser | Pro | Glu | Gln | Gln | Arg | Ile | Leu | Phe | Trp | Met | Phe | Leu |
|       |      |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser   | Met  | Tyr | Leu | Val | Thr | Val | Leu | Gly | Asn | Val | Leu | Ile | Ile | Leu | Ala |
|       |      | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile   | Ser  | Ser | Asp | Ser | His | Leu | His | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Ala |
|       | 50   |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn   | Leu  | Ser | Phe | Thr | Asp | Leu | Phe | Phe | Val | Thr | Asn | Thr | Ile | Pro | Lys |
| 65    |      |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met   | Leu  | Val | Asn | Phe | Gln | Ser | Gln | Asn | Lys | Ala | Ile | Ser | Tyr | Ala | Gly |
|       |      |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys   | Leu  | Thr | Gln | Leu | Tyr | Phe | Leu | Val | Ser | Leu | Val | Thr | Leu | Asp | Asn |
|       |      |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu   | Ile  | Leu | Ala | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Thr | Cys | Cys |
|       |      |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Pro   | Leu  | His | Tyr | Val | Thr | Ala | Met | Ser | Pro | Gly | Leu | Cys | Val | Leu | Leu |
|       | 130  |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu   | Ser  | Leu | Cys | Trp | Gly | Leu | Ser | Val | Leu | Tyr | Gly | Leu | Leu | Leu | Thr |
| 145   |      |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe   | Leu  | Leu | Thr | Arg | Val | Thr | Phe | Cys | Gly | Pro | Arg | Glu | Ile | His | Tyr |
|       |      |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu   | Phe  | Cys | Asp | Met | Tyr | Ile | Leu | Leu | Trp | Leu | Ala | Cys | Ser | Asn | Thr |
|       |      |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His   | Ile  | Ile | His | Thr | Ala | Leu | Ile | Ala | Thr | Gly | Cys | Phe | Ile | Phe | Leu |
|       |      | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr   | Pro  | Leu | Gly | Phe | Met | Thr | Thr | Ser | Tyr | Val | Arg | Ile | Val | Arg | Thr |
|       | 210  |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile   | Leu  | Gln | Met | Pro | Ser | Ala | Ser | Lys | Lys | Tyr | Lys | Thr | Phe | Ser | Thr |
| 225   |      |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys   | Ala  | Ser | His | Leu | Gly | Val | Val | Ser | Leu | Phe | Tyr | Gly | Thr | Leu | Ala |
|       |      |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met   | Val  | Tyr | Leu | Gln | Pro | Leu | His | Thr | Tyr | Ser | Met | Lys | Asp | Ser | Val |
|       |      |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |



Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu  
 290 295 300  
 Trp Arg Pro Phe Gln Arg Pro Lys  
 305 310

&lt;210&gt; 1088

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g4 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(305)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1088

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro  
 1 5 10 15  
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile  
 20 25 30  
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe  
 35 40 45  
 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Arg Leu Ser Thr Phe Asp  
 50 55 60  
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser  
 65 70 75 80  
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe  
 85 90 95  
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met  
 100 105 110  
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu  
 115 120 125  
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Val Pro Trp Leu  
 130 135 140  
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu  
 145 150 155 160  
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro  
 165 170 175  
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val  
 180 185 190  
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val  
 195 200 205  
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser  
 210 215 220  
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val  
 225 230 235 240  
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Tyr Leu Lys Ser  
 245 250 255  
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val  
 260 265 270  
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu  
 275 280 285  
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val  
 290 295 300  
 Cys  
 305

<210> 1089  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g5 protein)

<220>  
 <223> Synthetic construct

<400> 1089  
 Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu  
 20 25 30  
 Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu  
 35 40 45  
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln  
 65 70 75 80  
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser  
 85 90 95  
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe  
 100 105 110  
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp  
 115 120 125  
 Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu  
 130 135 140  
 Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr  
 145 150 155 160  
 Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His  
 165 170 175  
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr  
 180 185 190  
 Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met  
 195 200 205  
 Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile  
 245 250 255  
 Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys  
 260 265 270  
 Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu  
 290 295 300  
 Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr  
 305 310 315

<210> 1090  
 <211> 342  
 <212> PRT  
 <213> Unknown (H38g6 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(342)  
 <223> Xaa = Any Amino Acid

<400> 1090  
 Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Ile Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Thr Val Leu Glu Lys Leu Leu Ile Ile Met  
 35 40 45  
 Ala Val Ser Pro Asp Phe His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
 100 105 110  
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile  
 115 120 125  
 Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly  
 130 135 140  
 Phe Gln Asp Leu Leu Ser Leu Phe Phe Phe Ser Phe Phe Phe Phe  
 145 150 155 160  
 Leu Arg Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met  
 165 170 175  
 Thr Cys Phe Lys Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser  
 180 185 190  
 Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn  
 195 200 205  
 Leu Tyr Phe Pro Ala Ala Val Leu Gly Phe Leu Pro Ile Ser Gly Thr  
 210 215 220  
 Leu Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser  
 225 230 235 240  
 Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser  
 245 250 255  
 Ala Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser  
 260 265 270  
 Asp Val Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr  
 275 280 285  
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn  
 290 295 300  
 Arg Asp Met Lys Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Xaa  
 305 310 315 320  
 Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Lys  
 325 330 335  
 Lys Gly Ser Lys Val Lys  
 340

<210> 1091  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g7 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(313)  
 <223> Xaa = Any Amino Acid

<400> 1091  
 Met Val Lys Gly Asn His Ser Thr Val Thr Glu Phe Asn Leu Ala Gly

```

1      5      10      15
Leu Thr Asp Lys Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20      25      30
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Ser Met Ile Thr Leu
35      40      45
Ile Gly Phe Ser Ser His Leu His Thr Pro Met Tyr His Phe Leu Ser
50      55      60
Ser Leu Ser Phe Ile Asp Leu Cys Gln Ser Ser Val Ile Thr Pro Lys
65      70      75      80
Met Leu Val Asn Phe Val Ser Glu Arg Asn Ile Ile Ser Tyr Pro Ala
85      90      95
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Leu Val Ile Ser Glu Cys
100      105      110
His Met Leu Ala Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Asn
115      120      125
Pro Leu Leu Tyr His Val Ala Met Ser Tyr Gln Val Cys Ser Trp Met
130      135      140
Val Val Glu Val Tyr Phe Met Gly Phe Ile Gly Ala Ser Ala His Thr
145      150      155      160
Val Cys Met Leu Arg Val Leu Phe Cys Lys Ala Asp Val Ile Asn His
165      170      175
Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu Ser Arg Ser Ser Ile
180      185      190
Ser Ile Asn Glu Ile Val Val Cys Ala Cys Ser Ala Phe Asn Ile Leu
195      200      205
Phe Arg Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Val Ala Ser
210      215      220
Ile Leu Cys Ile Arg Ser Thr Glu Gly Arg Ser Lys Thr Phe Ser Thr
225      230      235      240
Cys Ser Ser His Ile Ser Ala Val Ser Val Phe Phe Gly Ser Ala Ala
245      250      255
Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
260      265      270
Val Ser Ser Val Phe Tyr Ala Thr Val Val Pro Met Leu Asn Pro Leu
275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Ile Lys Phe
290      295      300
Leu Glu Lys Arg Ser Phe Leu Xaa Lys
305      310

```

&lt;210&gt; 1092

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g8 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1092

```

Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu
1      5      10      15
Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu
20      25      30
Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu
35      40      45
Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser
50      55      60

```

Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val  
 65 70 75 80  
 Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe  
 85 90 95  
 Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu Ala Leu Cys Gly Ser  
 100 105 110  
 Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val  
 115 120 125  
 Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu  
 130 135 140  
 Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met  
 145 150 155 160  
 Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His  
 165 170 175  
 Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val  
 180 185 190  
 Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu  
 195 200 205  
 Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr  
 210 215 220  
 Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile  
 245 250 255  
 Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys  
 260 265 270  
 Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val  
 290 295 300  
 Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr  
 305 310 315 320  
 Leu Ser Ser Lys Pro Lys Arg Arg  
 325

&lt;210&gt; 1093

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g9 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1093

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala  
 20 25 30  
 Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala  
 35 40 45  
 Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln  
 65 70 75 80  
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly  
 85 90 95  
 Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys  
 100 105 110  
 Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met

|                         |                     |                         |
|-------------------------|---------------------|-------------------------|
| 130                     | 135                 | 140                     |
| Ile Ile Met Ile Trp Ser | Ile Ser Leu Ala Asn | Ser Val Val Leu Cys     |
| 145                     | 150                 | 155                     |
| Thr Leu Thr Leu Asn     | Leu Pro Thr Cys Gly | Asn Asn Ile Leu Asp His |
| 165                     | 170                 | 175                     |
| Phe Leu Cys Glu Leu Pro | Ala Leu Val Lys Ile | Ala Cys Val Asp Thr     |
| 180                     | 185                 | 190                     |
| Thr Thr Val Glu Met Ser | Val Phe Ala Leu Gly | Ile Ile Ile Val Leu     |
| 195                     | 200                 | 205                     |
| Thr Pro Leu Ile Leu Ile | Leu Ile Ser Tyr Gly | Tyr Ile Ala Lys Ala     |
| 210                     | 215                 | 220                     |
| Val Leu Arg Thr Lys Ser | Lys Ala Ser Gln Arg | Lys Ala Met Asn Thr     |
| 225                     | 230                 | 235                     |
| Cys Gly Ser His Leu Thr | Val Val Ser Met Phe | Tyr Gly Thr Ile Ile     |
| 245                     | 250                 | 255                     |
| Tyr Met Tyr Leu Gln Pro | Gly Asn Arg Ala Ser | Lys Asp Gln Gly Lys     |
| 260                     | 265                 | 270                     |
| Phe Leu Thr Leu Phe Tyr | Thr Val Ile Thr Pro | Ser Leu Asn Pro Leu     |
| 275                     | 280                 | 285                     |
| Ile Tyr Thr Leu Arg Asn | Lys Asp Met Lys Asp | Ala Leu Lys Lys Leu     |
| 290                     | 295                 | 300                     |
| Met Arg Phe His His Lys | Ser Thr Lys Ile Lys | Arg Asn Cys             |
| 305                     | 310                 | 315                     |

&lt;210&gt; 1094

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g10 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1094

|                         |                     |                     |
|-------------------------|---------------------|---------------------|
| His Thr Glu Pro Arg Asn | Leu Thr Gly Val Xaa | Glu Phe Leu Leu Leu |
| 1                       | 5                   | 10                  |
| Gly Leu Ser Glu Asp Pro | Glu Leu Gln Ser Val | Leu Ala Leu Leu Ser |
| 20                      | 25                  | 30                  |
| Leu Ser Leu Ser Thr Tyr | Leu Ala Thr Val Leu | Arg Asn Val Leu Asn |
| 35                      | 40                  | 45                  |
| Ile Leu Ala Val Ser Ser | Asp Ser Pro Leu His | Thr Pro Met Tyr Phe |
| 50                      | 55                  | 60                  |
| Phe Leu Ser Asn Leu Cys | Trp Ala Asp Ile Gly | Phe Thr Ser Ala Thr |
| 65                      | 70                  | 75                  |
| Val Pro Lys Met Ile Val | Asp Met Gln Ser Tyr | Ser Arg Val Ile Ser |
| 85                      | 90                  | 95                  |
| His Glu Gly Cys Leu Thr | Gln Met Ser Phe Leu | Val Leu Phe Ala Cys |
| 100                     | 105                 | 110                 |
| Ile Glu Gly Met Ile Leu | Thr Val Met Ala Tyr | Asp Cys Phe Val Ala |
| 115                     | 120                 | 125                 |
| Ile Cys Arg Pro Leu His | Tyr Pro Val Ile Val | Asn Pro His Leu Cys |
| 130                     | 135                 | 140                 |
| Val Phe Phe Val Leu Val | Ser Phe Phe Leu Ser | Leu Leu Asp Ser Gln |
| 145                     | 150                 | 155                 |
| Leu His Ser Xaa Ile Val | Leu Gln Phe Asn Ile | Ile Lys Asn Val Glu |
| 165                     | 170                 | 175                 |
| Ile Ser Asn Phe Val Cys | Asp Pro Ser Gln Phe | Leu Lys Leu Ala Cys |
| 180                     | 185                 | 190                 |

Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Phe Ser Xaa Phe Lys Ile  
 210 215 220  
 Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg  
 260 265 270  
 Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu  
 290 295 300  
 Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser  
 305 310 315 320  
 Phe Phe Leu Cys

&lt;210&gt; 1095

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g11 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1095

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly  
 1 5 10 15  
 Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu  
 20 25 30  
 Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Ile Leu Leu  
 35 40 45  
 Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys  
 65 70 75 80  
 Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu  
 85 90 95  
 Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys  
 100 105 110  
 Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu  
 130 135 140  
 Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile  
 145 150 155 160  
 Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met  
 180 185 190  
 Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu  
 195 200 205  
 Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr  
 210 215 220  
 Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala  
 225 230 235 240  
 Ser His Leu Val Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met  
 245 250 255  
 Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile

|     |                             |                                 |     |  |     |
|-----|-----------------------------|---------------------------------|-----|--|-----|
|     | 260                         |                                 | 265 |  | 270 |
| Ser | Ile Phe Tyr Ala Ile Val Thr | Pro Ser Leu Asn Pro Phe Ile Tyr |     |  |     |
|     | 275                         | 280                             | 285 |  |     |
| Cys | Leu Arg Asn Arg Glu Val Lys | Glu Ala Leu Lys Lys Leu Ala Tyr |     |  |     |
|     | 290                         | 295                             | 300 |  |     |
| Cys | Gln Ala Ser Arg Ser Asp     |                                 |     |  |     |
| 305 | 310                         |                                 |     |  |     |

&lt;210&gt; 1096

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g12 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1096

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Val | Asn | Lys | Thr | Val | Val | Arg | Glu | Phe | Val | Val | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Ser | Leu | Ala | Arg | Leu | Gln | Gln | Leu | Leu | Phe | Val | Ile | Phe | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Leu | Tyr | Leu | Phe | Thr | Leu | Gly | Thr | Asn | Ala | Ile | Ile | Ile | Ser | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Val | Leu | Asp | Arg | Ala | Leu | His | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Ser | Cys | Ser | Glu | Ile | Cys | Tyr | Thr | Phe | Val | Ile | Val | Pro | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Met | Leu | Val | Asp | Leu | Leu | Ser | Gln | Lys | Lys | Thr | Ile | Ser | Phe | Leu | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Cys | Ala | Ile | Gln | Met | Phe | Ser | Phe | Leu | Phe | Phe | Gly | Ser | Ser | His | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Leu | Leu | Ala | Ala | Met | Gly | Tyr | Asp | Arg | Tyr | Met | Ala | Ile | Cys | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Arg | Tyr | Ser | Val | Leu | Met | Gly | His | Gly | Val | Cys | Met | Gly | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Ala | Ala | Ala | Cys | Ala | Cys | Gly | Phe | Thr | Val | Ser | Leu | Val | Thr | Thr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Leu | Val | Phe | His | Leu | Pro | Phe | His | Ser | Ser | Asn | Gln | Leu | His | His |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Phe | Cys | Asp | Ile | Ser | Pro | Val | Leu | Lys | Leu | Ala | Ser | Gln | His | Ser |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Phe | Ser | Gln | Leu | Val | Ile | Phe | Met | Leu | Gly | Val | Phe | Ala | Leu | Val |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ile | Pro | Leu | Leu | Leu | Ile | Leu | Val | Ser | Tyr | Ile | Arg | Ile | Ile | Ser | Ala |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Ile | Leu | Lys | Ile | Pro | Ser | Ser | Val | Gly | Arg | Tyr | Lys | Thr | Phe | Ser | Thr |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Cys | Ala | Ser | His | Leu | Ile | Val | Val | Thr | Val | His | Tyr | Ser | Cys | Ala | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Phe | Ile | Tyr | Leu | Arg | Pro | Lys | Thr | Asn | Tyr | Thr | Ser | Ser | Gln | Asp | Thr |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Ile | Ser | Val | Ser | Tyr | Thr | Ile | Leu | Thr | Pro | Leu | Phe | Asn | Pro | Met |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ile | Tyr | Ser | Leu | Arg | Asn | Lys | Glu | Phe | Lys | Ser | Ala | Leu | Arg | Arg | Thr |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Ile | Gly | Gln | Thr | Phe | Tyr | Pro | Leu | Ser |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 1097

&lt;211&gt; 318

&lt;212&gt; PRT



<213> Unknown (H38g13 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1097

```

Cys Val Asp Ser Ser Leu Lys Xaa Glu Ile Thr Gln Xaa Cys Leu Ser
 1           5           10          15
Leu Leu Leu Xaa Met Ala Glu Gly Trp Arg Leu Tyr Phe Ile Ile Leu
          20          25          30
Ile Ile Ser Tyr Lys Phe Cys Thr Leu Leu Gly Asn Val Ile Phe Arg
          35          40          45
Thr Leu Val Cys Ser Leu Gly Phe His Thr Ser Cys Met Tyr Phe Phe
          50          55          60
Pro Xaa Lys Ile Ser Leu Xaa Leu Ala Xaa Val Cys His Ser Ile Ile
65          70          75          80
Ala Leu Pro Ser Thr Gln Lys Xaa Ala Ile Asn Val Gln Gly Ala Ala
          85          90          95
Val His Val Phe Ser Phe Pro Cys Leu Tyr Cys Pro Glu Ile Phe Leu
          100         105         110
His Ser Leu Thr Gln Cys His Pro Phe Ile Ala Ile Gly Tyr Pro Leu
          115         120         125
Gln Gly Met His Thr Ile Thr His Lys Leu Tyr Ile Leu Leu Thr Thr
          130         135         140
Gly Pro Trp Arg Gly Cys Xaa Leu His Val Asn Leu Leu Thr Ala Ile
145         150         155         160
Leu Gly Ser Tyr Pro Asn Pro Val Pro Thr Lys Leu Trp Leu Ser Phe
          165         170         175
Pro Ser Ile Pro Glu Val Lys Leu Xaa Pro Met Gln Ala Tyr Thr Lys
          180         185         190
Pro Tyr Ala Gly Leu Ser Leu Cys Leu Ser Leu Ser Leu Ser Leu Ser
          195         200         205
Phe Ser Leu Phe Ser Ile Ile Ser Ile Ser Tyr Ile Cys Asn Glu Ile
          210         215         220
Asp Ile Pro Lys Ile Ile Ser Ala Asp Ser Val His Gly Ala Phe Ser
225         230         235         240
Thr Cys Leu Ala His Leu Phe Ala Phe Ser Thr Cys Ile Ala Gln Pro
          245         250         255
Ala Val Cys Asn Ser Leu Trp Pro Trp Thr Glu Ala Gln Thr Glu Ser
          260         265         270
Ser Arg Asp Ser Val Ile Gln Arg Pro Asn Leu Cys Val Thr Ile Ser
          275         280         285
Leu Asn Ser Leu Ile Ser Ser Leu Arg Asn Glu Ser Val Lys Gln Ala
          290         295         300
Ser His Lys Ile Phe Lys Glu Gln Thr Leu Phe Met Lys Ile
305         310         315

```

<210> 1098

<211> 333

<212> PRT

<213> Unknown (H38g14 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1098

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1          5          10          15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
          20          25          30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
          35          40          45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
          65          70          75          80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
          85          90          95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
          130          135          140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
          145          150          155          160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
          195          200          205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
          210          215          220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
          225          230          235          240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
          245          250          255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
          275          280          285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
          290          295          300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
          305          310          315          320
Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
          325          330

```

<210> 1099

<211> 322

<212> PRT

<213> Unknown (H38g15 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1099

```

His Thr Gly Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Thr Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser  
 35 40 45  
 Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Xaa Ala Thr  
 65 70 75 80  
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Val Cys Leu Ile Gln Met Ser Leu Leu Val Leu Phe Ala Cys  
 100 105 110  
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala  
 115 120 125  
 Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Phe Val Leu Val Ser Phe Leu Leu Ser Leu Leu Asp Ser Gln  
 145 150 155 160  
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu  
 165 170 175  
 Ile Ser Asn Ser Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys  
 180 185 190  
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile  
 210 215 220  
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Arg  
 260 265 270  
 Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu  
 290 295 300  
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Arg  
 305 310 315 320  
 Phe Ser

&lt;210&gt; 1100

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g16 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1100

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile  
 1 5 10 15  
 Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn  
 20 25 30  
 Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu  
 35 40 45  
 Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu  
 50 55 60  
 Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu  
 65 70 75 80  
 Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu

```
<210> 1101
<211> 257
<212> PRT
<213> Unknown (H38q17 protein)
```

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(257)
<223> Xaa = Any Amino Acid
```

|                         |     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|-------------------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| <b>&lt;400&gt; 1101</b> |     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| Phe<br>1                | Ile | Leu        | Trp        | Gly<br>5   | Phe        | Phe        | Asp        | His        | Pro<br>10  | Xaa        | Pro        | Glu        | Met<br>15  | Phe        | Leu        |
| Phe                     | Ile | Met        | Gly<br>20  | Leu        | Val        | Gly        | Leu        | Ser<br>25  | Leu        | His        | Thr        | Gly        | Gly<br>30  | Gln        | His        |
| Leu                     | Asn | Tyr<br>35  | Cys        | Gly        | Thr        | Gln        | Gly<br>40  | Ile        | Phe        | Xaa        | Gly        | Ser<br>45  | Thr        | Lys        | Cys        |
| Ile<br>50               | Ile | Leu        | Ala        | Val        | Thr        | Ser<br>55  | Leu        | Asp        | Pro        | Tyr        | Ile<br>60  | Ala        | Ile        | Cys        | Lys        |
| His<br>65               | Leu | Arg        | Tyr        | Pro        | Ala<br>70  | Ile        | Met        | His        | Gln        | Gln<br>75  | Leu        | Cys        | Val        | Leu        | Leu<br>80  |
| Val                     | Ala | Met        | Ala        | Trp<br>85  | Leu        | Ser        | Ser        | Leu        | Ala<br>90  | Asn        | Ser        | Leu        | Gln        | Ser<br>95  | Ser        |
| Leu                     | Ala | Val        | Gln<br>100 | Leu        | Pro        | Leu        | Gly        | Gly<br>105 | Asn        | Lys        | Val        | Asp        | Asp<br>110 | Phe        | Leu        |
| Cys                     | Glu | Val<br>115 | Ser        | Ala        | Met        | Ile        | Lys<br>120 | Ile        | Ser        | Arg        | Phe        | Asp<br>125 | Thr        | Thr        | Phe        |
| Asn<br>130              | Val | Ser        | Met        | Leu        | Ser        | Ile<br>135 | Val        | Arg        | Ile        | Phe        | Xaa<br>140 | Ser        | Leu        | Val        | Leu        |
| Xaa<br>145              | Ser | Ile        | Ile        | Phe        | Ala<br>150 | Tyr        | Cys        | Gly        | Phe        | Ile<br>155 | Val        | Ala        | Thr        | Val        | Leu<br>160 |
| Arg                     | Ile | Gln        | Ser        | Ser<br>165 | Gly        | Gly        | Lys        | Lys        | Glu<br>170 | Val        | Phe        | Asn        | Thr        | Cys<br>175 | Gly        |

Ser His Ile Val Ser Leu Leu Tyr Gly Pro Val Ile Ser Met Tyr Val  
 180 185 190  
 Gln Pro Ser Ala Asn Ser Gln Asp Lys Asn Lys Phe Met Ser Leu Phe  
 195 200 205  
 Tyr Ser Leu Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Ser  
 210 215 220  
 Asn Arg Asp Ile Lys Gly Ala Met Arg Arg Leu Leu Val Phe Leu Tyr  
 225 230 235 240  
 His Gln Glu Glu Asn Lys Ser Asn Tyr Cys Leu Tyr Ser Thr Phe Phe  
 245 250 255  
 Ile

&lt;210&gt; 1102

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g18 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(334)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1102

Ser Thr Asp Pro Gln Asn Val Thr Asp Val Ser Arg Phe Leu Leu Leu  
 1 5 10 15  
 Lys Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro  
 65 70 75 80  
 Lys Met Val Val Asp Ile Gln Ser His Arg Val Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu  
 100 105 110  
 Asn Met Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys  
 115 120 125  
 His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe  
 130 135 140  
 Leu Leu Leu Leu Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu  
 145 150 155 160  
 His Asn Met Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile  
 165 170 175  
 Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys  
 180 185 190  
 Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Val Phe  
 195 200 205  
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val  
 210 215 220  
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Pro Cys  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Leu Ser Val Phe Cys Xaa Phe Tyr Gly Thr  
 245 250 255  
 Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys  
 260 265 270  
 Ala Ala Val Ala Ser Leu Met Tyr Lys Met Val Thr Pro Met Leu Asn

275                      280                      285  
 Pro Ser Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg  
 290                      295                      300  
 Gln Pro His Gly Ser Thr Val Xaa Ser Gln Asp Leu Leu Ile Cys Ser  
 305                      310                      315                      320  
 Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys  
                     325                      330

&lt;210&gt; 1103

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g19 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1103

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly  
 1                      5                      10                      15  
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser  
                     20                      25                      30  
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser  
                     35                      40                      45  
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala  
                     50                      55                      60  
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys  
 65                      70                      75                      80  
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly  
                     85                      90                      95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met  
                     100                      105                      110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys  
                     115                      120                      125  
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe  
                     130                      135                      140  
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu  
 145                      150                      155                      160  
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser  
                     165                      170                      175  
 Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr  
                     180                      185                      190  
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val  
                     195                      200                      205  
 Gly Thr Phe Phe Ile Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr  
                     210                      215                      220  
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu  
 225                      230                      235                      240  
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Gly Pro Pro Met Phe  
                     245                      250                      255  
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala  
                     260                      265                      270  
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr  
                     275                      280                      285  
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln  
                     290                      295                      300  
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu  
 305                      310                      315                      320

Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr  
 325 330

<210> 1104  
 <211> 339  
 <212> PRT  
 <213> Unknown (H38g20 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(339)  
 <223> Xaa = Any Amino Acid

<400> 1104  
 Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Pro Asp Ser Arg Phe Thr Ser Thr Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Asp Met Glu  
 100 105 110  
 Glu Asn Met Phe Leu Ser Val Val Ala Tyr Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly  
 130 135 140  
 Phe Leu Asp Ser Leu Ser Leu Phe Phe Phe Phe Phe Phe Leu Ser Leu  
 145 150 155 160  
 Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe  
 165 170 175  
 Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro  
 180 185 190  
 His Leu Ala Cys Cys Asp Ile Phe Thr Arg Asn Ile Asn Leu Tyr Phe  
 195 200 205  
 Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser  
 210 215 220  
 Tyr Tyr Lys Ile Val Ser Phe Ile Leu Arg Val Ser Ser Ser Gly Gly  
 225 230 235 240  
 Lys Tyr Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Tyr  
 245 250 255  
 Xaa Val Tyr Gly Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser  
 260 265 270  
 Ser Ser Pro Arg Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val  
 275 280 285  
 Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile  
 290 295 300  
 Lys Ser Val Leu Arg Gln Pro His Gly Ser Thr Val Xaa Ser Gln Tyr  
 305 310 315 320  
 Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser  
 325 330 335  
 Lys Val Lys

<210> 1105  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g21 protein)

<220>  
 <223> Synthetic construct

<400> 1105  
 Met Glu Thr Arg Lys Tyr Ser Ala Met Thr Glu Phe Phe Leu Val Gly  
 1 5 10 15  
 Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Cys Leu  
 20 25 30  
 Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Leu Leu Ile Ile Ile  
 35 40 45  
 Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ile Pro Pro  
 65 70 75 80  
 Met Leu Ile Ile Phe Met Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly  
 85 90 95  
 Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Thr Glu Cys  
 100 105 110  
 Val Leu Leu Ala Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Ser Ile Ile Met Asn Gly Val Leu Tyr Val Gln Met  
 130 135 140  
 Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Gln Thr  
 145 150 155 160  
 Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Val Ile Asp His  
 165 170 175  
 Ile Thr Cys Glu Ile Leu Ala Leu Leu Lys Leu Val Cys Ser Asp Ile  
 180 185 190  
 Thr Ile Asn Val Leu Ile Met Thr Val Thr Asn Ile Val Ser Leu Val  
 195 200 205  
 Ile Leu Leu Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser  
 210 215 220  
 Ile Leu Arg Ile Asn Cys Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Ser Ile Val Val Ile Leu Phe Tyr Gly Ser Ala Leu  
 245 250 255  
 Phe Met Tyr Met Lys Pro Lys Ser Lys Asn Thr Asn Thr Ser Asp Glu  
 260 265 270  
 Ile Ile Gly Leu Ser Tyr Gly Val Val Ser Pro Met Leu Asn Pro Ile  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Val Lys Lys Val  
 290 295 300  
 Leu Ser Arg His Leu His Leu Leu Lys Met  
 305 310

<210> 1106  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g22 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)  
 <223> Xaa = Any Amino Acid



<400> 1106  
Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr  
1 5 10 15  
Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu  
20 25 30  
Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Val Val Thr Ile Thr  
35 40 45  
Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu  
50 55 60  
Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ala Pro Lys Leu Ile  
65 70 75 80  
Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met  
85 90 95  
Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu  
100 105 110  
Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu  
115 120 125  
His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val  
130 135 140  
Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe  
145 150 155 160  
Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met  
165 170 175  
Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr  
180 185 190  
Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn  
195 200 205  
Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys  
210 215 220  
Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser  
225 230 235 240  
His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr  
245 250 255  
Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe  
260 265 270  
Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
275 280 285  
Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val  
290 295 300  
Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg  
305 310 315

<210> 1107

<211> 311

<212> PRT

<213> Unknown (H38g23 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1107

Met Arg Asn Phe Ser Val Val Ser Glu Phe Ile Leu Leu Gly Ile Pro  
1 5 10 15  
His Thr Glu Gly Leu Glu Thr Ile Leu Leu Val Leu Phe Leu Ser Phe  
20 25 30  
Tyr Ile Phe Thr Leu Met Gly Asn Leu Leu Ile Leu Leu Ala Ile Val

|   |     |     |
|---|-----|-----|
| 35  | 40  | 45  |
| Ser Ser Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Lys Leu |     |     |
| 50  | 55  | 60  |
| Ser Val Phe Asp Leu Phe Phe Pro Ser Val Ser Ser Pro Lys Met Leu |     |     |
| 65  | 70  | 75  |
| Cys Tyr Leu Ser Gly Asn Ser Arg Ala Ile Ser Tyr Ala Gly Cys Ala |     |     |
| 85  | 90  | 95  |
| Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu |     |     |
| 100   | 105 | 110 |
| Tyr Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu |     |     |
| 115   | 120 | 125 |
| Arg Tyr Thr Ile Ile Met Ser His Arg Ala Cys Ile Ile Leu Ala Met |     |     |
| 130   | 135 | 140 |
| Gly Thr Ser Phe Phe Gly Cys Ile Gln Ala Thr Phe Leu Thr Thr Leu |     |     |
| 145   | 150 | 155 |
| Thr Phe Gln Leu Pro Tyr Cys Val Pro Asn Glu Val Asp Tyr Tyr Phe |     |     |
| 165   | 170 | 175 |
| Cys Asp Ile Pro Val Met Leu Lys Leu Ala Cys Ala Asp Thr Ser Ala |     |     |
| 180   | 185 | 190 |
| Leu Glu Met Val Gly Phe Ile Ser Val Gly Leu Met Pro Leu Ser Cys |     |     |
| 195   | 200 | 205 |
| Phe Leu Leu Ile Leu Thr Ser Tyr Ser Gly Ile Val Phe Ser Ile Leu |     |     |
| 210   | 215 | 220 |
| Xaa Ile Cys Ser Ala Glu Gly Arg Arg Arg Ala Phe Ser Thr Cys Ser |     |     |
| 225   | 230 | 235 |
| Ala His Leu Thr Ala Ile Leu Leu Phe Tyr Met Pro Val Val Leu Ile |     |     |
| 245   | 250 | 255 |
| Tyr Leu Arg Pro Thr His Ser Leu Trp Leu Asp Ala Thr Val Gln Ile |     |     |
| 260   | 265 | 270 |
| Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu |     |     |
| 275   | 280 | 285 |
| Arg Asn Lys Glu Val Lys Leu Ser Leu Arg Lys Val Leu Tyr Gln Leu |     |     |
| 290   | 295 | 300 |
| Gly Phe Leu Pro Glu Gln Leu                                     |     |     |
| 305   | 310 |     |

&lt;210&gt; 1108

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g24 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1108

|   |     |
|---|-----|
| Met Asp Ile Pro Gln Asn Ile Thr Glu Phe Phe Met Leu Gly Leu Ser |     |
| 1   | 5   |
| Gln Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile |     |
| 20  | 25  |
| Tyr Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr |     |
| 35  | 40  |
| Ser Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu |     |
| 50  | 55  |
| Ser Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile |     |
| 65  | 70  |
| Ala Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met |     |
| 85  | 90  |
| Ala Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu |     |
| 100   | 105 |
| Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu |     |
| 115   | 120 |
|   | 125 |

```

His Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly
  130                135                140
Val Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu
 145                150                155                160
Val Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala
                165                170                175
Cys Asp Leu Tyr Pro Leu Leu Glu Val Ala Cys Thr Asn Thr Tyr Val
                180                185                190
Ile Gly Leu Leu Val Val Ala Asn Ser Gly Leu Ile Cys Leu Leu Asn
                195                200                205
Phe Leu Met Leu Ala Ala Ser Tyr Ile Val Ile Leu Tyr Ser Leu Arg
                210                215                220
Ser His Ser Ala Asp Gly Arg Cys Lys Ala Leu Ser Thr Cys Gly Ala
 225                230                235                240
His Phe Ile Val Val Ala Leu Phe Phe Val Pro Cys Ile Phe Thr Tyr
                245                250                255
Val His Pro Phe Ser Thr Leu Pro Ile Asp Lys Asn Met Ala Leu Phe
                260                265                270
Tyr Gly Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
                275                280                285
Asn Glu Glu Val Lys Asn Ala Met Arg Lys Leu Phe Thr Trp
 290                295                300

```

&lt;210&gt; 1109

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g25 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1109

```

Met Ile Thr Leu Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr
  1                5                10                15
Tyr Phe Leu Ser Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val
                20                25                30
Ile Thr Pro Lys Met Leu Val Asn Phe Ala Thr Glu Lys Asn Ile Ile
                35                40                45
Ser Tyr Pro Glu Cys Met Ala Gln Leu Tyr Leu Phe Ser Ile Phe Ala
                50                55                60
Ile Ala Glu Cys His Met Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val
 65                70                75                80
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His
                85                90                95
Cys Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser
                100                105                110
Thr Ile His Thr Ser Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn
                115                120                125
Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser
                130                135                140
Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala
 145                150                155                160
Phe Asn Ile Leu Met Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe
                165                170                175
Ile Ile Ala Ser Ile Leu Arg Ile His Ser Thr Glu Gly Arg Ser Lys
                180                185                190
Ala Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe
                195                200                205
Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met
 210                215                220
Asp Gln Arg Lys Val Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met

```

225                      230                      235                      240  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala  
                                  245                      250                      255  
 Val Lys Lys Ile Leu His Gln Thr Ala Cys  
                                  260                      265

<210> 1110  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g26 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(318)  
 <223> Xaa = Any Amino Acid

<400> 1110  
 Met Gly Asn Ser Asn Gln Ser Phe Met Thr Glu Phe Val Leu Leu Gly  
 1                      5                      10                      15  
 Leu Ser Gly Tyr Pro Glu Leu Glu Ala Ile Tyr Phe Val Leu Val Leu  
                                  20                      25                      30  
 Cys Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Ile Ile Ile Val  
                                  35                      40                      45  
 Ser Val Tyr Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
                                  50                      55                      60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Ile Pro Leu  
 65                      70                      75                      80  
 Phe Leu Ser Ser Phe Leu Thr Ser Lys Lys Thr Ile Ser Phe Ser Gly  
                                  85                      90                      95  
 Cys Gly Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys  
                                  100                      105                      110  
 Val Leu Leu Ser Met Met Ala Phe Asp Cys Tyr Val Ala Ile Cys Asn  
                                  115                      120                      125  
 Pro Leu Xaa Tyr Pro Ile Ile Met Ser Lys Ala Ser Tyr Met Ser Met  
                                  130                      135                      140  
 Ala Ala Gly Ser Trp Ile Gly Gly Gly Ile Asn Ser Val Leu Gln Thr  
 145                      150                      155                      160  
 Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His  
                                  165                      170                      175  
 Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asn Ile  
                                  180                      185                      190  
 Ser Ile Asn Ile Ile Ser Met Val Val Ala Ser Met Ile Phe Leu Val  
                                  195                      200                      205  
 Gly Pro Val Leu Phe Ile Phe Val Thr Tyr Val Phe Ile Leu Ser Thr  
                                  210                      215                      220  
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Ala Ser Ser Thr  
 225                      230                      235                      240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Arg Thr Ile Leu  
                                  245                      250                      255  
 Phe Met Tyr Ala Lys Pro Lys Ala Lys Asp Ser Ser Gly Ala Asp Lys  
                                  260                      265                      270  
 Glu Gln Val Thr Asp Lys Ile Ile Ser Leu Phe Tyr Gly Val Val Thr  
                                  275                      280                      285  
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
                                  290                      295                      300  
 Ala Ala Val Lys Ser Ile Leu Xaa Gln Lys Cys Phe Leu Glu  
 305                      310                      315

<210> 1111

<211> 329  
 <212> PRT  
 <213> Unknown (H38g27 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(329)  
 <223> Xaa = Any Amino Acid

<400> 1111  
 Lys Ser Met Lys Lys Met Asn Asn Val Ile Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr His Asn Pro Glu Leu Gln Lys Phe Leu Phe Val Met Phe Leu  
 20 25 30  
 Ile Thr Tyr Leu Ile Thr Leu Ala Gly Asn Leu Phe Ile Ser Val Ile  
 35 40 45  
 Ile Phe Ile Ser Pro Ala Leu Gly Ser Pro Met Tyr Ser Phe Pro Ser  
 50 55 60  
 Tyr Leu Phe Ile Ile Asp Ile Phe Cys Ser Ser Ser Ile Ala Pro Lys  
 65 70 75 80  
 Met Asn Phe Asp Leu Ile Ser Glu Lys Asn Thr Ile Ser Phe Asn Gly  
 85 90 95  
 Cys Met Thr Gln Leu Phe Thr Glu His Phe Phe Thr Glu His Phe Phe  
 100 105 110  
 Glu Ala Ala Glu Ile Ile Leu Leu Ser Val Met Ala Tyr Asp His Tyr  
 115 120 125  
 Val Ala Ile Arg Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro  
 130 135 140  
 Met Cys Gly Phe Leu Met Val Val Ala Gly Ile Leu Gly Phe Val His  
 145 150 155 160  
 Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro  
 165 170 175  
 Asn Val Ile Asn His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu  
 180 185 190  
 Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser  
 195 200 205  
 Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val  
 210 215 220  
 Ile Ile Leu Cys Phe Leu Arg Thr His Ser Ser Glu Gly Arg Arg Lys  
 225 230 235 240  
 Ala Leu Ser Ser Cys Ala Ser His Ile Phe Ile Val Ile Leu Phe Phe  
 245 250 255  
 Val Pro Phe Ser Tyr Leu Tyr Leu Arg Pro Ile His Ser Phe Pro Thr  
 260 265 270  
 Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu Asn  
 275 280 285  
 Pro Leu Ile Tyr Thr Leu Lys Asn Lys Glu Val Lys Asn Val Ile Lys  
 290 295 300  
 Lys Leu Trp Lys Gln Ile Met Thr Thr Asp Asp Lys Xaa Val Leu Xaa  
 305 310 315 320  
 His Lys His Leu Gly Lys Asn Ile Trp  
 325

<210> 1112  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g28 protein)

<220>

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 1112

```

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1           5           10           15
Leu Ser Gly His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
          20           25           30
Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
          35           40           45
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
          50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
          65           70           75           80
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly
          85           90           95
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
          100          105          110
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met
          130          135          140
Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Ser
          145          150          155          160
Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His
          165          170          175
Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
          180          185          190
Ser Asp Asn Glu Phe Ile Met Leu Val Ala Thr Thr Leu Phe Ile Leu
          195          200          205
Thr Pro Leu Leu Leu Ile Ile Val Ser Tyr Thr Leu Ile Ile Val Ser
          210          215          220
Ile Phe Lys Ile Ser Ser Ser Glu Gly Arg Ser Lys Ala Ser Ser Thr
          225          230          235          240
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
          245          250          255
Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
          260          265          270
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
          275          280          285
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
          290          295          300
Glu Ala Val Lys His Leu Leu Asn Arg Arg Phe Phe Ser Lys
          305          310          315

```

&lt;210&gt; 1113

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g29 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

## &lt;400&gt; 1113

```

Met Val Asp Asn Leu Ile Ile Val Val Thr Ile Thr Thr Ser Pro Ala
 1           5           10           15
Leu Asp Ser Pro Val Tyr Phe Phe Leu Ser Phe Phe Ser Phe Ile Asp
          20           25           30
Gly Cys Ser Ser Ser Thr Met Ala Pro Lys Met Ile Phe Asp Leu Leu
          35           40           45
Thr Glu Lys Lys Thr Ile Ser Phe Ser Gly Cys Met Thr Gln Leu Phe
          50           55           60

```

Val Glu His Phe Phe Gly Gly Val Glu Ile Ile Leu Leu Val Val Met  
 65 70 75 80  
 Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu Tyr Tyr Leu Ile  
 85 90 95  
 Thr Met Asn Arg Gln Val Cys Gly Leu Leu Val Ala Met Ala Trp Val  
 100 105 110  
 Gly Gly Phe Leu His Ala Leu Ile Gln Met Leu Leu Ile Val Trp Leu  
 115 120 125  
 Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile Cys Asp Leu Phe  
 130 135 140  
 Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe  
 145 150 155 160  
 Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu  
 165 170 175  
 Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser  
 180 185 190  
 Thr Cys Ala Phe His Ile Thr Val Val Leu Phe Phe Val Pro Cys  
 195 200 205  
 Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala  
 210 215 220  
 Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile  
 225 230 235 240  
 Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp  
 245 250 255  
 Ser Gln Ile Ile Trp Gly Asn Asn  
 260

&lt;210&gt; 1114

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g30 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1114

Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro  
 1 5 10 15  
 Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val  
 20 25 30  
 Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys  
 35 40 45  
 His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu  
 50 55 60  
 Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met  
 65 70 75 80  
 Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe  
 85 90 95  
 Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser  
 100 105 110  
 Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu  
 115 120 125  
 Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val  
 130 135 140  
 Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg  
 145 150 155 160  
 Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe  
 165 170 175  
 Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe  
 180 185 190  
 Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp

```

      195              200              205
Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
  210              215              220
Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Ile
  225              230              235              240
Ser His Ile Ser Cys Val Leu Ile Phe Tyr Val Thr Val Met Gly Leu
      245              250              255
Thr Phe Ile Tyr Arg Phe Gly Lys Asn Val Pro Glu Val Val His Ile
      260              265              270
Ile Met Ser Tyr Ile Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Val
      275              280              285
Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
      290              295              300
Leu Ser Lys His Arg Phe Ser Arg
  305              310

```

&lt;210&gt; 1115

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g31 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(285)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1115

```

Asp Thr Glu Pro Gln Asn Leu Thr Ala Val Ser Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Phe
      20              25              30
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35              40              45
Ala Ile Gly Ser Asp Ser His Leu Asp Thr Pro Met Tyr Phe Phe Leu
      50              55              60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
      65              70              75              80
Lys Met Ile Glu Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly
      85              90              95
Asp Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp
      100              105              110
Asp Met Ile Leu Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys
      115              120              125
His Pro Leu Asn Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu
      130              135              140
Leu Val Leu Val Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      145              150              155              160
Asn Leu Ile Val Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser
      165              170              175
Asn Phe Phe Cys Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp
      180              185              190
Ser Asp Ile Asn Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly
      195              200              205
Phe Leu Arg Ile Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe
      210              215              220
Pro Ile Leu Arg Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser
      225              230              235              240
Thr Xaa Gly Ser Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255

```



Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp  
                   260                  265                  270  
 Val Val Ala Ser Val Met Tyr Ala Val Val Val Thr Pro  
                   275                  280                  285

<210> 1116  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g32 protein)

<220>  
 <223> Synthetic construct

<400> 1116  
 Met Gly Glu Ile Asn Gln Thr Leu Val Ser Glu Phe Leu Leu Leu Gly  
   1                  5                  10                  15  
 Leu Ser Gly Tyr Pro Lys Ile Glu Ile Val Tyr Phe Ala Leu Ile Leu  
                   20                  25                  30  
 Val Met Tyr Leu Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala  
                   35                  40                  45  
 Ser Ile Phe Asp Ser His Phe His Thr Pro Met Tyr Phe Phe Leu Gly  
                   50                  55                  60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Val Pro Ser  
  65                  70                  75                  80  
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly  
                   85                  90                  95  
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys  
                   100                  105                  110  
 Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn  
                   115                  120                  125  
 Pro Leu Arg Tyr Pro Ile Ile Leu Ser Lys Val Ala Tyr Val Leu Met  
                   130                  135                  140  
 Ala Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Ala Val Gln Thr  
  145                  150                  155                  160  
 Leu Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn Ile Ile Asn His  
                   165                  170                  175  
 Phe Ala Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile  
                   180                  185                  190  
 Ser Leu Asn Ile Ile Thr Met Val Ile Ser Asn Met Ala Phe Leu Val  
                   195                  200                  205  
 Leu Pro Leu Met Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr  
                   210                  215                  220  
 Ile Leu Gln Met Asn Ser Ala Thr Gly Arg Arg Lys Ala Phe Ser Thr  
  225                  230                  235                  240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe  
                   245                  250                  255  
 Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Ile Gly Glu Glu Lys  
                   260                  265                  270  
 Leu Gln Ala Leu Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr  
                   275                  280                  285  
 Pro Met Leu Asn Pro Ile Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys  
                   290                  295                  300  
 Ala Ala Val Lys Tyr Leu Leu Asn Lys Lys Pro Ile His  
  305                  310                  315

<210> 1117  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g33 protein)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1117

```

Met Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe
 1           5           10           15
Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe
 20           25           30
His Val Leu Thr Val Leu Gly Asn Leu Leu Val Ile Ile Thr Ile Asn
 35           40           45
Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu
 50           55           60
Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile
 65           70           75           80
Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met
 85           90           95
Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu
100           105           110
Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu
115           120           125
His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly
130           135           140
Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu
145           150           155           160
Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe
165           170           175
Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met
180           185           190
Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser
195           200           205
Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg
210           215           220
Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser
225           230           235           240
His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr
245           250           255
Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe
260           265           270
Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275           280           285
Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg
290           295           300
Ser Leu Gly Glu Lys
305

```

&lt;210&gt; 1118

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g34 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1118

```

Ala Thr Cys His Leu Xaa Thr His Asn Ala Ala Pro Phe Leu Leu Pro
 1           5           10           15
Gly Phe Ser Val Leu Glu Ala Thr Tyr His Ser Ile Ser Ile Pro Phe
 20           25           30

```

Phe Ala Val Tyr Val Cys Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr  
 35 40 45  
 Leu Ile Lys His Asp His Ser Leu His Glu Pro Met Tyr Cys Phe Leu  
 50 55 60  
 Ala Thr Leu Arg Gln Asp Leu Met Val Lys Leu Thr Met Met Pro Thr  
 65 70 75 80  
 Val Met Gly Val Leu Trp Met Asn His Lys Glu Val Ile His Gly Ala  
 85 90 95  
 Cys Phe Leu Gln Val Tyr Ile Ile His Ser His Tyr Pro Leu Ala Glu  
 100 105 110  
 Ser Gly Ile Leu Leu Ser Met Ala Tyr Asp Arg Phe Ile Ile Ile His  
 115 120 125  
 Met Leu Leu Arg Tyr Asn Ser Ile Ser Thr Lys Ser Trp Val Lys Ile  
 130 135 140  
 Glu Leu Trp Leu Phe Met Arg Asp Phe Leu Ser Leu Val Pro Pro Ile  
 145 150 155 160  
 Leu Pro Leu His Cys Phe Pro Tyr Cys His Ser His Val Leu Phe His  
 165 170 175  
 Thr Phe Phe Leu His Gln Asp Val Leu Lys Leu Ala Cys Ala Asp Ile  
 180 185 190  
 Thr Phe Asn His Leu Tyr Pro Ala Ile Leu Val Ala Leu Ile Phe Phe  
 195 200 205  
 Leu Asp Ala Leu Ile Ile Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr  
 210 215 220  
 Val Ile Gly Ile Ala Ser Arg Lys Glu Gln Ala Lys Ala Leu Asn Met  
 225 230 235 240  
 Cys Val Ser His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Ile  
 245 250 255  
 Ser Glu Thr Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val  
 260 265 270  
 His Ile Thr Val Ser Tyr Asp Ser Phe Leu Phe Pro Pro Phe Met Asn  
 275 280 285  
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Val  
 290 295 300  
 Arg Leu Phe Ser Gly His Arg Met Ala Xaa Ala Leu Phe Ser Glu Phe  
 305 310 315 320  
 Cys Asp Leu His Asp Phe Trp Ala Phe  
 325

&lt;210&gt; 1119

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g35 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1119

Leu Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met  
 1 5 10 15  
 Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His  
 20 25 30  
 Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu  
 35 40 45  
 Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg  
 50 55 60  
 Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr  
 65 70 75 80  
 Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Leu Thr Val Met Ser Tyr  
 85 90 95  
 Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met

```

      100      105      110
Arg Pro Tyr Val Cys Ile Gly Thr Val Val Phe Ser Trp Val Gly Gly
      115      120      125
Phe Leu Ser Val Leu Phe Pro Thr Ile Leu Ile Ser Gln Leu Pro Phe
      130      135      140
Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ser Gly Pro Leu
      145      150      155      160
Leu Ala Leu Ala Cys Ala Asp Thr Thr Ala Ile Glu Leu Met Asp Phe
      165      170      175
Met Leu Ser Ser Met Val Ile Leu Cys Cys Ile Val Leu Val Ala Tyr
      180      185      190
Ser Tyr Thr Tyr Ile Ile Leu Thr Ile Met Arg Ile Pro Ser Ala Ser
      195      200      205
Gly Arg Lys Lys Ala Phe Asn Thr Cys Ala Ser His Leu Thr Ile Val
      210      215      220
Ile Ile Ser Ser Gly Ile Thr Val Phe Ile Tyr Val Thr Pro Ser Gln
      225      230      235      240
Lys Glu Tyr Leu Glu Ile Asn Lys Ile Pro Ser Val Leu Ser Ser Leu
      245      250      255
Val Thr Pro Phe Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Asp Thr
      260      265      270
Val Gln Gly Val Leu Arg Asp Val Trp Val Arg Val Arg Gly Val Phe
      275      280      285
Glu Lys Arg Met Arg Ala Val Leu
      290      295

```

&lt;210&gt; 1120

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g36 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1120

```

Met Trp Tyr Asn Asn Ser Ala Gly Pro Phe Leu Leu Thr Gly Phe Leu
  1      5      10      15
Gly Ser Glu Ala Val His Tyr Arg Ile Ser Met Ser Phe Phe Val Ile
      20      25      30
Tyr Phe Ser Val Leu Phe Gly Asn Gly Thr Leu Leu Val Leu Ile Trp
      35      40      45
Asn Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
      50      55      60
Ala Asp Thr Asp Leu Gly Met Thr Phe Thr Thr Met Pro Thr Val Leu
      65      70      75      80
Gly Val Leu Leu Leu Asp Gln Arg Glu Ile Ala His Ala Ala Cys Phe
      85      90      95
Thr Gln Ser Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Ile Leu
      100      105      110
Leu Val Leu Ala Tyr Asp Cys Phe Ile Ala Ile Arg Thr Pro Leu Arg
      115      120      125
Tyr Asn Cys Ile Leu Thr Asn Ser Arg Val Met Asn Ile Gly Leu Gly
      130      135      140
Val Leu Met Arg Gly Phe Met Ser Ile Leu Pro Ile Ile Leu Ser Leu
      145      150      155      160
Tyr Cys Tyr Pro Tyr Cys Gly Ser Arg Ala Leu Leu His Thr Phe Cys
      165      170      175
Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn
      180      185      190
His Ile Tyr Pro Ile Ile Gln Thr Ser Leu Thr Val Phe Leu Asp Ala
      195      200      205

```

Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Met Gly  
 210 215 220  
 Ile Ala Ser Gly Gln Glu Glu Ala Lys Ser Leu Asn Thr Cys Val Ser  
 225 230 235 240  
 His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Met Gly Leu Ser  
 245 250 255  
 Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val Pro Ile Thr  
 260 265 270  
 Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe Val Asn Pro Ile Ile  
 275 280 285  
 Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Ile Arg Leu Phe  
 290 295 300  
 Ser Gly Gln Ser Arg Ala  
 305 310

<210> 1121  
 <211> 332  
 <212> PRT  
 <213> Unknown (H38g37 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(332)  
 <223> Xaa = Any Amino Acid

<400> 1121  
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Pro Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile  
 35 40 45  
 Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr  
 65 70 75 80  
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ala Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Phe Leu Phe Ala Cys  
 100 105 110  
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala  
 115 120 125  
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys  
 130 135 140  
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln  
 145 150 155 160  
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Phe Lys Asn Val Glu  
 165 170 175  
 Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys  
 180 185 190  
 Ser Asp Gly Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile  
 210 215 220  
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Gly Ser His Gln Ala Val Val Cys Xaa Phe Tyr Arg  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg

```

      260      265      270
Asn Gly Val Val Ala Ser Leu Ile Tyr Ala Val Val Thr Pro Met Leu
      275      280      285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290      295      300
Arg Arg Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro
305      310      315      320
Phe Ser Trp Trp Val Arg Lys Gly Asn His Ile Lys
      325      330

```

<210> 1122  
 <211> 310  
 <212> PRT  
 <213> Unknown (H38g38 protein)

<220>  
 <223> Synthetic construct

```

<400> 1122
Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe
 1      5      10      15
Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
      20      25      30
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
      35      40      45
Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
      50      55      60
Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
      65      70      75      80
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
      85      90      95
Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
      100      105      110
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
      115      120      125
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130      135      140
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
      145      150      155      160
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
      165      170      175
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
      180      185      190
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
      195      200      205
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
      210      215      220
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
      225      230      235      240
Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
      245      250      255
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
      260      265      270
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
      275      280      285
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
      290      295      300
Gly Val Glu Arg Ala Leu
      305      310

```

<210> 1123

<211> 323  
 <212> PRT  
 <213> Unknown (H38g39 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(323)  
 <223> Xaa = Any Amino Acid

<400> 1123  
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Thr  
 20 25 30  
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Ser Met Tyr Phe Val Leu  
 50 55 60  
 Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe Phe Ala Cys Ile Glu  
 100 105 110  
 Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln Phe Leu Ala Ile Cys  
 115 120 125  
 His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys Val Phe  
 130 135 140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp  
 180 185 190  
 Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Gly  
 195 200 205  
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro  
 210 215 220  
 Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys Tyr Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu Phe Tyr Gly Ala Gly  
 245 250 255  
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Ser Gly Asn Gly  
 260 265 270  
 Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Pro Trp Arg  
 290 295 300  
 Leu Arg Ser Thr Thr Val Glu Ser Pro Xaa Ser Leu Pro Ser Phe Phe  
 305 310 315 320  
 Leu Cys Leu

<210> 1124  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g40 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1124

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Glu | Pro | Gln | Asn | Leu | Thr | Gly | Val | Xaa | Glu | Phe | Leu | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Ser | Glu | Asp | Pro | Glu | Leu | Gln | Pro | Ile | Leu | Ala | Gly | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Met | Tyr | Leu | Val | Thr | Val | Leu | Arg | Asn | Leu | Leu | Ile | Ile | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Ser | Ser | Asp | Pro | His | Leu | His | Thr | Pro | Met | Cys | Phe | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asn | Leu | Cys | Trp | Ala | Asp | Ile | Gly | Phe | Thr | Leu | Ala | Thr | Val | Pro |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Met | Ile | Val | Asp | Met | Gln | Ser | His | Thr | Arg | Val | Ile | Ser | Tyr | Glu |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Gly | Cys | Leu | Thr | Arg | Ile | Ser | Phe | Leu | Val | Leu | Phe | Ala | Cys | Ile | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Met | Leu | Leu | Thr | Val | Met | Ala | Tyr | Asp | Cys | Phe | Val | Ala | Ile | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Pro | Leu | His | Tyr | Pro | Val | Ile | Val | Asn | Pro | His | Leu | Cys | Val | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Phe | Leu | Leu | Val | Tyr | Phe | Phe | Leu | Ser | Leu | Leu | Asp | Ser | Gln | Leu | His |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Trp | Ile | Val | Leu | Gln | Phe | Thr | Ile | Ile | Lys | Asn | Val | Glu | Ile | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Phe | Val | Cys | Asp | Pro | Ser | Gln | Leu | Leu | Lys | Leu | Ala | Cys | Ser | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Val | Ile | Asn | Ser | Ile | Phe | Met | Tyr | Phe | His | Ser | Thr | Met | Phe | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Leu | Pro | Ile | Ser | Gly | Ile | Leu | Leu | Ser | Tyr | Tyr | Lys | Ile | Val | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ile | Leu | Arg | Ile | Ser | Ser | Ser | Asp | Gly | Lys | Tyr | Lys | Ala | Phe | Ser |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Cys | Gly | Ser | His | Leu | Ala | Val | Val | Cys | Xaa | Phe | Tyr | Gly | Thr | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Gly | Val | Tyr | Leu | Thr | Ser | Ala | Val | Ser | Pro | Pro | Pro | Arg | Asn | Gly |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Val | Ala | Ser | Val | Met | Tyr | Ala | Val | Val | Thr | Pro | Met | Leu | Asn | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Phe | Ile | Tyr | Ser | Leu | Arg | Asn | Arg | Asp | Ile | Gln | Ser | Ala | Leu | Arg | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Leu | Ser | Arg | Thr | Val | Glu | Ser | His | Asp | Leu | Phe | His | Pro | Phe | Ser |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |

<210> 1125

<211> 327

<212> PRT

<213> Unknown (H38g41 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1125



Ser Thr Asp Xaa Gln Ser Leu Thr Gly Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Lys Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
 100 105 110  
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly  
 130 135 140  
 Phe Leu Val Leu Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn  
 145 150 155 160  
 Leu Ile Ala Leu Lys Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn  
 165 170 175  
 Phe Leu Cys Asp Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr  
 180 185 190  
 Phe Thr Asn His Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser  
 210 215 220  
 Ile Leu Arg Val Ser Ser Arg Gly Arg Cys Lys Ala Phe Ser His  
 225 230 235 240  
 Leu Xaa Val Val Cys Xaa Tyr Tyr Gly Thr Gly Phe Gly Gly Tyr Leu  
 245 250 255  
 Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val  
 260 265 270  
 Met Tyr Met Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu  
 275 280 285  
 Arg Asn Arg Asp Ile Lys Ser Val Val Gln Arg Pro His Gly Ser Thr  
 290 295 300  
 Val Xaa Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp  
 305 310 315 320  
 Val Lys Lys Gly Ser Lys Val  
 325

&lt;210&gt; 1126

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g42 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1126

Met Gly Asn Trp Ser Thr Val Thr Glu Ile Thr Leu Ile Ala Phe Pro  
 1 5 10 15  
 Ala Leu Leu Glu Ile Arg Ile Ser Leu Phe Val Val Leu Val Val Thr  
 20 25 30  
 Tyr Thr Leu Thr Ala Thr Gly Asn Ile Thr Ile Ile Ser Leu Ile Trp  
 35 40 45  
 Ile Asp His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 Ser Phe Leu Asp Ile Leu Tyr Thr Thr Val Ile Thr Pro Lys Leu Leu

```

65          70          75          80
Ala Cys Leu Leu Gly Glu Glu Lys Thr Ile Ser Phe Ala Gly Cys Met
      85          90          95
Ile Gln Thr Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Ile Leu
      100        105        110
Leu Ala Val Met Ser Phe Asp Arg Tyr Met Ala Ile Cys Asp Pro Leu
      115        120        125
His Tyr Thr Val Ile Met Asn Ser Arg Ala Cys Leu Leu Val Leu
      130        135        140
Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Phe Pro Thr Ile Val
      145        150        155        160
Val Thr Arg Leu Pro Tyr Cys Arg Lys Glu Ile Asn His Phe Phe Cys
      165        170        175
Asp Ile Ala Pro Leu Leu Gln Val Ala Cys Ile Asn Thr His Leu Ile
      180        185        190
Glu Lys Ile Asn Phe Leu Leu Ser Ala Leu Val Ile Leu Ser Ser Leu
      195        200        205
Ala Phe Thr Thr Gly Ser Tyr Val Tyr Ile Ile Ser Thr Ile Leu Arg
      210        215        220
Ile Pro Ser Thr Gln Gly Arg Gln Lys Ala Phe Ser Thr Cys Ala Ser
      225        230        235        240
His Ile Thr Val Val Ser Ile Ala His Gly Ser Asn Ile Phe Val Tyr
      245        250        255
Val Arg Pro Asn Gln Asn Ser Ser Leu Asp Tyr Asp Lys Val Ala Ala
      260        265        270
Val Leu Ile Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser
      275        280        285
Leu Arg Asn Glu Lys Val Gln Glu Val Leu Arg Glu Thr Val Asn Arg
      290        295        300
Ile Met Thr Leu Ile Gln Arg Lys Thr
305          310

```

&lt;210&gt; 1127

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g43 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(247)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1127

```

Met Gly Asn Ile Asn Ile Ser Leu Glu Asn Tyr Phe Ile Leu Leu Gly
  1          5          10          15
Leu Ser Asn Xaa Pro Pro Leu Glu Ile Val Ile Phe Val Val Leu Leu
      20          25          30
Ile Phe Cys Phe Met Thr Leu Ile Gly Lys Leu Phe Ser Ile Ile Leu
      35          40          45
Ser Tyr Leu Asp Ser His Pro His Thr Pro Arg Tyr Leu Phe Ser Phe
      50          55          60
Leu Asp Phe Cys Tyr Thr Ile Ser Ser Ile Phe Xaa Leu Gln Tyr Asn
      65          70          75          80
Leu Trp Gly Pro Gln Lys Asn Ile Ser Tyr Ala Ser Gly Met Ile Gln
      85          90          95
Ile Tyr Phe Val Leu Thr Leu Gly Thr Met Asp Cys Ala Leu Leu Val
      100        105        110
Val Met Ser Arg Thr Val Tyr Ala Ala Gly His Arg His Leu Pro Tyr
      115        120        125

```

```

Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser
  130                      135                      140
Ala Phe Asp Ser Phe Phe Thr Phe Trp Val Thr Leu Cys Gly His His
145                      150                      155                      160
Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp
                      165                      170                      175
Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala
                      180                      185                      190
Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile
                      195                      200                      205
Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His
                      210                      215                      220
Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met
225                      230                      235                      240
Arg Pro Ile Leu Gly Asn Ser
                      245

```

&lt;210&gt; 1128

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g44 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1128

```

Asp Ile Gln Asn Gln Thr Thr Val Thr Glu Phe Thr Leu Thr Ala Phe
  1                      5                      10                      15
Pro Val Leu Gln Gln Leu Gln Ile Ser Leu Leu Ala Val Leu Trp Phe
                      20                      25                      30
Thr Tyr Met Leu Thr Leu Thr Gly Asn Val Ala Ile Ile Ser Leu Thr
                      35                      40                      45
Trp Ala Asn His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
                      50                      55                      60
Trp Ser Ile Trp Asp Ile Phe Phe Thr Thr Ser Val Ile Pro Lys Leu
65                      70                      75                      80
Leu Ala Cys Leu Leu Gln Asp Lys Lys Thr Ile Ser Leu Ala Gly Cys
                      85                      90                      95
Ile Thr Gln Thr Tyr Phe Leu Gly Phe Leu Gly Thr Val Glu Phe Ile
                      100                      105                      110
Leu Trp Ala Val Met Ser Phe Asp Cys Tyr Val Ala Ile Cys Asp Pro
                      115                      120                      125
Leu His Tyr Thr Ile Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val
                      130                      135                      140
Leu Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Cys Pro Thr Ile
145                      150                      155                      160
Val Val Ser Arg Leu Pro Phe Cys Tyr Lys Glu Ile Ser His Phe Phe
                      165                      170                      175
Cys Asp Ile Thr Pro Leu Leu His Val Ser Cys Ile Asp Thr His Phe
                      180                      185                      190
Ile Glu Met Ile Asn Phe Leu Leu Ser Ser Leu Ile Leu Leu Thr Ser
                      195                      200                      205
Leu Val Leu Thr Thr Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
210                      215                      220
His Ile Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala
225                      230                      235                      240
Ser His Ile Thr Val Ile Ser Ile Ala Tyr Ile Ser Asn Ile Phe Arg

```

245 250 255  
 Tyr Val Arg Pro Ser Gln Ser His Ser Met Gly Phe Asp Lys Val Thr  
 260 265 270  
 Ala Val Pro Thr Met Val Thr Pro Leu Leu Asn Pro Phe Thr Tyr Ser  
 275 280 285  
 Leu Arg Asn Glu Lys Val Lys Ala Val Leu Lys Glu Ala Val Ser Lys  
 290 295 300  
 Ile Met Ser Ser Trp His Arg Arg Thr Xaa Asn Phe  
 305 310 315

&lt;210&gt; 1129

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g45 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1129

Met Glu Pro Gln Asn Thr Thr Gln Val Ser Met Phe Val Leu Leu Gly  
 1 5 10 15  
 Phe Ser Gln Thr Gln Glu Leu Gln Lys Phe Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr  
 35 40 45  
 Val Thr Phe Asp Cys Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg  
 50 55 60  
 Asn Leu Ala Leu Ile Asp Leu Cys Tyr Ser Thr Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly  
 85 90 95  
 Cys Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val  
 100 105 110  
 Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln  
 115 120 125  
 Pro Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu  
 130 135 140  
 Val Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu  
 145 150 155 160  
 Ala Leu Ile Leu Pro Leu Pro Phe Cys Asp Pro Asn Ile Ile Asp Asn  
 165 170 175  
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Leu Leu Glu Phe Leu Met Ile Phe Asn Ser Gly Leu Leu Val Ile  
 195 200 205  
 Ile Trp Phe Leu Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Val Met  
 210 215 220  
 Leu Arg Ser His Ser Gly Lys Ala Arg Arg Lys Ala Ala Ser Thr Cys  
 225 230 235 240  
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr  
 245 250 255  
 Ile Tyr Thr Trp Pro Phe Thr Pro Phe Leu Met Asp Lys Ala Val Ser  
 260 265 270  
 Ile Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys  
 290 295 300  
 Leu Val Ile Cys Arg Glu  
 305 310

&lt;210&gt; 1130

<211> 311  
 <212> PRT  
 <213> Unknown (H38g46 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(311)  
 <223> Xaa = Any Amino Acid

<400> 1130  
 Asp Gln Glu Asn Gln Thr Ser Glu Val Thr Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Ser Glu Tyr Pro Asp Leu Gln Thr Pro Leu Phe Leu Val Phe Leu Thr  
 20 25 30  
 Ile Tyr Thr Val Thr Val Leu Gly Asn Leu Gly Met Ile Ile Val Ile  
 35 40 45  
 Arg Ile Ser Pro Lys Leu His Thr Pro Met Cys Phe Phe Leu Ser His  
 50 55 60  
 Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu  
 65 70 75 80  
 Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys  
 85 90 95  
 Thr Met Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe  
 100 105 110  
 Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro  
 115 120 125  
 Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val  
 130 135 140  
 Ala Thr Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa  
 145 150 155 160  
 Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe  
 165 170 175  
 Val Cys Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys  
 180 185 190  
 Val Ser Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser  
 195 200 205  
 Ser Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro  
 210 215 220  
 Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu  
 225 230 235 240  
 Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val  
 245 250 255  
 Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe  
 260 265 270  
 Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg  
 275 280 285  
 Asn Lys Asp Val Lys Glu Thr Val Arg Arg Leu Leu Ile Thr Lys Leu  
 290 295 300  
 Leu Cys Leu Ile Leu Xaa Asn  
 305 310

<210> 1131  
 <211> 334  
 <212> PRT  
 <213> Unknown (H38g47 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(334)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1131

```

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Val Ser Gly Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile
115          120          125
Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala
130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln
145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu
165          170          175
Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Ser His Leu Ala Cys
180          185          190
Cys Asp Thr Phe Thr Ile Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
195          200          205
Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Phe Ser Lys Ile
210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225          230          235          240
Leu Ser Thr Cys Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly
245          250          255
Thr Gly Val Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Leu Val Thr Pro Met Leu
275          280          285
Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Val Leu
290          295          300
Arg Gln Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Ile Cys Ser
305          310          315          320
Ile Pro Phe Val Val Trp Val Gln Lys Gly Ser Lys Val Lys
325          330

```

&lt;210&gt; 1132

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g48 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1132

```

Met Glu Thr Gly Asn Leu Thr Trp Val Ser Asp Phe Val Phe Leu Gly
 1          5          10          15
Leu Ser Gln Thr Arg Glu Leu Gln Arg Phe Leu Phe Leu Met Phe Leu
 20          25          30

```

Phe Val Tyr Ile Thr Thr Val Met Gly Asn Ile Leu Ile Ile Ile Thr  
 35 40 45  
 Val Thr Ser Asp Ser Gln Leu His Thr Pro Met Tyr Phe Leu Leu Arg  
 50 55 60  
 Asn Leu Ala Val Leu Asp Leu Cys Phe Ser Ser Val Thr Ala Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Tyr Gln Gly  
 85 90 95  
 Cys Met Gly Gln Ile Phe Phe Phe His Phe Leu Gly Gly Ala Met Val  
 100 105 110  
 Phe Phe Leu Ser Val Met Ala Phe Asp Arg Leu Ile Ala Ile Ser Arg  
 115 120 125  
 Pro Leu Arg Tyr Val Thr Val Met Asn Thr Gln Leu Trp Val Gly Leu  
 130 135 140  
 Val Val Ala Thr Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu  
 145 150 155 160  
 Ala Leu Met Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn  
 165 170 175  
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Leu Leu Glu Phe Leu Lys Ile Ser Asn Ser Gly Leu Leu Asp Val  
 195 200 205  
 Val Trp Phe Phe Leu Leu Leu Met Ser Tyr Leu Phe Ile Leu Val Met  
 210 215 220  
 Leu Arg Ser His Pro Gly Glu Ala Arg Arg Lys Ala Ala Ser Thr Cys  
 225 230 235 240  
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Val Pro Ser Ile Tyr  
 245 250 255  
 Leu Tyr Ala Arg Pro Phe Thr Pro Phe Pro Met Asp Lys Leu Val Ser  
 260 265 270  
 Ile Gly His Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Asp Met Gln Ala Ala Val Arg Arg Leu Gly Arg His  
 290 295 300  
 Arg Leu Val  
 305

&lt;210&gt; 1133

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g49 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1133

His Thr Glu Pro Gln Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser  
 35 40 45  
 Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Asn Leu Cys  
 50 55 60  
 Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val  
 65 70 75 80  
 Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Gln | Met | Ser | Phe | Phe | Ile | Leu | Phe | Ala | Cys | Ile | Glu | Gly | Met | Leu | Leu |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Thr | Val | Met | Ala | Tyr | Asp | Cys | Phe | Val | Ala | Ile | Cys | Arg | Pro | Leu | His |  |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |  |
| Tyr | Pro | Val | Ile | Val | Asn | Pro | His | Leu | Cys | Val | Phe | Phe | Val | Leu | Val |  |  |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |  |  |
| Ser | Phe | Phe | Leu | Ser | Leu | Leu | Asp | Ser | Gln | Leu | His | Ser | Xaa | Ile | Val |  |  |
| 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |  |  |
| Leu | Gln | Phe | Thr | Ile | Ile | Lys | Asn | Val | Glu | Ile | Ser | His | Phe | Phe | Cys |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |  |
| Asp | Pro | Ser | Gln | Leu | Leu | Lys | Leu | Ala | Cys | Ser | Asp | Ser | Val | Ile | Asn |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Ser | Ile | Phe | Ile | Tyr | Phe | Asp | Ser | Thr | Met | Phe | Gly | Phe | Leu | Pro | Ile |  |  |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |  |  |
| Ser | Gly | Ile | Leu | Trp | Ser | Tyr | Tyr | Lys | Ile | Ile | Pro | Ser | Ile | Leu | Arg |  |  |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |  |  |
| Ile | Ser | Ser | Ser | Tyr | Gly | Lys | Tyr | Lys | Ala | Phe | Ser | Thr | Cys | Ala | Ser |  |  |
| 225 |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |  |  |
| His | Leu | Ala | Val | Val | Cys | Xaa | Phe | Tyr | Val | Thr | Gly | Ile | Gly | Met | Tyr |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |  |
| Leu | Thr | Ser | Ala | Val | Ser | Pro | Pro | Pro | Ser | Asn | Gly | Val | Val | Ala | Ser |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Val | Met | Tyr | Ala | Ala | Val | Thr | Pro | Met | Leu | Asn | Pro | Phe | Ile | Tyr | Ser |  |  |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |  |  |
| Leu | Arg | Asn | Arg | Asp | Ile | Gln | Ser | Ala | Leu | Arg | Arg | Val | Leu | Ser | Arg |  |  |
| 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |     |     |  |  |
| Thr | Val | Glu | Phe | His | Asp | Leu | Phe | His | Pro | Phe | Ser |     |     |     |     |  |  |
| 305 |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |     |     |  |  |

<210> 1134

**<211> 123**

<212> PRT

<213> Unknown (H38q50 protein)

**<220>**

<223> Synthetic construct

<400> 1134

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Ser | Pro | Thr | Gln | Leu | Thr | Ala | Gly | Pro | Arg | Thr | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Cys | Val | Ile | Met | Ile | Cys | Phe | Ala | Leu | Thr | Val | Leu | Ser | Tyr | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ile | Leu | Ala | Thr | Val | Val | Gln | Ile | Arg | Ser | Ala | Ala | Ser | Arg | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ala | Phe | Ser | Thr | Cys | Ser | Ser | His | Leu | Gly | Met | Val | Leu | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Gly | Thr | Gly | Ser | Ser | Thr | Tyr | Met | Arg | Pro | Thr | Thr | Arg | Tyr | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Leu | Glu | Gly | Arg | Leu | Ala | Ala | Val | Phe | Tyr | Ser | Ile | Leu | Ile | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Leu | Asn | Pro | Leu | Ile | Tyr | Ser | Leu | Arg | Asn | Gln | Asp | Met | Lys | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Trp | Lys | Leu | Tyr | Leu | Gln | Val | Pro | Tyr |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

<210> 1135

**<211> 356**

<212> PRT

<213> Unknown (H38g51 protein)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(356)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1135

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10           15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe Phe
          20           25           30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
          35           40           45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
 50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
65           70           75           80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
          85           90           95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
          100          105          110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
          115          120          125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
130          135          140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
145          150          155          160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
          165          170          175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
          180          185          190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
          195          200          205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
225          230          235          240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
          245          250          255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
          260          265          270
Gly Lys Leu Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
          275          280          285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
290          295          300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
305          310          315          320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
          325          330          335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
340          345          350
Arg Xaa Tyr Pro
          355

```

&lt;210&gt; 1136

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g52 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1136

```

Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met Leu Leu Gly Phe Pro
 1           5           10           15
Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly Val Val Phe Phe Phe
 20           25           30
Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu Ile Leu Leu Pro Leu
 35           40           45
Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe Phe Leu Arg Asn Leu
 50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
 65           70           75           80
Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr Phe Gly Gly Cys Ala
 85           90           95
Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr Val Glu Cys Met Leu
 100          105          110
Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala Val Cys Lys Pro Leu
 115          120          125
Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys Gln Gly Leu Val Ala
 130          135          140
Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met Ile Leu Ser Pro Cys
 145          150          155          160
Pro Val Ser Leu Pro Arg Cys Gly Asp His His Leu Asp His Tyr Phe
 165          170          175
Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys Gly Ala Thr Thr Val
 180          185          190
Met Glu Glu Lys Pro Tyr Leu His Cys Val Val Val Val Val Phe Ile
 195          200          205
Phe Leu Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
 210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
 225          230          235          240
Gly Thr Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr
 245          250          255
Val Arg Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu
 260          265          270
Gly Lys Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn
 275          280          285
Pro Tyr Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu
 290          295          300
Ile Gly Lys Glu Lys Gly Ser Gly Asp Thr Ile Gly His
 305          310          315

```

&lt;210&gt; 1137

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g53 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1137

```

Met Val Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1           5           10           15
Glu His Pro Gly Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
 20           25           30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
 35           40           45
Leu Asp Pro Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50           55           60

```

Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu  
 65 70 75 80  
 Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser  
 85 90 95  
 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu  
 100 105 110  
 Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu  
 115 120 125  
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser  
 130 135 140  
 Val Ala Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser  
 145 150 155 160  
 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val  
 165 170 175  
 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr  
 180 185 190  
 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro  
 195 200 205  
 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu  
 210 215 220  
 Arg Ile Asn Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly Thr Cys Ser  
 225 230 235 240  
 Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val  
 245 250 255  
 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe  
 260 265 270  
 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Thr Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Gly  
 290 295 300  
 Lys Glu Met Gly Leu Thr Gln Ser  
 305 310

&lt;210&gt; 1138

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g54 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(343)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1138

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser  
 1 5 10 15  
 Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser  
 20 25 30  
 Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp  
 35 40 45  
 Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe  
 50 55 60  
 Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn  
 65 70 75 80  
 Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln  
 85 90 95  
 Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr  
 100 105 110  
 Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His

```

      115      120      125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
  130      135      140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
  145      150      155      160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
      165      170      175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
      180      185      190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
      195      200      205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
      210      215      220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
  225      230      235      240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
      245      250      255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
      260      265      270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275      280      285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
      290      295      300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
  305      310      315      320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
      325      330      335
Tyr Leu Ser Tyr Thr His His
      340

```

&lt;210&gt; 1139

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g55 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1139

```

Met Phe Ala Ala Leu Val Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly
  1      5      10      15
Asn Ser Ala Leu Val Leu Leu Ala Val Arg Asp Pro Arg Leu His Thr
      20      25      30
Pro Met Tyr Tyr Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe
      35      40      45
Thr Thr Ser Val Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala
      50      55      60
Leu Trp Leu Pro Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu
  65      70      75      80
Ala Leu Gly Ser Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Asp
      85      90      95
Arg Ala Ala Lys Lys Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser
      100      105      110
Leu Gly Arg Gly Gln Ala Gly Gln Ser Ala Ser Trp Leu Ser Gly Leu
      115      120      125
Thr Asn Ser Val Ala Gln Thr Ala Leu Leu Ala Glu Arg Pro Leu Cys
      130      135      140
Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu
  145      150      155      160
Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe
      165      170      175

```

Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala  
 180 185 190  
 Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly  
 195 200 205  
 Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val  
 210 215 220  
 Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln  
 225 230 235 240  
 Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val  
 245 250 255  
 Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys  
 260 265 270  
 Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln  
 275 280 285  
 Ala Gly Gln  
 290

&lt;210&gt; 1140

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g56 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(307)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1140

Glu Leu Ile Thr Asn Ser Ser Ser Val Pro Ser Cys Glu Arg Thr Ile  
 1 5 10 15  
 Gln Ile Phe Leu Phe Ser Leu Ile Thr Thr Ile Tyr Ala Leu Thr Ile  
 20 25 30  
 Thr Gly Asn Gly Ala Ile Ala Phe Ala Leu Trp Cys Asp Arg Arg Leu  
 35 40 45  
 His Thr Pro Met Tyr Met Phe Leu Gly Asp Phe Ser Phe Leu Glu Ile  
 50 55 60  
 Trp Tyr Val Phe Ser Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser  
 65 70 75 80  
 Glu Lys Thr Asn Ile Ser Phe Ala Gly Cys Phe Leu Gln Ile Tyr Phe  
 85 90 95  
 Phe Phe Ser Leu Asn Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala  
 100 105 110  
 Phe Asp Gln Asn Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Asn Ile  
 115 120 125  
 Met Thr Gly His Leu Cys Ala Lys Leu Ala Ile Leu Cys Trp Val Cys  
 130 135 140  
 Gly Phe Leu Trp Phe Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro  
 145 150 155 160  
 Phe Cys Gly Pro Asn Ile Ile Asp His Val Val Cys Asp Pro Gly Pro  
 165 170 175  
 Leu Phe Ala Leu Asp Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys  
 180 185 190  
 Tyr Thr Leu Ser Ser Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile  
 195 200 205  
 Gly Ser Tyr Thr Ile Val Leu Lys Val Val Leu Gly Thr Pro Ser Ser  
 210 215 220  
 Thr Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val  
 225 230 235 240  
 Val Ser Leu Cys Tyr Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly

245 250 255  
 Leu Gly His Ser Thr Glu Met Gln Lys Ile Val Thr Leu Phe Tyr Ala  
 260 265 270  
 Met Val Thr Ser Leu Phe Asn Pro Leu Ile Tyr Ser Leu Gln Asn Lys  
 275 280 285  
 Glu Ile Lys Ala Ala Leu Arg Lys Val Leu Val Ser Ser Asn Ile Ile  
 290 295 300  
 Xaa Gly Ile  
 305

<210> 1141  
 <211> 221  
 <212> PRT  
 <213> Unknown (H38g57 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(221)  
 <223> Xaa = Any Amino Acid

<400> 1141  
 Ala Cys Lys His Asp Met Ile Leu Thr Val Met Ala Tyr Asp Cys Leu  
 1 5 10 15  
 Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His  
 20 25 30  
 Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Ile Ser Met Xaa Asp  
 35 40 45  
 Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Ile Ile Lys Asn  
 50 55 60  
 Val Glu Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Phe Leu Lys Leu  
 65 70 75 80  
 Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser  
 85 90 95  
 Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Phe  
 100 105 110  
 Lys Ile Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr  
 115 120 125  
 Lys Ala Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe  
 130 135 140  
 Tyr Gly Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Leu Ser Pro Pro  
 145 150 155 160  
 Pro Arg Asn Gly Val Met Ala Ser Val Met Tyr Ala Val Val Thr Pro  
 165 170 175  
 Met Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser  
 180 185 190  
 Ala Leu Trp Arg Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe  
 195 200 205  
 His Pro Phe Ser Cys Val Gly Lys Gly Asn His Ile Lys  
 210 215 220

<210> 1142  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g58 protein)

<220>  
 <223> Synthetic construct

<400> 1142

```

Met Ala Lys Asn Asn Leu Thr Arg Val Thr Glu Phe Ile Leu Met Gly
 1           5           10           15
Phe Met Asp His Pro Lys Leu Glu Ile Pro Leu Phe Leu Val Phe Leu
          20           25           30
Ser Phe Tyr Leu Val Thr Leu Leu Gly Asn Val Gly Met Ile Met Leu
          35           40           45
Ile Gln Val Asp Val Lys Leu Tyr Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
His Leu Ser Leu Leu Asp Ala Cys Tyr Thr Ser Val Ile Thr Pro Gln
65           70           75           80
Ile Leu Ala Thr Leu Ala Thr Gly Lys Thr Val Ile Ser Tyr Gly His
          85           90           95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Ile Cys Ala Gly Thr Glu Cys
          100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Arg Asn
          115          120          125
Pro Leu Leu Tyr Thr Val Ala Met Asn Pro Arg Leu Cys Trp Ser Leu
          130          135          140
Val Val Gly Ala Tyr Val Cys Gly Val Ser Gly Ala Ile Leu Arg Thr
145          150          155          160
Thr Cys Thr Phe Thr Leu Ser Phe Cys Lys Asp Asn Gln Ile Asn Phe
          165          170          175
Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr
          180          185          190
Ala Asn Ile Glu Ile Val Ile Ile Phe Phe Gly Asn Phe Val Ile Leu
          195          200          205
Ala Asn Ala Ser Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile Lys Thr
          210          215          220
Ile Leu Lys Val Lys Ser Ser Gly Gly Arg Ala Lys Thr Phe Ser Thr
225          230          235          240
Cys Ala Ser His Ile Thr Ala Val Ala Leu Phe Phe Gly Ala Leu Ile
          245          250          255
Phe Met Tyr Leu Gln Ser Gly Ser Gly Lys Ser Leu Glu Glu Asp Lys
          260          265          270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Arg Lys Val
          290          295          300
Ala Arg Arg Leu Gln Val Ser Leu Ser Met
305          310

```

&lt;210&gt; 1143

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g59 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1143

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1           5           10           15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Leu
          20           25           30
Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
          35           40           45
Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

```

|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |
| Phe | Phe | Leu | Ser | Thr | Leu |
| 65  |     |     |     |     | 70  |
| Trp | Glu | Leu | Xaa | Val | Leu |
|     |     |     |     |     | 85  |
| Ser | Tyr | Asn | Ser | Cys | Ser |
|     |     |     |     |     | 100 |
| Thr | Ala | Gln | Cys | Leu | Leu |
|     |     |     |     |     | 115 |
| Glu | Ile | Ser | Tyr | Leu | Leu |
|     |     |     |     |     | 130 |
| Cys | Ile | Gln | Leu | Ala | Leu |
| 145 |     |     |     |     | 150 |
| Val | Thr | Leu | Ile | Ile | Ala |
|     |     |     |     |     | 165 |
| Ile | Asn | His | Phe | Thr | Cys |
|     |     |     |     |     | 180 |
| Ser | Asp | Thr | Leu | Val | Ser |
|     |     |     |     |     | 195 |
| Thr | Leu | Pro | Leu | Pro | Phe |
|     |     |     |     |     | 210 |
| Phe | Val | Arg | Ala | Val | Glu |
| 225 |     |     |     |     | 230 |
| Ser | His | Leu | Thr | Gly | Val |
|     |     |     |     |     | 245 |
| Tyr | Leu | Lys | Pro | Gln | Ser |
|     |     |     |     |     | 260 |
| Ser | Lys | Leu | Tyr | Gly | Ala |
|     |     |     |     |     | 275 |
| Ile | Gln | Arg | Asn | Lys | Asp |
|     |     |     |     |     | 290 |
| Gly | Asn | Glu | Lys | Ser | Xaa |
| 305 |     |     |     |     | 310 |

&lt;210&gt; 1144

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g61 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(351)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1144

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ile | Leu | Val | Ile | Asp | Asn | Gly | Ser | Glu | Val | Thr | Glu | Phe | Ile |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Val | Gly | Leu | Tyr | Asn | His | Pro | Lys | Phe | Gln | Ile | Ala | Phe | Tyr | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Met | Val | Val | Val | Tyr | Leu | Ile | Thr | Phe | Val | Gly | Ser | Ser | Leu | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Val | Val | Val | Lys | Val | Asp | Gly | Trp | Leu | His | Thr | Pro | Met | Cys | Phe |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Phe | Leu | Ser | Asn | Leu | Ser | Phe | Leu | Asp | Ile | Cys | Tyr | Ser | Ser | Asn | Ser |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Pro | Phe | Leu | Leu | Phe | Asn | Gly | Leu | Arg | Asp | Tyr | Pro | Thr | Ile | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Tyr | Asn | Ser | Cys | Tyr | Ala | Gln | Met | Thr | Ser | Ala | Phe | Phe | Leu | Gly | Met |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |



Thr Gly Cys Leu Leu Leu Ala Val Met Ala Tyr Glu Arg Phe Val Val  
 115 120 125  
 Ile Ser Asn Pro Leu Arg Tyr Ile Ile Ile Met Asn Asn Lys Val Cys  
 130 135 140  
 Ile Gln Leu Ala Met Val Thr Trp Ala Ser Ala Ser Pro Tyr Val Ile  
 145 150 155 160  
 Asn Thr Ile Ile Ala Ile Ile His Cys Asn Asn Thr Leu Ile Ala Met  
 165 170 175  
 Ile Ala Leu Ser Ile Pro Ala His Phe Cys Gly His Asn Val Ile Asn  
 180 185 190  
 His Phe Thr Cys Glu Val Gln Glu Leu Leu Lys Leu Val Cys Ser Asp  
 195 200 205  
 Ile Pro Gly Ser Leu Ile Leu Gly Leu Val Ile Gly Ile Phe Thr Leu  
 210 215 220  
 Ser Leu Pro Phe Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Phe Ala  
 225 230 235 240  
 Tyr Ala His Ile Val Val Ala Val Leu Arg Ile Asn Ser Ala Glu Ala  
 245 250 255  
 Arg Leu Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Ile Ile  
 260 265 270  
 Ile Phe Tyr Gly Thr Ala Thr Tyr Met Tyr Leu Lys Pro Gln Ser Arg  
 275 280 285  
 Glu Ser Gln Asp Glu Gly Lys Val Ile Ser Val Phe Phe Leu Lys Val  
 290 295 300  
 Glu Lys Gln His Gln Asn Asp Ser Ile Ser Val Phe Tyr Gly Val Val  
 305 310 315 320  
 Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asp Lys Asp Ala  
 325 330 335  
 Lys His Ala Leu Arg Lys Ile Ile Arg Lys Lys Glu Ser Xaa Lys  
 340 345 350

&lt;210&gt; 1145

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g62 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1145

Met Asp Lys Ile Asn Gln Thr Phe Val Arg Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Gly Tyr Pro Lys Leu Glu Ile Ile Phe Phe Ala Leu Ile Leu  
 20 25 30  
 Val Met Tyr Val Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala  
 35 40 45  
 Ser Ile Leu Asp Ser Arg Leu His Met Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Ser  
 65 70 75 80  
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Pro Ile Ile Met Asn Lys Val Val Tyr Val Leu Leu  
 130 135 140  
 Thr Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Thr Val Gln Thr  
 145 150 155 160  
 Ser Leu Ala Met Arg Trp Pro Phe Cys Gly Asn Asn Ile Ile Asn His

```

      165      170      175
Phe Leu Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ser Asp Ile
      180      185      190
Ser Val Asn Ile Val Thr Leu Ala Val Ser Asn Ile Ala Phe Leu Val
      195      200      205
Leu Pro Leu Leu Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr
      210      215      220
Ile Leu Arg Thr Asn Ser Ala Thr Gly Arg His Lys Ala Phe Ser Thr
      225      230      235
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
      245      250      255
Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Leu Gly Lys Asp Asn
      260      265      270
Leu Gln Ala Thr Glu Gly Leu Val Ser Met Phe Tyr Gly Val Val Thr
      275      280      285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290      295      300
Ala Ala Ile Lys Tyr Leu Leu Ser Arg Lys Ala Ile Asn Gln
      305      310      315

```

&lt;210&gt; 1146

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g63 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1146

```

Met Phe Pro Ala Asn Trp Thr Ser Val Lys Val Phe Phe Phe Leu Gly
1      5      10      15
Phe Phe His Tyr Pro Lys Val Gln Val Ile Ile Phe Ala Val Cys Leu
      20      25      30
Leu Met Tyr Leu Ile Thr Leu Leu Gly Asn Ile Phe Leu Ile Ser Ile
      35      40      45
Thr Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Leu Asp Ile Trp Tyr Ser Ser Ala Leu Ser Pro
      65      70      75      80
Met Leu Ala Asn Phe Val Ser Gly Arg Asn Thr Ile Ser Phe Ser Gly
      85      90      95
Cys Ala Thr Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
      100      105      110
Val Leu Leu Pro Met Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115      120      125
Pro Leu Arg Tyr Pro Val Ile Met Asn Arg Arg Thr Cys Val Gln Ile
      130      135      140
Ala Ala Gly Ser Trp Met Thr Gly Cys Leu Thr Ala Met Val Glu Met
      145      150      155      160
Met Ser Val Leu Pro Leu Ser Leu Cys Gly Asn Ser Ile Ile Asn His
      165      170      175
Phe Thr Cys Glu Ile Leu Ala Ile Leu Lys Leu Val Cys Val Asp Thr
      180      185      190
Ser Leu Val Gln Leu Ile Met Leu Val Ile Ser Val Leu Leu Leu Pro
      195      200      205
Met Pro Met Leu Leu Ile Cys Ile Ser Tyr Ala Phe Ile Leu Ala Ser
      210      215      220
Ile Leu Arg Ile Ser Ser Val Glu Gly Arg Ser Lys Ala Phe Ser Thr
      225      230      235      240
Cys Thr Ala His Leu Met Val Val Val Leu Phe Tyr Gly Thr Ala Leu
      245      250      255

```

Ser Met His Leu Lys Pro Ser Ala Val Asp Ser Gln Glu Ile Asp Lys  
                   260                  265                  270  
 Phe Met Ala Leu Val Tyr Ala Gly Gln Thr Pro Met Leu Asn Pro Ile  
                   275                  280                  285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Val Ala Leu Lys Lys Leu  
                   290                  295                  300  
 Leu Ile Arg Asn His Phe Asn Thr Ala Phe Ile Ser Ile Leu Lys  
 305                  310                  315

<210> 1147

<211> 310

<212> PRT

<213> Unknown (H38g64 protein)

<220>

<223> Synthetic construct

<400> 1147

Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala  
 1                  5                  10                  15  
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu  
                   20                  25                  30  
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu  
                   35                  40                  45  
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser  
                   50                  55                  60  
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln  
 65                  70                  75                  80  
 Met Leu Ala Val Leu Leu Glu His Gly Ala Ala Leu Ser Tyr Thr Arg  
                   85                  90                  95  
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys  
                   100                  105                  110  
 Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln  
                   115                  120                  125  
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu  
                   130                  135                  140  
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr  
 145                  150                  155                  160  
 Val Ser Ala Phe Thr Leu Ser Phe Cys Gly Thr Ser Glu Ile Asp Phe  
                   165                  170                  175  
 Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Thr Cys Gly Glu Ser  
                   180                  185                  190  
 Tyr Thr Gln Glu Val Leu Ile Ile Met Phe Ala Ile Phe Val Ile Pro  
                   195                  200                  205  
 Ala Ser Met Val Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala  
                   210                  215                  220  
 Ile Met Gly Ile Pro Ala Gly Ser Gln Ala Lys Thr Phe Ser Thr Cys  
 225                  230                  235                  240  
 Thr Ser His Leu Thr Ala Val Ser Leu Phe Phe Gly Thr Leu Ile Phe  
                   245                  250                  255  
 Met Tyr Leu Arg Gly Asn Ser Asp Gln Ser Ser Glu Lys Asn Arg Val  
                   260                  265                  270  
 Val Ser Val Leu Tyr Thr Glu Val Ile Pro Met Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Arg Lys Ile Leu  
                   290                  295                  300  
 Asn Arg Ala Lys Leu Ser  
 305                  310

<210> 1148

<211> 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g65 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1148

```

Met Gly Met Glu Gly Leu Leu Gln Asn Ser Thr Asn Phe Val Leu Thr
 1          5          10          15
Gly Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Ile Val
 20          25          30
Phe Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu
 35          40          45
Leu Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu
 50          55          60
Ser Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro
 65          70          75          80
Lys Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu
 85          90          95
Gly Cys Ala Val Gln Ile Phe Leu Tyr Leu Thr Leu Ile Gly Gly Glu
100          105          110
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
115          120          125
Asn Pro Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe
130          135          140
Met Val Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu
145          150          155          160
Thr Pro Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn
165          170          175
His Phe Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp
180          185          190
Thr Ser Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu
195          200          205
Leu Ile Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu
210          215          220
Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala
225          230          235          240
Thr Cys Ser Ser His Ile Met Ala Val Ser Val Phe Tyr Gly Ala Ala
245          250          255
Phe Tyr Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp
260          265          270
Lys Val Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Leu Arg Lys
290          295          300
Val Leu Gly Arg Cys Gly Ser Ser Gln Ser Ile Arg Val Ala Thr Val
305          310          315          320
Ile

```

&lt;210&gt; 1149

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g66 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1149

```

Met Ala His Thr Asn Glu Ser Met Val Ser Glu Phe Val Leu Leu Gly
 1          5          10          15

```

Leu Ser Asn Ser Trp Gly Leu Gln Leu Phe Phe Phe Ala Ile Phe Ser  
 20 25 30  
 Ile Val Tyr Val Thr Ser Val Leu Gly Asn Val Leu Ile Ile Val Ile  
 35 40 45  
 Ile Ser Phe Asp Ser His Leu Asn Ser Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ile Asp Ile Cys Gln Ser Asn Phe Ala Thr Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Phe Phe Ile Glu Arg Lys Thr Ile Ser Phe Glu Gly  
 85 90 95  
 Cys Met Ala Gln Ile Phe Val Leu His Ser Phe Val Gly Ser Glu Met  
 100 105 110  
 Met Leu Leu Val Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Ser Thr Ile Met Asn Arg Arg Leu Cys Val Ile Phe  
 130 135 140  
 Val Ser Ile Ser Trp Ala Val Gly Val Leu His Ser Val Ser His Leu  
 145 150 155 160  
 Ala Phe Thr Val Asp Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Leu Val Ile Glu Leu Ala Cys Met Asp Thr  
 180 185 190  
 Tyr Glu Met Glu Ile Met Thr Leu Thr Asn Ser Gly Leu Ile Ser Leu  
 195 200 205  
 Ser Cys Phe Leu Ala Leu Ile Ile Ser Tyr Thr Ile Ile Leu Ile Gly  
 210 215 220  
 Val Arg Cys Arg Ser Ser Ser Gly Ser Ser Lys Ala Leu Ser Thr Leu  
 225 230 235 240  
 Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Cys Ile Tyr  
 245 250 255  
 Phe Tyr Ile Trp Pro Phe Ser Arg Leu Pro Val Asp Lys Phe Leu Ser  
 260 265 270  
 Val Phe Tyr Thr Val Cys Thr Pro Leu Leu Asn Pro Ile Ile Tyr Ser  
 275 280 285  
 Leu Arg Asn Glu Asp Val Lys Ala Ala Met Trp Lys Leu Arg Asn Arg  
 290 295 300  
 His Val Asn Ser Trp Lys Asn  
 305 310

&lt;210&gt; 1150

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g67 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1150

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Leu Leu  
 20 25 30  
 Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu  
 35 40 45  
 Ser His Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Phe Ser  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln  
 65 70 75 80  
 Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly  
 85 90 95  
 Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys

```

      100      105      110
Val Leu Leu Gly Val Met Val Phe Asp Arg Tyr Ala Ala Val Cys Arg
      115      120      125
Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met
      130      135      140
Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr
      145      150      155      160
Val Leu Ile Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His
      165      170      175
Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr
      180      185      190
Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu
      195      200      205
Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala
      210      215      220
Val Met Arg Ile Lys Leu Ala Thr Gly Gln Arg Lys Val Phe Gly Thr
      225      230      235      240
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
      245      250      255
Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys
      260      265      270
Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val
      290      295      300
Leu Trp Lys Asn Tyr Asp Ser Arg
305      310

```

&lt;210&gt; 1151

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g68 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1151

```

Met Cys Ser Gly Asn Gln Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp
  1      5      10      15
Phe Thr Leu Thr Gly Leu Phe Ala Glu Ser Lys His Ala Ala Leu Leu
      20      25      30
Tyr Thr Val Thr Phe Leu Leu Phe Leu Met Ala Leu Thr Gly Asn Ala
      35      40      45
Leu Leu Ile Leu Leu Ile His Ser Glu Pro Arg Leu His Thr Pro Met
      50      55      60
Tyr Phe Phe Ile Ser Gln Leu Ala Leu Met Asp Leu Met Tyr Leu Cys
      65      70      75      80
Val Thr Val Pro Lys Met Leu Val Gly Gln Val Thr Gly Asp Asp Thr
      85      90      95
Ile Ser Pro Ser Gly Cys Gly Ile Gln Met Phe Phe His Leu Thr Leu
      100      105      110
Ala Gly Ala Glu Val Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr
      115      120      125
Ala Ala Val Cys Arg Pro Leu His Tyr Pro Leu Leu Met Asn Gln Arg
      130      135      140
Val Cys Gln Leu Leu Val Ser Ala Cys Trp Val Leu Gly Met Val Asp
      145      150      155      160
Gly Leu Leu Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Gln Ser
      165      170      175
Arg Lys Ile Leu Ser Phe Phe Cys Glu Thr Pro Ala Leu Leu Lys Leu
      180      185      190

```

Ser Cys Ser Asp Val Ser Leu Tyr Lys Met Leu Thr Tyr Leu Cys Cys  
 195 200 205  
 Ile Leu Met Leu Leu Thr Pro Ile Met Val Ile Ser Ser Ser Tyr Thr  
 210 215 220  
 Leu Ile Leu His Leu Ile His Arg Met Asn Ser Ala Ala Gly Arg Arg  
 225 230 235 240  
 Lys Ala Leu Ala Thr Cys Ser Ser His Met Ile Ile Val Leu Leu Leu  
 245 250 255  
 Phe Gly Ala Ser Phe Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr  
 260 265 270  
 Ala Glu Gln Asp Met Met Val Ser Ala Phe Tyr Thr Ile Phe Thr Pro  
 275 280 285  
 Val Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Arg  
 290 295 300  
 Ala Met Arg Ser Met Met Gln Ser Arg  
 305 310

&lt;210&gt; 1152

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g69 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1152

Met Asp Val Gly Asn Lys Ser Thr Met Ser Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Ser Asn Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser  
 20 25 30  
 Leu Leu Tyr Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr  
 35 40 45  
 Val Ile Val Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr  
 50 55 60  
 Asn Leu Ser Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys  
 65 70 75 80  
 Met Ile Thr Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly  
 85 90 95  
 Cys Leu Thr Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile  
 100 105 110  
 Ile Leu Leu Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu  
 130 135 140  
 Val Val Ala Ser Trp Ile Met Gly Val Met His Ser Met Ser Gln Val  
 145 150 155 160  
 Ile Phe Ala Leu Thr Leu Pro Phe Cys Gly Pro Tyr Glu Val Asp Ser  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Val Val Phe Gln Leu Ala Cys Val Asp Thr  
 180 185 190  
 Tyr Val Leu Gly Leu Phe Met Ile Ser Thr Ser Gly Ile Ile Ala Leu  
 195 200 205  
 Ser Cys Phe Ile Val Leu Phe Asn Ser Tyr Val Ile Val Leu Val Thr  
 210 215 220  
 Val Lys His His Ser Ser Arg Gly Ser Ser Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Thr Ala His Phe Ile Val Val Phe Leu Phe Phe Gly Pro Cys Ile Phe  
 245 250 255  
 Ile Tyr Met Trp Pro Leu Ser Ser Phe Leu Thr Asp Lys Ile Leu Ser  
 260 265 270  
 Val Phe Tyr Thr Ile Phe Thr Pro Thr Leu Asn Pro Ile Ile Tyr Thr

275                      280                      285  
 Leu Arg Asn Gln Glu Val Lys Ile Ala Met Arg Lys Leu Lys Asn Arg  
 290                      295                      300  
 Phe Leu Asn Phe Asn Lys Ala Met Pro Ser  
 305                      310

<210> 1153  
 <211> 310  
 <212> PRT  
 <213> Unknown (H38g70 protein)

<220>  
 <223> Synthetic construct

<400> 1153  
 Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe  
 1                      5                      10                      15  
 Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu  
 20                      25                      30  
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile  
 35                      40                      45  
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His  
 50                      55                      60  
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met  
 65                      70                      75                      80  
 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg  
 85                      90                      95  
 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu  
 100                      105                      110  
 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro  
 115                      120                      125  
 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala  
 130                      135                      140  
 Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val  
 145                      150                      155                      160  
 Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe  
 165                      170                      175  
 Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His  
 180                      185                      190  
 Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly  
 195                      200                      205  
 Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile  
 210                      215                      220  
 Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys  
 225                      230                      235                      240  
 Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile  
 245                      250                      255  
 Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr  
 260                      265                      270  
 Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile  
 275                      280                      285  
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu  
 290                      295                      300  
 Gly Val Glu Arg Ala Leu  
 305                      310

<210> 1154  
 <211> 323  
 <212> PRT  
 <213> Unknown (H38g71 protein)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1154

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Leu Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Ala Val Ser Ser Asp Ser Pro His Thr Pro Val Tyr Phe Phe
          50           55           60
Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Pro Thr Val
65          70          75          80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His
          85          90          95
Ala Gly Cys Leu Ala Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile
          100         105         110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Ser Phe Val Ala Ile
          115         120         125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
          130         135         140
Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
145         150         155         160
His Gly Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile
          165         170         175
Ser Asn Phe Leu Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser
          180         185         190
Asp Ser Val Thr Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe
          195         200         205
Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val
          210         215         220
Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe
225         230         235         240
Thr Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr
          245         250         255
Gly Ile Gly Met Tyr Leu Thr Ser Ala Leu Ser Pro Pro Pro Arg Asn
          260         265         270
Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn
          275         280         285
Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg
          290         295         300
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe
305         310         315         320
Phe Leu Cys

```

&lt;210&gt; 1155

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g72 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1155

Met Ala Trp Ser Asn Gln Ser Ala Val Thr Glu Phe Ile Leu Arg Gly

```

1           5           10           15
Leu Ser Ser Ser Leu Glu Leu Gln Ile Phe Tyr Phe Leu Phe Phe Ser
20           25           30
Ile Val Tyr Ala Ala Thr Val Leu Gly Asn Leu Leu Ile Val Val Thr
35           40           45
Ile Ala Ser Glu Pro His Leu His Ser Pro Thr Tyr Phe Leu Leu Gly
50           55           60
Asn Leu Ser Phe Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys
65           70           75           80
Met Ile Ala Asp Phe Leu Arg Glu His Lys Ala Ile Ser Phe Glu Gly
85           90           95
Cys Met Thr Gln Met Phe Phe Leu His Leu Leu Gly Gly Ala Glu Ile
100          105          110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Lys
115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Arg Arg Met Cys Val Gly Leu
130          135          140
Val Ile Leu Ser Trp Ile Val Gly Ile Phe His Ala Leu Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser
165          170          175          180
Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Val Asp Thr
180          185          190
Tyr Ile Leu Gly Val Phe Met Ile Ser Thr Ser Gly Met Ile Ala Leu
195          200          205
Val Cys Phe Ile Leu Leu Val Ile Ser Tyr Thr Ile Ile Leu Val Thr
210          215          220
Val Arg Gln Arg Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Cys
225          230          235          240
Ser Ala His Phe Thr Val Val Thr Leu Phe Phe Gly Pro Cys Thr Phe
245          250          255
Ile Tyr Val Trp Pro Phe Thr Asn Phe Pro Ile Asp Lys Val Leu Ser
260          265          270
Val Phe Tyr Thr Ile Tyr Thr Pro Leu Leu Asn Pro Val Ile Tyr Thr
275          280          285
Val Arg Asn Lys Asp Val Lys Tyr Ser Met Arg Lys Leu Ser Ser His
290          295          300
Ile Phe Lys Ser Arg Lys Thr Asp His Thr Pro
305          310          315

```

&lt;210&gt; 1156

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g73 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1156

```

Met Lys Lys Tyr Met Glu Arg Thr Asn Xaa Thr Thr Glu Phe Glu Leu
1           5           10           15
Ile Leu Ile Ser Leu Xaa Val Leu Ile Ser Xaa Gln Lys Leu Leu Phe
20           25           30
Val Thr Cys Leu Val Val Tyr Leu Val Thr Leu Leu Gly Asn Arg Ile
35           40           45
Gln Ile Ile Pro Thr Leu Leu Val Ser His Leu Tyr Leu Cys His Gly
50           55           60

```

```

Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro Ser
65          70          75          80
Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr Asp
      85          90          95
Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu Cys
      100        105        110
Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser Lys
      115        120        125
Phe Leu Arg Tyr Pro Leu Ile Asn Lys Val Asn Lys Ile Lys Lys
      130        135        140
Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe Leu
145          150        155        160
Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys Gly
      165        170        175
Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Ala Leu
      180        185        190
Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly Lys
      195        200        205
Val Asn Phe Ser Phe Thr Leu Leu Leu Pro Phe Gln Phe Phe Ile Phe
      210        215        220
Ser Phe Leu Tyr Phe His His Leu Cys Cys Ile Glu Ile Asn Ser Ala
225          230        235        240
Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr Val
      245        250        255
Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser Thr
      260        265        270
Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly Val
      275        280        285
Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met Glu
      290        295        300
Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp Cys
305          310        315        320
Trp

```

&lt;210&gt; 1157

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g74 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1157

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20          25          30
Leu Ser Leu Ser Met Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu
      35          40          45
Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Gln Leu His Thr Pro Met
      50          55          60
Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser
65          70          75          80
Pro Met Val Pro Lys Met Ile Met Asp Met Gln Ser His Ser Arg Val
      85          90          95
Ile Ser His Ala Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe

```

|   |     |     |
|---|-----|-----|
| 100   | 105 | 110 |
| Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe |     |     |
| 115   | 120 | 125 |
| Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His |     |     |
| 130   | 135 | 140 |
| Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp |     |     |
| 145   | 150 | 155 |
| Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Asn Asn |     |     |
| 165   | 170 | 175 |
| Val Glu Ile Ala Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu |     |     |
| 180   | 185 | 190 |
| Asp Cys Ser Asp Thr Val Ile Asn Ser Val Phe Ile Tyr Phe Asp Ser |     |     |
| 195   | 200 | 205 |
| Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys |     |     |
| 210   | 215 | 220 |
| Ile Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys |     |     |
| 225   | 230 | 235 |
| Ala Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp |     |     |
| 245   | 250 | 255 |
| Gly Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro |     |     |
| 260   | 265 | 270 |
| Arg Asn Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met |     |     |
| 275   | 280 | 285 |
| Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala |     |     |
| 290   | 295 | 300 |
| Leu Gln Arg Leu Ser Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro |     |     |
| 305   | 310 | 315 |
| Ser Phe Phe Leu Cys   |     | 320 |
| 325   |     |     |

&lt;210&gt; 1158

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g75 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1158

|   |  |
|---|--|
| Met Gly Asn Trp Thr Ala Ala Val Thr Glu Phe Val Leu Leu Gly Phe |  |
| 1 5 10 15   |  |
| Ser Leu Ser Arg Glu Val Glu Leu Leu Leu Val Leu Leu Leu Pro     |  |
| 20 25 30  |  |
| Thr Phe Leu Leu Thr Leu Leu Gly Asn Leu Leu Ile Ile Ser Thr Val |  |
| 35 40 45  |  |
| Leu Ser Cys Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn |  |
| 50 55 60  |  |
| Leu Ser Ile Leu Asp Ile Leu Phe Thr Ser Val Ile Ser Pro Lys Val |  |
| 65 70 75 80   |  |
| Leu Ala Asn Leu Gly Ser Arg Asp Lys Thr Ile Ser Phe Ala Gly Cys |  |
| 85 90 95  |  |
| Ile Thr Gln Cys Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Leu |  |
| 100 105 110   |  |
| Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Thr Ile Cys Cys Pro |  |
| 115 120 125   |  |
| Leu Arg Tyr Thr Thr Ile Met Arg Pro Ser Val Cys Ile Gly Thr Val |  |
| 130 135 140   |  |
| Val Phe Ser Trp Val Gly Gly Phe Leu Ser Val Leu Phe Pro Thr Ile |  |
| 145 150 155 160   |  |
| Leu Ile Ser Gln Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe |  |
| 165 170 175   |  |

Phe Cys Asp Ser Gly Pro Leu Leu Ala Leu Ala Cys Ala Asp Thr Thr  
 180 185 190  
 Ala Ile Glu Leu Met Asp Phe Met Leu Ser Ser Met Val Ile Leu Cys  
 195 200 205  
 Cys Ile Val Leu Val Ala Tyr Ser Tyr Thr Tyr Ile Ile Leu Thr Ile  
 210 215 220  
 Val Arg Ile Pro Ser Ala Ser Gly Arg Lys Lys Ala Phe Asn Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Thr Ile Val Ile Ile Pro Ser Gly Ile Thr Val Phe  
 245 250 255  
 Ile Tyr Val Thr Pro Ser Gln Lys Glu Tyr Leu Glu Ile Asn Lys Ile  
 260 265 270  
 Pro Leu Val Leu Ser Ser Val Val Thr Pro Phe Leu Asn Pro Phe Ile  
 275 280 285  
 Tyr Thr Val Arg Asn Asp Thr Val Gln Gly Val Leu Arg Asp Val Trp  
 290 295 300  
 Val Arg Val Arg Gly Val Phe Glu Lys Arg Met Arg Ala Val Leu  
 305 310 315

&lt;210&gt; 1159

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g76 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1159

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly  
 1 5 10 15  
 Leu Ser Gln Thr Arg Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu  
 20 25 30  
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr  
 35 40 45  
 Ile Arg Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ala Leu Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Lys  
 65 70 75 80  
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Val Gly Ala Ser Glu Met  
 100 105 110  
 Phe Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ala Thr Ile Met Asn Arg Arg Leu Cys Cys Ile Leu  
 130 135 140  
 Val Ala Leu Ser Trp Met Gly Gly Phe Ile His Ser Ile Ile Gln Val  
 145 150 155 160  
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser  
 165 170 175  
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr  
 180 185 190  
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val  
 195 200 205  
 Val Trp Phe Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu  
 210 215 220  
 Leu Lys Lys His Ser Gly Ser Asp Glu Asn Thr Asn Arg Ala Met Ser  
 225 230 235 240  
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser  
 245 250 255  
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 260 |     | 265 |     | 270 |     |     |     |     |     |     |     |     |     |     |
| Val | Ser | Val | Phe | His | Thr | Val | Ile | Phe | Pro | Leu | Leu | Asn | Pro | Ile | Ile |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Tyr | Thr | Leu | Arg | Asn | Lys | Glu | Val | Lys | Ala | Ala | Met | Arg | Lys | Val | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Lys | Tyr | Ile | Leu | Cys | Glu | Glu | Lys |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 1160

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g77 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1160

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Gln | Arg | Asn | Ile | Xaa | Lys | Phe | Ile | Leu | Met | Ser | Leu | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ile | Gln | Asn | Ile | Gln | Ile | Phe | Val | Phe | Val | Phe | Leu | Phe | Cys | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Val | Ala | Ile | Leu | Val | Gly | Asn | Phe | Leu | Ile | Leu | Ile | Ser | Ile | Xaa | Cys |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Pro | Leu | Phe | Asn | Gln | Pro | Met | His | Tyr | Phe | Leu | Gly | Tyr | Met | Asn |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ile | Tyr | Tyr | Thr | Ser | Cys | Val | Thr | Pro | Lys | Ile | Ile | Gly | Asp | Leu | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Gly | Arg | Ile | Asn | Ile | Ser | Tyr | Asp | Arg | Ile | Phe | Pro | Met | His | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Gly | Ile | Ile | Glu | Ile | Phe | Ile | Leu | Thr | Val | Met | Ala | Phe | Asp | His |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Tyr | Val | Ala | Ile | Cys | Lys | Pro | Pro | Arg | Tyr | Leu | Ile | Ile | Met | Asn | Arg |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Thr | Lys | Tyr | Asn | Thr | Leu | Ile | Ser | Val | Ala | Trp | Leu | Leu | Gly | Leu | Ile |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| His | Ser | Leu | Phe | Gln | Phe | Ser | Met | Lys | Ile | Trp | Leu | Pro | Phe | Cys | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Asn | Lys | Val | Asp | Asp | Xaa | Tyr | Xaa | Asp | Ile | Phe | Pro | Leu | Leu | Lys |
|     |     |     | 165 |     |     | 170 |     |     |     |     |     |     |     | 175 |     |
| Val | Ala | Cys | Thr | Asp | Thr | Cys | Ile | Thr | Gly | Val | Leu | Val | Val | Ala | Asn |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| Ser | Gly | Met | Phe | Ala | Leu | Val | Thr | Phe | Val | Leu | Ser | Phe | Gly | Ser | Tyr |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Val | Ile | Ile | Leu | Phe | Pro | Leu | Lys | Asn | His | Ser | Val | Glu | Gly | Arg | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Ala | Leu | Ser | Thr | Cys | Gly | Ser | His | Ile | Thr | Met | Val | Ile | Phe | Phe |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Phe | Glu | Pro | Ser | Ile | Phe | Ala | Tyr | Leu | Arg | Pro | Ser | Thr | Phe | Pro | Glu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Asp | Lys | Ile | Ser | Ala | Leu | Phe | Tyr | Thr | Ile | Ile | Ala | Pro | Met | Phe | Asn |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| His | Leu | Ile | Tyr | Asn | Leu | Arg | Asn | Thr | Glu | Met | Lys | Lys | Ala | Met | Arg |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Lys | Val | Trp | Tyr | Gln | Ile | Ser | Phe | Ser | Glu | Glu | Lys | Gln | Leu | Ile | Cys |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Pro | Thr | Xaa | Cys | Thr | Lys | Glu | Leu | Tyr |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

<210> 1161  
 <211> 304  
 <212> PRT  
 <213> Unknown (H38g78 protein)

<220>  
 <223> Synthetic construct

<400> 1161  
 Met Arg Asn Gly Thr Val Ile Thr Glu Phe Ile Leu Leu Gly Phe Pro  
 1 5 10 15  
 Val Ile Gln Gly Leu Gln Thr Pro Leu Phe Ile Ala Ile Phe Leu Thr  
 20 25 30  
 Tyr Ile Leu Thr Leu Ala Gly Asn Gly Leu Ile Ile Ala Thr Val Trp  
 35 40 45  
 Ala Glu Pro Arg Leu Gln Ile Pro Met Tyr Phe Phe Leu Cys Asn Leu  
 50 55 60  
 Ser Phe Leu Glu Ile Trp Tyr Thr Thr Thr Val Ile Pro Lys Leu Leu  
 65 70 75 80  
 Gly Thr Phe Val Val Ala Arg Thr Val Ile Cys Met Ser Cys Cys Leu  
 85 90 95  
 Leu Gln Ala Phe Phe His Phe Phe Val Gly Thr Thr Glu Phe Leu Ile  
 100 105 110  
 Leu Thr Ile Met Ser Phe Asp Arg Tyr Leu Thr Ile Cys Asn Pro Leu  
 115 120 125  
 His His Pro Thr Ile Met Thr Ser Lys Leu Cys Leu Gln Leu Ala Leu  
 130 135 140  
 Ser Ser Trp Val Val Gly Phe Thr Ile Val Phe Cys Gln Thr Met Leu  
 145 150 155 160  
 Leu Ile Gln Leu Pro Phe Cys Gly Asn Asn Val Ile Ser His Phe Tyr  
 165 170 175  
 Cys Asp Val Gly Pro Ser Leu Lys Ala Ala Cys Ile Asp Thr Ser Ile  
 180 185 190  
 Leu Glu Leu Leu Gly Val Ile Ala Thr Ile Leu Val Ile Pro Gly Ser  
 195 200 205  
 Leu Leu Phe Asn Met Ile Ser Tyr Ile Tyr Ile Leu Ser Ala Ile Leu  
 210 215 220  
 Arg Ile Pro Ser Ala Thr Gly His Gln Lys Thr Phe Ser Thr Cys Ala  
 225 230 235 240  
 Ser His Leu Thr Val Val Ser Leu Leu Tyr Gly Ala Val Leu Phe Met  
 245 250 255  
 Tyr Leu Arg Pro Thr Ala His Ser Ser Phe Lys Ile Asn Lys Val Val  
 260 265 270  
 Ser Val Leu Asn Thr Ile Leu Thr Pro Leu Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Thr Ile Arg Asn Lys Glu Val Lys Gly Ala Leu Arg Lys Ala Met Thr  
 290 295 300

<210> 1162  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g79 protein)

<220>  
 <223> Synthetic construct

<400> 1162  
 Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu  
 1 5 10 15  
 Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro

```

      20      25      30
Phe Cys Phe Ile Tyr Leu Thr Val Ile Leu Gly Asn Leu Thr Ile Leu
      35      40      45
His Val Ile Cys Thr Asp Ala Thr Leu His Gly Pro Met Tyr Tyr Phe
      50      55      60
Leu Gly Met Leu Ala Val Thr Asp Leu Gly Leu Cys Leu Ser Thr Leu
      65      70      75      80
Pro Thr Val Leu Gly Ile Phe Trp Phe Asp Thr Arg Glu Ile Gly Ile
      85      90      95
Pro Ala Cys Phe Thr Gln Leu Phe Phe Ile His Thr Leu Ser Ser Met
      100      105      110
Glu Ser Ser Val Leu Leu Ser Met Ser Ile Asp Arg Tyr Val Ala Val
      115      120      125
Cys Asn Pro Leu His Asp Ser Thr Val Leu Thr Pro Ala Cys Ile Val
      130      135      140
Lys Met Gly Leu Ser Ser Val Leu Arg Ser Ala Leu Leu Ile Leu Pro
      145      150      155      160
Leu Pro Phe Leu Leu Lys Arg Phe Gln Tyr Cys His Ser His Val Leu
      165      170      175
Ala His Ala Tyr Cys Leu His Leu Glu Ile Met Lys Leu Ala Cys Ser
      180      185      190
Ser Ile Ile Val Asn His Ile Tyr Gly Leu Phe Val Val Ala Cys Thr
      195      200      205
Val Gly Val Asp Ser Leu Leu Ile Phe Leu Ser Tyr Ala Leu Ile Leu
      210      215      220
Arg Thr Val Leu Ser Ile Ala Ser His Gln Glu Arg Leu Arg Ala Leu
      225      230      235      240
Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe Tyr Ile Pro
      245      250      255
Met Ile Gly Leu Ser Leu Val His Arg Phe Gly Glu His Leu Pro Arg
      260      265      270
Val Val His Leu Phe Met Ser Tyr Val Tyr Leu Leu Val Pro Pro Leu
      275      280      285
Met Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Arg Gln Arg
      290      295      300
Ile Ile Lys Lys Phe Gln Phe Ile Lys Ser Leu Arg Cys Phe Trp Lys
      305      310      315      320
Asp

```

&lt;210&gt; 1163

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g80 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1163

```

Met Gly Asn His Thr Thr Val Thr Glu Phe Val Leu Leu Gly Leu Ser
  1      5      10      15
Glu Thr Cys Glu Leu Gln Met Leu Ile Phe Leu Gly Leu Leu Leu Thr
      20      25      30
Tyr Leu Leu Thr Leu Leu Gly Asn Leu Val Ile Val Val Ile Thr Leu
      35      40      45
Met Asp Arg Arg Leu His Thr Met Tyr Tyr Phe Leu Arg Asn Phe
      50      55      60

```



```

Ala Val Pro Glu Ile Trp Phe Thr Ser Val Ile Phe Pro Lys Val Leu
65      70      75      80
Ala Asn Ile Leu Thr Gly Tyr Lys Thr Ile Ser Leu Pro Gly Cys Phe
      85      90      95
Leu Gln Ser Leu Leu Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu
      100     105     110
Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Asn Pro Leu
      115     120     125
His Tyr Ala Thr Ile Met Ser Lys Arg Val Cys Val Gln Leu Val Leu
      130     135     140
Cys Xaa Trp Met Thr Gly Phe Leu Leu Ile Ile Ile Pro Ser Phe Leu
145      150     155     160
Val Leu Gln Gln Pro Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe
      165     170     175
Cys Asp Asn Phe Pro Leu Leu Lys Leu Ile Cys Ala Asp Met Thr Leu
      180     185     190
Ile Glu Leu Leu Gly Phe Val Ile Ala Asn Val Ser Leu Leu Gly Thr
      195     200     205
Leu Ser Met Thr Ala Thr Cys Tyr Gly His Ile Leu His Ala Ile Leu
      210     215     220
His Ile Pro Ser Ala Lys Glu Lys Gln Lys Ala Phe Ser Ala Cys Ser
225      230     235     240
Ser His Ile Ile Val Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met
      245     250     255
Tyr Ile Gln Ser Gly Lys Ser Asp Gln Lys Glu Asp Arg Asn Lys Val
      260     265     270
Ala Ala Leu Leu Asn Thr Val Val Thr Leu Met Leu Asn Pro Phe Ile
      275     280     285
Tyr Thr Leu Arg Asn Lys Gln Val Lys Gln Val Phe Arg Gln Gln Val
      290     295     300
Ser Lys Leu Leu Ile Xaa Ser Cys Val Lys Lys Lys Leu Lys Leu Ser
305      310     315     320
Ile Pro Arg

```

&lt;210&gt; 1164

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g81 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1164

```

Glu Ile Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu
1      5      10      15
Gly Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile
      20      25      30
Leu Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe
      35      40      45
Thr Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu
      50      55      60
Gly Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro
65      70      75      80
Arg Met Leu Val Asp Phe Leu Ser Ala Lys Asn Val Ile Ser Tyr Arg
      85      90      95
Gly Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu
      100     105     110
Gly Leu Leu Leu Val Ile Val Ala Phe Asp Arg Tyr Ile Ala Ile Cys
      115     120     125
Arg Pro Leu His Tyr Ser Thr Leu Met Asn Pro Arg Ala Cys Tyr Ala

```

```

      130              135              140
Met Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln
145              150              155
Val Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp
      165              170              175
Asn Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp
      180              185              190
Thr Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr
      195              200              205
Leu Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys
      210              215              220
His Val Arg Lys Ala Ala Ser Glu Leu Lys Asn Lys Ala Met Ser Thr
225              230              235
Cys Thr Thr His Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile
      245              250              255
Phe Ile Tyr Met His Pro Phe Arg Ala Leu Pro Ala Asp Lys Val Val
      260              265              270
Ser Phe Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr
      275              280              285
Thr Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser
      290              295              300
Arg His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
305              310              315

```

&lt;210&gt; 1165

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g82 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(287)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1165

```

Val Ile Arg Asn Gln Thr Met Val Thr Glu Phe Thr Leu Val Ser Leu
1      5      10      15
Pro Ala Val Gln Glu Leu Gln Ile Trp Leu Cys Val Leu Leu Trp Leu
      20      25      30
Val His Met Leu Thr Ile Thr Gly Asn Leu Phe Val Ile Phe Leu Thr
      35      40      45
Trp Thr Asp Asn Cys Leu Gln Thr Pro Met Asp Leu Phe Leu Glu Lys
      50      55      60
Lys Val Ile Ser Phe Ser Gly Cys Ile Thr Gln Ile Tyr Phe Tyr Phe
65      70      75      80
Phe Leu Gly Thr Val Ala Phe Ile Pro Leu Ala Val Thr Ser Phe Lys
      85      90      95
His Cys Met Ala Thr Cys Asp Pro Leu Cys Ser Thr Ile Ile Ala Lys
      100      105      110
Ser Arg Ala Cys Leu Leu Leu Ala Leu Gly Cys Trp Met Gly Thr Phe
      115      120      125
Leu Ala Val Leu Arg Leu Thr Ile Val Val Ser Arg Leu Pro Asp Cys
      130      135      140
Thr Glu Lys Ile Ser Pro Phe Phe Cys Asp Ile Ala Ser Leu Leu Gln
145      150      155      160
Val Ala Cys Ile Asp Ile His Phe Ile Glu Met Ile Ser Phe Leu Xaa
      165      170      175
Ser Ser Leu Met Val Leu Thr Ser Leu Val Leu Asn Ala Thr Ser Tyr
      180      185      190

```

Ala Tyr Ile Ile Ser Thr Leu Leu Cys Ile Pro Ser Ala Gln Gly Cys  
 195 200 205  
 Gln Glu Ala Phe Ser Thr Cys Ala Ser His Ile Thr Ile Ile Phe Ile  
 210 215 220  
 Ala Cys Arg Asn Ser Ile Ser Thr Cys Val Arg Pro Asn Pro Arg Tyr  
 225 230 235 240  
 Xaa Leu Asp Phe Asp Lys Val Thr Ala Ile Leu Thr Ile Val Val Thr  
 245 250 255  
 Ser Phe Leu Asn Pro Arg Ile Tyr Ser Leu Arg Xaa Arg Lys Tyr Glu  
 260 265 270  
 Gly Ser Thr Ile Cys Thr Ile Leu Ser Pro His Ser Lys Gly Thr  
 275 280 285

&lt;210&gt; 1166

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g83 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1166

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr Gln Ser Gln Asp Ile Gln Leu Val Phe Val Leu Val Leu  
 20 25 30  
 Ile Phe Tyr Phe Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr  
 35 40 45  
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Thr Val Ala Pro Arg  
 65 70 75 80  
 Met Leu Val Asp Phe Leu Ser Ala Lys Lys Ile Ile Ser Tyr Arg Gly  
 85 90 95  
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly  
 100 105 110  
 Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Val Met Asn Pro Arg Thr Cys Tyr Ala Met  
 130 135 140  
 Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val  
 145 150 155 160  
 Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn  
 165 170 175  
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu  
 195 200 205  
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg  
 210 215 220  
 Ile Arg Gly Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys  
 225 230 235 240  
 Ile Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe  
 245 250 255  
 Ile Tyr Thr Arg Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser  
 260 265 270  
 Leu Phe His Thr Val Ile Phe Pro Leu Leu Asn Pro Val Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys  
 290 295 300  
 His Ile Ala

```

Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
 50          55          60
Ser Leu Ala Phe Val Asp Ala Ser Leu Ser Ser Thr Val Thr Pro Lys
65          70          75          80
Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu
          85          90          95
Cys Met Val Gln Phe Phe Ser Leu Val Thr Thr Val Thr Thr Glu Cys
          100          105          110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile Gln Leu
          130          135          140
Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu
145          150          155          160
Ala Phe Ser Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His
          165          170          175
Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser
          180          185          190
Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ala Gly Ser Val Gln Val
          195          200          205
Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Ile Ile Leu Phe Thr
          210          215          220
Ile Leu Glu Lys Lys Ser Ile Lys Gly Ile Arg Lys Ala Val Ser Thr
225          230          235          240
Cys Gly Ala His Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Thr
          245          250          255
Phe Lys Tyr Leu Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
          260          265          270
Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met
          290          295          300
Phe Lys Ser Asn Val
305

```

&lt;210&gt; 1207

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g124 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(308)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1207

```

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
          20          25          30
Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr Ala
          35          40          45
Ser Pro Ser Leu Arg Ser Pro Met Xaa Phe Phe Leu Ala Tyr Leu Ser
          50          55          60
Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Val Ser Lys Leu Ile Thr
65          70          75          80
Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr
          85          90          95
Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu Leu

```

305

&lt;210&gt; 1167

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g84 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1167

```

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1           5           10           15
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met
 20           25           30
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile
 35           40           45
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu
 50           55           60
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile
 65           70           75           80
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu
 85           90           95
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu
 100          105          110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115          120          125
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly
 130          135          140
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe
 145          150          155          160
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile
 165          170          175
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile
 180          185          190
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile
 195          200          205
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys
 210          215          220
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
 225          230          235          240
His Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245          250          255
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser
 260          265          270
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275          280          285
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu
 290          295          300
Ala Leu Ala Gly Lys
305

```

&lt;210&gt; 1168

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g85 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1168

```

Val Glu Asp Met Val Pro Phe Ser Met Arg Ile Ser Gly Ile Phe Gln
 1          5          10          15
Ile Phe Phe Tyr Gly Tyr His His Leu Ile Tyr Xaa Tyr Ser Val Leu
 20          25          30
Thr Cys Val Pro Phe Gln Phe Thr Tyr Ser His Ile Val Lys Cys Xaa
 35          40          45
Leu Gln Gly Asn Leu Pro Gln Thr Gln Thr Ile Asn Val Thr Ser Glu
 50          55          60
Thr Ile Trp Ile Lys Ile Ile His Asp Phe Leu His Glu Pro Lys Thr
 65          70          75          80
Ile Ser Phe Glu Gly Cys Met Ala Gln Ile Phe Leu Phe His Val Phe
 85          90          95
Ala Gly Gly Glu Met Val Leu Leu Val Ala Met Ala Tyr Asp Ile Tyr
 100         105         110
Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Asn Leu Cys
 115         120         125
Thr Cys Thr Gly Leu Val Val Gly Ser Trp Val Thr Gly Val Met His
 130         135         140
Ser Leu Ser Gln Leu Ala Phe Thr Val Ser Leu Pro Phe Cys Gly Pro
 145         150         155         160
Asn Ile Val Asp Ser Tyr Tyr Cys Asp Leu Thr Leu Val Ile Lys Leu
 165         170         175
Ala Cys Thr Asp Thr Tyr Ile Pro Glu Ala Leu Met Leu Leu Asp Ser
 180         185         190
Gly Leu Met Gly Val Thr Ser Phe Leu Leu Leu Ile Ser Tyr Thr
 195         200         205
Val Ile Leu Ile Thr Val Gln Arg Pro Ser Ser Ala Gly Met Ala Lys
 210         215         220
Ala Arg Ser Thr Leu Thr Ala His Val Thr Val Val Thr Leu Phe Phe
 225         230         235         240
Gly Pro Cys Ile Phe Ile Tyr Ala Trp Pro Phe Ser Asn Leu Pro Val
 245         250         255
Asp Asn Ile Leu Ser Val Phe Ser Thr Val Phe Thr Pro Ile Leu Asn
 260         265         270
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala Ile His
 275         280         285
Asn Leu Lys Thr Gln Tyr Val Thr Ser Arg Leu Ser Ser Gln Leu Ser
 290         295         300
Leu Ile Gly Leu Asp Leu Leu
 305         310

```

&lt;210&gt; 1169

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g86 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(210)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1169

```

Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr
 1          5          10          15
Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu

```

```

      20      25      30
Gly His Ser Val Leu Gly Leu Ser Leu Leu Asn Ile His Gly Glu
      35      40      45
Leu Val Phe Ser Leu Phe Ser Phe Val Phe Val Phe Gln Met Ser Tyr
      50      55      60
Ser Phe Val Ile Leu Ile Lys Met Ile Met Asn Ser Ile Ser Glu Arg
      65      70      75      80
Tyr Ile Thr Thr Asn Leu Lys Cys Lys Thr Ser Ala Leu Val Phe Ile
      85      90      95
Cys Phe Ala Ile Ser Glu Thr Leu Ile Leu Leu Ala Trp Gly His Cys
      100      105      110
Gly Ile Cys Val Pro Gln Val Cys Ser Leu Thr Met Leu Gly Leu His
      115      120      125
Gly Val Gly Ile Asp Gly Val Met Ala His Pro Glu Ala Met Val Ser
      130      135      140
Leu Ser Phe Cys Asp Arg Ser Ile Ile Asn His Cys Val Trp His Thr
      145      150      155      160
Ser Phe His Gln Thr Leu Leu Arg Ala Pro Ala Ser Gln Ala Gly Asp
      165      170      175
Phe Val Val Ile Ala Xaa Xaa Leu Ile Ile Phe Ile Ser Asp Ile Leu
      180      185      190
Ile Leu Ser Thr Ile Leu His Phe Leu Phe Pro Glu Ala Asn Ser Lys
      195      200      205
Ala Phe
      210

```

&lt;210&gt; 1170

&lt;211&gt; 274

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g87 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1170

```

Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile Asn Pro Lys Leu
1      5      10      15
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Val Asp Phe
      20      25      30
Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu Asn Leu Val Val
      35      40      45
Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met Gln Phe Phe Phe
      50      55      60
Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu Ala Ala Met Ala
      65      70      75      80
Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala
      85      90      95
Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala Ser Tyr Ser Trp
      100      105      110
Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu Leu Thr Leu Ser
      115      120      125
Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys Glu His Ala Ala
      130      135      140
Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser Gln Lys Val Ile
      145      150      155      160
Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Ile Leu
      165      170      175
Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr
      180      185      190
Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala
      195      200      205

```

Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn  
 210 215 220  
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr  
 225 230 235 240  
 Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys  
 245 250 255  
 Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr Lys Leu Leu Cys  
 260 265 270  
 His Lys

<210> 1171

<211> 348

<212> PRT

<213> Unknown (H38g88 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400> 1171

Met Thr Asn Ser Ser Val Lys Gly Asp Phe Ile Leu Val Gly Phe Ser  
 1 5 10 15  
 His Gln Pro His Leu Glu Lys Ile Leu Phe Val Ala Val Leu Ile Ser  
 20 25 30  
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Val Ile Ile Leu Ile Cys Ser  
 35 40 45  
 Val Asp Pro Lys Leu Lys Thr Pro Met Tyr Phe Phe Leu Ser His Leu  
 50 55 60  
 Ser Leu Val Asp Ile Cys Phe Thr Thr Ser Ile Val Pro Gln Leu Leu  
 65 70 75 80  
 Trp Asn Leu Lys Gly Pro Asp Lys Thr Ile Thr Phe Leu Gly Cys Val  
 85 90 95  
 Ile Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys Val Leu  
 100 105 110  
 Leu Ala Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu  
 115 120 125  
 His Tyr Thr Ala Val Met Asn Pro Gln Leu Cys Gln Val Leu Ala Gly  
 130 135 140  
 Val Ala Trp Leu Ser Gly Val Gly Asn Thr Leu Ile Gln Gly Thr Val  
 145 150 155 160  
 Thr Leu Trp Leu Pro Arg Cys Gly His Arg Leu Leu Gln His Phe Phe  
 165 170 175  
 Cys Glu Val Pro Ser Met Ile Lys Leu Ala Cys Val Asp Ile His Asp  
 180 185 190  
 Asn Glu Val Gln Leu Phe Val Ala Ser Leu Val Leu Leu Leu Leu Pro  
 195 200 205  
 Leu Val Leu Ile Leu Leu Ser Tyr Gly His Ile Ala Lys Val Val Ile  
 210 215 220  
 Arg Ile Lys Ser Val Gln Ala Trp Cys Lys Gly Leu Gly Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Ile Val Val Ser Leu Phe Cys Gly Thr Ile Thr Ala Val  
 245 250 255  
 Tyr Ile Gln Ser Asn Ser Ser Tyr Ala His Ala His Gly Lys Phe Ile  
 260 265 270  
 Ser Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Thr Leu Arg Asn Asn Asp Val Lys Gly Ala Leu Arg Leu Phe Asn Arg



|   |     |     |
|---|-----|-----|
| 290   | 295 | 300 |
| Asp Leu Gly Thr Xaa Lys Met Lys Gln Ser Thr Gln Arg Ser Thr Phe |     |     |
| 305   | 310 | 315 |
| Phe Thr Lys Gln Leu Xaa Arg Ser Tyr Leu Tyr Asn Phe Ser Leu Lys |     |     |
|   | 325 | 330 |
| Asn Phe Ala Ser Leu Xaa Arg Lys Arg Cys Asn Leu                 |     | 335 |
| 340   | 345 |     |

&lt;210&gt; 1172

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g89 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1172

|   |     |
|---|-----|
| Met Asp Lys Ser Asn Ser Ser Val Val Ser Glu Phe Val Leu Leu Gly |     |
| 1   | 5   |
| Leu Cys Ser Ser Gln Lys Leu Gln Leu Phe Tyr Phe Cys Phe Phe Ser |     |
|   | 20  |
| Val Leu Tyr Thr Val Ile Val Leu Gly Asn Leu Leu Ile Ile Leu Thr |     |
|   | 35  |
| Val Thr Ser Asp Thr Ser Leu His Ser Pro Met Tyr Phe Leu Leu Gly |     |
|   | 50  |
| Asn Leu Ser Phe Val Asp Ile Cys Gln Ala Ser Phe Ala Thr Pro Lys |     |
|   | 65  |
| Met Ile Ala Asp Phe Leu Ser Ala His Glu Thr Ile Ser Phe Ser Gly |     |
|   | 80  |
| Cys Ile Ala Gln Ile Phe Phe Ile His Leu Phe Thr Gly Gly Glu Met |     |
|   | 100 |
| Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys |     |
|   | 115 |
| Pro Leu Tyr Tyr Val Val Ile Met Ser Arg Arg Thr Cys Thr Val Leu |     |
|   | 130 |
| Val Met Ile Ser Trp Ala Val Ser Leu Val His Thr Leu Ser Gln Leu |     |
|   | 145 |
| Ser Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Val Val Asp Ser |     |
|   | 160 |
| Phe Phe Cys Asp Leu Pro Arg Val Thr Lys Leu Ala Cys Leu Asp Ser |     |
|   | 175 |
| Tyr Ile Ile Glu Ile Leu Ile Val Val Asn Ser Gly Ile Leu Ser Leu |     |
|   | 190 |
| Ser Thr Phe Ser Leu Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Thr |     |
|   | 205 |
| Val Trp Leu Lys Ser Ser Ala Ala Met Ala Lys Ala Phe Ser Thr Leu |     |
|   | 220 |
| Ala Ser His Ile Ala Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe |     |
|   | 235 |
| Ile Tyr Val Trp Pro Phe Thr Ile Ser Pro Leu Asp Lys Phe Leu Ala |     |
|   | 250 |
| Ile Phe Tyr Thr Val Phe Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr |     |
|   | 265 |
| Leu Arg Asn Arg Asp Met Lys Ala Ala Val Arg Lys Ile Val Asn His |     |
|   | 280 |
| Tyr Leu Arg Pro Arg Arg Ile Ser Glu Met Ser Leu Val Val Arg     |     |
|   | 295 |
| 305   | 310 |
|   | 315 |

&lt;210&gt; 1173

&lt;211&gt; 312

&lt;212&gt; PRT

<213> Unknown (H38g90 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1173

```

Met Pro Ala Lys Asn Ser Ser Ser Val Thr Ala Phe Ile Leu Ser Gly
 1          5          10          15
Leu Thr Asp Gln Pro Gly Leu Gln Ile Pro Ala Phe Phe Leu Phe Leu
          20          25          30
Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu
          35          40          45
Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe
          50          55          60
Asn Leu Ser Phe Ile Asp Phe Ser Tyr Ser Thr Thr Leu Ala Pro Lys
          65          70          75          80
Met Leu Met Ser Phe Val Ser Glu Asn Ile Ile Ser Tyr Ala Gly Cys
          85          90          95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser Tyr
          100          105          110
Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Gly Ile Cys Asn Pro
          115          120          125
Leu Leu Tyr Thr Val Thr Met Ser Pro Gln Met Cys Leu Leu Leu Leu
          130          135          140
Leu Gly Val Tyr Gly Met Gly Tyr Phe Gly Ala Val Ala His Met Gly
          145          150          155          160
Asn Ile Met Phe Met Ser Phe Cys Gly Asp Asn Leu Val Asn His Tyr
          165          170          175
Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr
          180          185          190
Ile Asn Leu Leu Val Val Phe Ile Ile Val Thr Val Gly Ile Gly Val
          195          200          205
Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly Phe Ile Leu Ser Ser Ile
          210          215          220
Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
          225          230          235          240
Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe
          245          250          255
Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys Val
          260          265          270
Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met Phe Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Arg Thr Phe
          290          295          300
Cys Arg Lys Leu Val Ser Xaa Lys
          305          310

```

<210> 1174

<211> 357

<212> PRT

<213> Unknown (H38g91 protein)

<220>

<223> Synthetic construct

<400> 1174

Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu Val

```

1           5           10           15
Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe Leu
20           25           30
Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
35           40           45
Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50           55           60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
65           70           75           80
Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly Gly
85           90           95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys
100           105           110
Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys Arg
115           120           125
Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln Leu
130           135           140
Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
145           150           155           160
Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp His
165           170           175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
180           185           190
Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val Leu Phe Leu Leu
195           200           205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
210           215           220
Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly Thr
225           230           235           240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
245           250           255
Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
260           265           270
Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
275           280           285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg Leu
290           295           300
Val Ala Lys Ser Leu Leu Asn Gln Glu Ile Arg Asn Met Gln Met Ile
305           310           315           320
Ser Phe Ala Lys Asp Thr Val Leu Thr Tyr Leu Thr Asn Phe Ser Ala
325           330           335
Ser Cys Pro Ile Phe Val Ile Thr Ile Glu Asn Tyr Cys Asn Leu Pro
340           345           350
Gln Arg Lys Phe Pro
355

```

&lt;210&gt; 1175

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g92 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1175

```

His Thr Glu Pro Arg Asn Leu Thr Gly Ala Xaa Glu Leu Leu Leu Leu
1           5           10           15

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser  
 20 25 30  
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ser Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Arg Ser His Ser Gly Val Ile Ser Tyr Ala  
 85 90 95  
 Asp Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Val Glu  
 100 105 110  
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe  
 130 135 140  
 Leu Val Ser Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu Arg  
 145 150 155 160  
 Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Val Cys Asp Pro Ser Gln Pro Leu Lys Leu Ala Cys Ser Asp  
 180 185 190  
 Ser Ile Ile Asp Ser Met Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly  
 195 200 205  
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro  
 210 215 220  
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Xaa Tyr Lys Ala Phe Ser  
 225 230 235 240  
 Ala Cys Gly Ser His Leu Pro Val Val Cys Leu Phe Tyr Gly Thr Gly  
 245 250 255  
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly  
 260 265 270  
 Val Val Ala Ser Val Thr Tyr Ala Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg  
 290 295 300  
 Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His Pro Phe Ser  
 305 310 315 320

&lt;210&gt; 1176

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g93 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1176

Met Glu Gly Phe Asn Cys Ser Arg Val Ser Glu Phe Met Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Ser Pro Glu Leu Gln Arg Phe Phe Phe Val Val Phe Ser  
 20 25 30  
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr  
 35 40 45  
 Val Leu Ser Thr Ser His Leu His Ser Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Asn Leu Ser Leu Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys

```

65      70      75      80
Met Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly
      85      90      95
Cys Ile Ser Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
      100     105     110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
      115     120     125
Pro Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu
      130     135     140
Val Ala Val Ser Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145      150     155     160
Ala Phe Thr Leu Tyr Leu Pro Phe Cys Gly Pro Asn Val Glu Ser Phe
      165     170     175
Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Met Asp Ile Tyr
      180     185     190
Val Leu Gly Ile Phe Met Ile Ser Thr Ser Gly Val Ile Ala Leu Ile
      195     200     205
Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Ile Thr Val
      210     215     220
Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys Thr
225      230     235     240
Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe Ile
      245     250     255
Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser Val
      260     265     270
Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu
      275     280     285
Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Xaa Leu Asn Ile Gln
290      295     300
Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305      310

```

&lt;210&gt; 1177

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g94 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(338)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1177

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
1      5      10      15
Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro
      20      25      30
Gln Leu Glu His Ile Ile Ser Val Val Val Phe Ile Ile Tyr Ile Val
      35      40      45
Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr
50      55      60
Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
65      70      75      80
Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln
      85      90      95
Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe
      100     105     110
Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Leu Ala Val
115      120     125

```

Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr  
 130 135 140  
 Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala  
 145 150 155 160  
 Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly  
 165 170 175  
 His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys  
 180 185 190  
 Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe  
 195 200 205  
 Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr  
 210 215 220  
 Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu  
 225 230 235 240  
 Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu  
 245 250 255  
 Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile  
 260 265 270  
 Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro  
 275 280 285  
 Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser  
 290 295 300  
 Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ser Ala Glu Xaa Met  
 305 310 315 320  
 Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala  
 325 330 335  
 Phe Ile

&lt;210&gt; 1178

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g95 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1178

Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly  
 1 5 10 15  
 Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu  
 20 25 30  
 Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Thr Val Pro Lys  
 65 70 75 80  
 Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly  
 85 90 95  
 Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn  
 100 105 110  
 Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Thr Val Val Val Leu Ser Pro Lys Asn Cys Ala Leu  
 130 135 140  
 Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His

```

145          150          155          160
Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Phe Tyr
          165          170          175
Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
          180          185          190
Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Phe
          195          200          205
Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
          210          215          220
Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
225          230          235          240
Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
          245          250          255
Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
          260          265          270
Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
          275          280          285
Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
          290          295          300
Ser Arg Gln Gly Phe Ser Gly Val Val Ser
305          310

```

&lt;210&gt; 1179

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g96 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1179

```

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
 1          5          10          15
Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu
          20          25          30
Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu
          35          40          45
Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser
          50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
          65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
          85          90          95
Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
          100          105          110
Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu
          130          135          140
Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His
          165          170          175
Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr
          180          185          190
Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val
          195          200          205
Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr
          210          215          220
Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr
225          230          235          240

```

Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile  
 245 250 255  
 Gly Leu Tyr Leu Cys Pro Leu Thr Asn His Asn Thr Val Lys Asp Thr  
 260 265 270  
 Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Asn Pro Gly Gln Ser  
 290 295 300  
 Leu Gln His Lys Glu Asn Phe Phe Val Phe  
 305 310

<210> 1180

<211> 331

<212> PRT

<213> Unknown (H38g97 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1180

Met Ala Ala Glu Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Ala Gly  
 1 5 10 15  
 Leu Ile His Gln Pro Gly Leu Gln Val Pro Val Phe Phe Leu Phe Leu  
 20 25 30  
 Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu  
 35 40 45  
 Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe  
 50 55 60  
 Asn Leu Ser Leu Val Asp Phe Ser Phe Ser Thr Thr Ile Ile Pro Lys  
 65 70 75 80  
 Met Leu Met Ser Phe Val Ser Arg Lys Asn Ile Ile Ser Phe Thr Gly  
 85 90 95  
 Cys Met Ser Gln Phe Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser  
 100 105 110  
 Phe Ile Leu Ser Ala Met Val Xaa Asp Arg Tyr Val Gly Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Ile Thr Met Ser Pro Gln Val Cys Leu Leu Leu  
 130 135 140  
 Leu Leu Gly Val Tyr Gly Met Gly Val Phe Gly Ala Val Ala His Thr  
 145 150 155 160  
 Gly Asn Ile Val Phe Leu Thr Phe Cys Ala Asp Asn Leu Val Asn His  
 165 170 175  
 Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Gly Ser  
 180 185 190  
 Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val Thr Val Gly Ile Gly  
 195 200 205  
 Val Pro Ile Val Ala Val Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser  
 210 215 220  
 Ile Leu Arg Val Ser Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Ser  
 225 230 235 240  
 Cys Ser Ser Tyr Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala  
 245 250 255  
 Phe Thr Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys  
 260 265 270  
 Val Ser Ser Leu Phe Tyr Thr Thr Val Val Pro Met Phe Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Arg Thr



290                      295                      300  
 Phe Ser Arg Ile Ser Phe Ser Glu Lys Asn Phe Arg Asn Arg Lys Glu  
 305                      310                      315                      320  
 Ile Leu Gly Phe Phe Xaa Asn Gln Ile Ala Phe  
                     325                      330

<210> 1181  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g98 protein)

<220>  
 <223> Synthetic construct

<400> 1181  
 Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu  
 1                      5                      10                      15  
 Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu  
                     20                      25                      30  
 Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu  
                     35                      40                      45  
 Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met  
                     50                      55                      60  
 Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser  
 65                      70                      75                      80  
 Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met  
                     85                      90                      95  
 Ile Ser Leu Ser Glu Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly  
                     100                      105                      110  
 Gly Thr Thr Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr  
                     115                      120                      125  
 Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser  
                     130                      135                      140  
 Leu Cys Ile Arg Leu Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His  
 145                      150                      155                      160  
 Ala Leu Ile His Glu Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser  
                     165                      170                      175  
 Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile  
                     180                      185                      190  
 Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser  
                     195                      200                      205  
 Gly Ser Ile Gln Val Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr  
                     210                      215                      220  
 Phe Ala Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg  
 225                      230                      235                      240  
 Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr  
                     245                      250                      255  
 Tyr Gly Pro Leu Ile Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala  
                     260                      265                      270  
 Asp Asp Gln Asp Met Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro  
                     275                      280                      285  
 Leu Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp  
                     290                      295                      300  
 Ser Phe Thr Lys Met Val Lys Arg Asn Val  
 305                      310

<210> 1182  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g99 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct.

&lt;400&gt; 1182

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1           5           10           15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
 20           25           30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
 35           40           45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
 65           70           75           80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
 85           90           95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
 100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
 115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
 130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
 145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
 165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
 180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
 195          200          205
Ile Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr
 210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
 225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
 245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
 260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
 290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
305          310

```

&lt;210&gt; 1183

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g100 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1183

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu

```

```

      20      25      30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val
      35      40      45
Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly
      50      55      60
Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys
      65      70      75      80
Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Val Ser Leu Pro Glu
      85      90      95
Ser Lys Ile Gln Phe Phe Ser Phe Ala Ile Ser Val Thr Thr Glu Cys
      100      105      110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115      120      125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys Ile Arg Leu
      130      135      140
Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Gly Phe Leu Phe Arg
      145      150      155      160
Leu Thr Phe Cys Asn Ser Asn Val Val His His Ile Tyr Cys Asp Ile
      165      170      175
Ile Pro Leu Ser Lys Ile Ser Cys Thr Asp Ser Ser Ile Asn Phe Leu
      180      185      190
Met Val Phe Ile Phe Ser Gly Ser Ile Gln Val Phe Thr Ile Gly Thr
      195      200      205
Gly Leu Ile Ser Tyr Thr Phe Val Leu Phe Thr Ile Leu Lys Lys Lys
      210      215      220
Ser Val Lys Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ala His Leu
      225      230      235      240
Leu Ser Val Ser Leu Tyr His Gly Pro Leu Asp Phe Met Tyr Met Gly
      245      250      255
Ser Ala Ser Pro Gln Ala Asp Asp Glu Asp Met Met Glu Ser Leu Phe
      260      265      270
Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met Thr Tyr Ser Leu Arg
      275      280      285
Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met Phe Lys Arg Asn Asn
      290      295      300
Ile Xaa Ile Ser Tyr Ser
      305      310

```

&lt;210&gt; 1184

&lt;211&gt; 231

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g101 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(231)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1184

```

Phe Cys Leu Phe Pro Ala Thr Val Ser Lys Ala Val Val Lys Phe Leu
1      5      10      15
Ala Glu Thr Ile Ser Phe Ser Tyr Tyr Val Ile Gln Met Leu Val Phe
      20      25      30
Leu Phe Phe Val Thr Thr Glu Cys Asn Leu Leu Ala Ser Leu Gly Lys
      35      40      45
Asp Ile Tyr Met Pro Ile Arg Gln Pro Met Leu Tyr Pro Val Thr Met
      50      55      60
Ser Gln Val Cys Cys Ile Gln Leu Val Ala Ser Cys Tyr Gly His Gly
      65      70      75      80

```

```

Val Ile His Thr Met Phe Leu Gly Gly Ser Ile Ser Ile Phe Ala Phe
      85          90          95
Cys Lys Ser Gln Thr Ile Ile Ser Phe Phe Gly Asp Ser Phe Pro Leu
      100        105        110
Leu Val Leu Ser Cys Ser Asp Thr Tyr Ile Met Asn Ser Leu Phe Phe
      115        120        125
Phe Thr Gly Cys Phe Ile Trp Met Ser Ser Xaa Pro Val Ile Leu Val
      130        135        140
Ser His Met Phe Ile Ile Val Thr Phe Leu Arg Ile Phe Ser Val Val
      145        150        155        160
Val Glu Ser Lys Gly Phe Leu Ala Phe Ser Ser His Leu Thr Ala Ile
      165        170        175
Ile Leu Phe Tyr Gly Asp Ile Met Ser Leu Tyr Met Xaa His Ser Ser
      180        185        190
Asn Tyr Phe Leu Asn Gln Asp Gln Thr Val Ser Ile Phe Tyr Met Val
      195        200        205
Arg Ile Leu Leu Leu Ser Pro Ile Ile Tyr Cys Leu Ile Lys Met Gln
      210        215        220
Val Ile Cys Phe Leu Glu Asn
      225        230

```

<210> 1185  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g102 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(216)  
 <223> Xaa = Any Amino Acid

```

<400> 1185
Leu Phe Phe Phe Val Xaa His Ser Ile Leu Thr Xaa Xaa Glu Gly Val
  1      5      10      15
Lys Glu Ile Trp Tyr Phe Gln Glu Phe Leu Thr Tyr Pro Arg His Arg
      20      25      30
Xaa Leu Leu Phe Val Ser Ser Cys Met Tyr Tyr Ser Ser Arg Ile Phe
      35      40      45
Leu Arg Arg Thr Val Asn Ile Leu Phe Leu Leu Lys Val Ile Ser Leu
      50      55      60
Leu Cys Tyr Gly Ser Lys Leu Ser Leu Phe Ile Phe Val Val Thr Ala
      65      70      75      80
Glu Phe Xaa Leu Leu Ala Ser Arg Ile Cys His Cys Tyr Ile Ile Ile
      85      90      95
Cys Asn Pro Phe Ser Thr Gln Phe Ser His Xaa Lys Leu Leu Ile Ser
      100     105     110
Ile Leu Thr Ala His Tyr Asn Lys Arg Val Cys Ile Ser Ile Thr Thr
      115     120     125
Ser Asn Thr Met Ser Xaa Leu Phe Phe Gly Arg Ser Asn Val Val Asn
      130     135     140
Asn Phe Ser Asp Leu Leu Leu Leu Asp Leu Ser Cys Thr Phe Val
      145     150     155     160
Ser Phe Xaa Ser Pro Ser Gln Leu Pro Asp His Ser Pro Gly Pro His
      165     170     175
Asn Phe Ile Ile Val Val Asn Ile Lys Ile Xaa Leu Ala Glu Gly Lys
      180     185     190
His Lys Asp Phe Ser Ile Cys Pro Leu Xaa Phe Ala Thr Val Ser Asn
      195     200     205
Phe Leu Met Ala His Ile His Ile

```

210

215

<210> 1186  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g103 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(312)  
 <223> Xaa = Any Amino Acid

<400> 1186  
 Phe Met Glu Asn Arg Asn Ile Val Thr Val Phe Ile Leu Leu Gly Leu  
 1 5 10 15  
 Ser Gln Asn Lys Asn Ile Glu Val Phe Trp Phe Val Leu Phe Val Phe  
 20 25 30  
 Cys Tyr Ile Ala Ile Trp Met Glu Asn Phe Ile Ile Met Ile Ser Ile  
 35 40 45  
 Met Tyr Ile Xaa Leu Ile Asp Gln Pro Met Tyr Phe Phe Leu Asn Tyr  
 50 55 60  
 Leu Ala Leu Ser Asp Leu Cys Tyr Ile Ser Thr Val Ala Pro Lys Leu  
 65 70 75 80  
 Met Ile Asp Leu Leu Thr Glu Arg Lys Ile Val Ser Tyr Asn Asn Cys  
 85 90 95  
 Met Ile Gln Leu Phe Ile Thr His Phe Leu Gly Asp Ile Glu Ile Phe  
 100 105 110  
 Ile Leu Lys Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Lys His  
 115 120 125  
 Leu His Tyr Thr Ile Ile Thr Lys Gln Ser Cys Asn Thr Ile Ile  
 130 135 140  
 Ile Ala Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu  
 145 150 155 160  
 Leu Thr Ile Phe Leu Pro Phe Cys Gly Leu Asn Glu Ile Asp Gln Tyr  
 165 170 175  
 Phe Cys Tyr Val Tyr Pro Leu Leu Lys Leu Ala Arg Ile Asp Ile Tyr  
 180 185 190  
 Arg Ile Gly Phe Leu Val Ile Val Asn Ser Gly Leu Ile Ser Leu Leu  
 195 200 205  
 Ala Phe Val Ile Leu Met Val Ser Tyr Tyr Leu Ile Leu Ser Thr Ile  
 210 215 220  
 Arg Val Tyr Ser Ala Glu Ser His Thr Lys Ala Leu Ser Thr Cys Ser  
 225 230 235 240  
 Ser His Ile Ile Val Val Val Leu Phe Phe Val Pro Ala Leu Phe Ile  
 245 250 255  
 Tyr Ile Arg Pro Ala Ile Thr Phe Pro Glu Asp Lys Val Phe Val Leu  
 260 265 270  
 Phe Cys Ala Ile Ile Ala Pro Met Phe Ser Leu Leu Ile Tyr Met Leu  
 275 280 285  
 Arg Lys Val Glu Met Lys Asn Ala Val Arg Lys Met Trp Cys His Gln  
 290 295 300  
 Leu Leu Leu Ala Arg Lys Xaa Leu  
 305 310

<210> 1187  
 <211> 308  
 <212> PRT  
 <213> Unknown (H38g104 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1187

```

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly
 1           5           10           15
Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
          20           25           30
Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
          35           40           45
Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
65           70           75           80
Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
          85           90           95
Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
          100          105          110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
          115          120          125
Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
          130          135          140
Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
145          150          155          160
Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
          165          170          175
Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
          180          185          190
Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
          195          200          205
Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
          210          215          220
Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
          245          250          255
Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
          260          265          270
Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
          290          295          300
Leu Lys Arg Thr
305

```

&lt;210&gt; 1188

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g105 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1188

```

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu

```

```

      20      25      30
Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35      40      45
Val Ser Ser Asp Ser His Leu His Ser Pro Met Xaa Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Val Asp Thr Cys Phe Ile Cys Thr Thr Val Pro Lys
      65      70      75      80
Met Leu Val Asn Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
      85      90      95
Cys Leu Thr Gln Val Tyr Phe Xaa Met Met Phe Ala Gly Met Asp Thr
      100      105      110
Phe Leu Leu Ala Val Ile Ala Tyr Asp Arg Phe Val Ala Ile Cys His
      115      120      125
Pro Leu Gln Tyr Met Val Ile Ile Asn Pro His Leu Cys Gly Leu Leu
      130      135      140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
      145      150      155      160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
      165      170      175
Phe Phe Cys Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Ala
      180      185      190
Leu Leu Ile Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
      195      200      205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
      210      215      220
Leu Met Arg Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
      245      250      255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
      260      265      270
Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg Leu
      290      295      300
Leu Ser Arg Ala Ala Ser Cys Pro Leu Thr Val His Asn Leu Arg Thr
      305      310      315      320
Lys Arg Met Leu

```

&lt;210&gt; 1189

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g106 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1189

```

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
1      5      10      15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
      20      25      30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
      35      40      45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
      50      55      60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
      65      70      75      80
Ile Met Asp Phe Phe Ala Leu Arg Asn Thr Ile Ser Phe Glu Gly Cys
      85      90      95

```

Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val  
 100 105 110  
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro  
 115 120 125  
 Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val  
 130 135 140  
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu  
 145 150 155 160  
 Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile  
 180 185 190  
 Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu  
 195 200 205  
 Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile  
 210 215 220  
 Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe  
 245 250 255  
 Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser  
 260 265 270  
 Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn  
 290

&lt;210&gt; 1190

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g107 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1190

Tyr Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Glu  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp  
 100 105 110  
 Asp Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
 115 120 125  
 His Pro Leu His Tyr Arg Ile Ile Met Asn Pro Arg Leu Cys Gly Phe  
 130 135 140  
 Leu Ile Leu Leu Ser Phe Phe Ile Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Asn Leu Ile Met Leu Gln Leu Thr Cys Phe Lys Asp Val Asp Ile Ser  
 165 170 175  
 Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu His Leu Arg Cys Ser Asp  
 180 185 190  
 Thr Phe Ile Asn Glu Met Val Ile Tyr Phe Met Gly Ala Ile Phe Gly



```

      195              200              205
Cys Leu Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
  210              215              220
Pro Ile Leu Arg Val Pro Thr Ser Asp Gly Lys Tyr Lys Ala Phe Ser
  225              230              235              240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255
Leu Val Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser
      260              265              270
Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Gln Ser Ala Leu Cys Arg
      290              295              300
Leu His Gly Arg Ile Ile Lys Ser His His Leu His Pro Phe Val Ile
  305              310              315              320
Trp Asp Arg Asn Gly Ser Lys Ile
      325

```

&lt;210&gt; 1191

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g108 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1191

```

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
  1              5              10              15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
      20              25              30
Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met
      35              40              45
Ile Leu Leu Val Val Ile Leu Glu Pro Asn Leu His Glu Pro Met Tyr
      50              55              60
Cys Phe Leu Phe Met Leu Ser Ala Ala Asp Leu Gly Leu Thr Leu Ser
      65              70              75              80
Thr Met Pro Thr Thr Leu Ser Val Leu Trp Phe Ser Ala Arg Glu Ile
      85              90              95
Ile Leu Asn Ala Cys Ile Ile Gln Leu Phe Phe Leu His Ser Ser Gly
      100              105              110
Phe Met Glu Ser Ser Val Leu Met Ala Met Ala Phe Asp Arg Phe Val
      115              120              125
Ala Ile Cys Arg Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Ser Arg
      130              135              140
Ile Leu Lys Ile Gly Val Ala Ile Val Leu Arg Thr Leu Ile Ser Leu
      145              150              155              160
Ser Pro Ser Leu Phe Leu Ile Lys Arg Leu Ser Phe Cys Lys Val Asn
      165              170              175
Val Leu Ser His Ser Tyr Cys Phe His Pro Asp Ala Leu Lys Val Ala
      180              185              190
Cys Ser Asp Ser Arg Met Asn Ser Tyr Gly Gly Leu Ala Val Leu Ile
      195              200              205
Leu Val Thr Gly Val Gly Thr Pro Cys Val Ala Leu Ser Tyr Ile Leu
      210              215              220
Ile Ile His Ser Val Leu Asn Ile Ile Ser Ser Glu Gly Arg Arg Lys
      225              230              235              240

```

Ala Phe Asp Thr Cys Gly Ser His Ile Gly Ala Val Ala Val Phe Tyr  
 245 250 255  
 Ile Pro Trp Val Val Leu Ser Val Val His Arg Phe Phe His Lys Ala  
 260 265 270  
 Ser Pro Tyr Val His Pro Leu Leu Ser Asn Ile Tyr Phe Leu Gly Pro  
 275 280 285  
 Ser Arg Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg  
 290 295 300  
 Arg Ala Ile Leu Lys Leu Phe Gln Thr Lys Ser Lys Glu Met Xaa Trp  
 305 310 315 320  
 Gly Leu Phe Phe Leu  
 325

&lt;210&gt; 1192

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g109 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(295)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1192

Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr  
 1 5 10 15  
 Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu  
 20 25 30  
 Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile  
 35 40 45  
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu  
 50 55 60  
 Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu  
 65 70 75 80  
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu  
 85 90 95  
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
 100 105 110  
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile  
 115 120 125  
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe  
 130 135 140  
 Cys Asp Pro Ser Gln His Pro Thr Leu Ala Cys Cys Asp Thr Phe Thr  
 145 150 155 160  
 Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro  
 165 170 175  
 Ile Ser Gly Thr Phe Ser Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu  
 180 185 190  
 Arg Val Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly  
 195 200 205  
 Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly  
 210 215 220  
 Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala  
 225 230 235 240  
 Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr  
 245 250 255  
 Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg  
 260 265 270  
 Ile Val Xaa Ser His Phe Leu Ile Ile Cys Ser Ile Pro Ser Val Val

275 280 285  
 Xaa Val Arg Lys Gly Ser Lys  
 290 295

<210> 1193  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g110 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(320)  
 <223> Xaa = Any Amino Acid

<400> 1193  
 Tyr Thr Asp Ser Gln Asn Leu Thr Gly Val Leu Glu Phe Leu Phe Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Val Gly Leu Phe  
 20 25 30  
 Leu Ser Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Cys Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Leu Thr Ser Ala Thr Ile Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ile Ile Ser Tyr Glu  
 85 90 95  
 Gly Cys Leu Met Gln Met Tyr Phe Ile Tyr Phe Val Cys Met Asn Asp  
 100 105 110  
 Met Val Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu  
 130 135 140  
 Val Leu Val Ser Phe Ile Leu Ser Leu Leu Asn Ser Gln Leu His Asn  
 145 150 155 160  
 Gln Ile Val Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Phe Asn  
 165 170 175  
 Phe Phe Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser  
 180 185 190  
 Val Ile Asn Asn Ile Phe Met Tyr Leu Asp Ser Val Ile Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu  
 245 250 255  
 Gly Ala Tyr Leu Ser Ser Ala Ala Ser Ser Phe Pro Arg Lys Gly Ala  
 260 265 270  
 Val Thr Ser Val Met Tyr Thr Val Ile Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Ala Leu Trp Arg Leu  
 290 295 300  
 His Ser Arg Thr Val Xaa Ser His Tyr Leu Phe His Pro Phe Cys Ser  
 305 310 315 320

<210> 1194  
 <211> 318  
 <212> PRT

<213> Unknown (H38g111 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1194

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Glu | Pro | Gln | Asn | Leu | Thr | Gly | Val | Ser | Glu | Phe | Leu | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Ser | Glu | Asp | Pro | Glu | Leu | Gln | Pro | Leu | Leu | Ala | Gly | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Met | Cys | Leu | Val | Thr | Met | Leu | Gly | Asn | Leu | Leu | Ile | Ile | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Ser | Pro | Asp | Ser | His | Leu | His | Ile | Pro | Met | Tyr | Phe | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asn | Leu | Ser | Leu | Pro | Asp | Ile | Gly | Phe | Thr | Leu | Ala | Thr | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Met | Ile | Val | Asp | Met | Gln | Ser | His | Ser | Arg | Val | Ile | Ser | His | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Cys | Leu | Thr | Gln | Ile | Pro | Phe | Phe | Val | Leu | Phe | Val | Cys | Ile | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Met | Leu | Leu | Thr | Val | Met | Ala | Tyr | Asp | Xaa | Phe | Val | Ala | Ile | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Pro | Leu | His | Tyr | Pro | Val | Ile | Met | Asn | Pro | His | Leu | Cys | Val | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Leu | Val | Leu | Met | Ser | Phe | Ile | Leu | Ser | Leu | Leu | Asp | Ser | Xaa | Leu | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Trp | Ile | Val | Gln | Phe | Thr | Cys | Phe | Lys | Asn | Val | Glu | Ile | Ser | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Phe | Cys | Asp | Xaa | Ser | Gln | Leu | Leu | Asn | Leu | Ala | Cys | Ser | Asp | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ser | Asn | Ile | Phe | Ile | His | Leu | Asp | Ser | Thr | Ile | Phe | Gly | Phe | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Ile | Ser | Gly | Ile | Leu | Leu | Ser | Tyr | Tyr | Lys | Ile | Val | Pro | Ser | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Arg | Ile | Pro | Leu | Ser | Asp | Gly | Lys | Tyr | Lys | Ala | Phe | Ser | Thr | Cys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Ser | His | Leu | Ala | Ile | Val | Cys | Leu | Phe | Tyr | Gly | Thr | Gly | Ile | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met | Tyr | Leu | Thr | Ser | Ala | Val | Ser | Pro | Ala | Pro | Arg | Asn | Gly | Val | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Ser | Val | Leu | Tyr | Ala | Met | Val | Thr | Pro | Met | Leu | Asn | Pro | Phe | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Ser | Leu | Arg | Asn | Arg | Gly | Ile | Gln | Ser | Ala | Leu | Trp | Arg | Leu | Cys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Arg | Lys | Val | Xaa | Ser | His | Asp | Leu | Phe | His | Pro | Phe | Ser |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |

<210> 1195

<211> 350

<212> PRT

<213> Unknown (H38g112 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400> 1195

```

Met Ser Gln Leu Gly Arg Asp Asn Ile Thr Trp Val Ser Glu Phe Ile
 1           5           10           15
Leu Met Gly Leu Ser Ser Asp Arg Gln Thr Gln Ala Gly Leu Phe Ile
           20           25           30
Leu Phe Gly Ala Ala Tyr Leu Leu Thr Leu Leu Gly Asn Gly Leu Ile
           35           40           45
Leu Leu Leu Ile Trp Leu Asp Val Arg Leu His Leu Pro Met Tyr Phe
           50           55           60
Phe Leu Cys Asn Leu Ser Leu Val Asn Ile Cys Tyr Thr Ser Ser Arg
65           70           75           80
Val Pro Gln Met Leu Val His Leu His Gln Gln Arg Lys Thr Ile Ser
           85           90           95
Phe Ala Arg Cys Gly Thr Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly
           100          105          110
Thr Glu Phe Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala
           115          120          125
Val Cys Asp Pro Leu Cys Tyr Ile Ala Val Met Ser Pro Arg Leu Cys
           130          135          140
Met Ala Leu Ala Ala Val Ser Trp Leu Val Gly Leu Ala Asn Ser Ala
145          150          155          160
Met Glu Thr Ala Leu Thr Met His Leu Pro Thr Cys Gly His Asn Val
           165          170          175
Leu Asn His Val Ala Cys Glu Thr Leu Ala Leu Val Arg Ser Ala Cys
           180          185          190
Val Asp Ile Thr Phe Asn Gln Val Val Ile Val Ala Ser Ser Val Val
           195          200          205
Val Leu Leu Val Pro Cys Cys Leu Val Ser Leu Ser Tyr Thr Leu Ile
           210          215          220
Val Val Ala Val Leu Gln Ile His Ser Thr Gln Gly His Arg Lys Ala
225          230          235          240
Phe Gly Thr Cys Ala Ser His Leu Thr Val Val Ser Ile Ser Tyr Gly
           245          250          255
Met Ala Leu Phe Thr Tyr Met Gln Pro Arg Ser Met Ala Ser Ala Glu
           260          265          270
Gln Glu Lys Val Met Val Leu Ser Tyr Ala Val Val Thr Pro Met Leu
           275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu
           290          295          300
Ser Arg Ala Leu Met Arg Ser Ser Glu Leu Lys His Xaa Arg Val Val
305          310          315          320
Xaa Val Thr Arg Arg Pro His Ser Glu Asn Ser Gly His Trp Thr Val
           325          330          335
Leu Ser Ser Ile Thr Cys Val Arg Met Cys Val Tyr Val Cys
           340          345          350

```

<210> 1196

<211> 320

<212> PRT

<213> Unknown (H38g113 protein)

<220>

<223> Synthetic construct

<400> 1196

```

Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln
 1           5           10           15
Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu
           20           25           30

```

Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val  
 35 40 45  
 Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys  
 50 55 60  
 Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg  
 65 70 75 80  
 Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile  
 85 90 95  
 Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly  
 100 105 110  
 Gly Ala Glu Cys Phe Leu Leu Ala Ala Met Ala Asn Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu  
 130 135 140  
 Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser  
 145 150 155 160  
 Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg  
 165 170 175  
 Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala  
 180 185 190  
 Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu  
 195 200 205  
 Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala  
 210 215 220  
 Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys  
 225 230 235 240  
 Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr  
 245 250 255  
 Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro  
 260 265 270  
 Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu  
 275 280 285  
 Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala  
 290 295 300  
 Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly  
 305 310 315 320

&lt;210&gt; 1197

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g114 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1197

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu  
 1 5 10 15  
 Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu  
 20 25 30  
 Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu  
 35 40 45  
 Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe  
 50 55 60  
 Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu  
 65 70 75 80  
 Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala  
 85 90 95  
 Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu  
 100 105 110  
 Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile

|   |     |     |
|---|-----|-----|
| 115   | 120 | 125 |
| Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly |     |     |
| 130   | 135 | 140 |
| Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro |     |     |
| 145   | 150 | 155 |
| Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu |     |     |
|   | 165 | 170 |
| Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr |     |     |
|   | 180 | 185 |
| Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr |     |     |
|   | 195 | 200 |
| Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu |     |     |
|   | 210 | 215 |
| Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu |     |     |
| 225   | 230 | 235 |
| Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro |     |     |
|   | 245 | 250 |
| Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro |     |     |
|   | 260 | 265 |
| Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val |     |     |
|   | 275 | 280 |
| Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly |     |     |
|   | 290 | 295 |
| Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe                     |     |     |
| 305   | 310 | 315 |

&lt;210&gt; 1198

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g115 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(289)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1198

|   |     |     |
|---|-----|-----|
| Phe His Gly Trp Ile Ser Met Pro Phe Cys Cys Ile Tyr Leu Met Pro |     |     |
| 1   | 5   | 10  |
| Leu Leu Ser Asn Ala Thr Ile Leu Leu Thr Ile Trp Ser Asp Arg Thr |     |     |
|   | 20  | 25  |
| Leu Arg Asp Pro Met Phe Tyr Phe Leu Ala Ile Leu Ser Ala Ile Asp |     |     |
|   | 35  | 40  |
| Leu Ala Leu Ser Thr Ser Ser Val Pro Arg Met Leu Gly Ile Phe Trp |     |     |
|   | 50  | 55  |
| Phe Asp Ala His Lys Ile Gly Phe Gly Ala Trp Val Ala Gln Met Phe |     |     |
| 65  | 70  | 75  |
| Leu Ile His Thr Phe Thr Gly Met Glu Ser Thr Val Leu Leu Ala Met |     |     |
|   | 85  | 90  |
| Ala Phe Asp Arg Tyr Val Ala Ile Cys Thr Ser Leu His Tyr Thr Ser |     |     |
|   | 100 | 105 |
| Thr Leu Thr Pro Arg Val Leu Ala Gly Ile Gly Val Ser Ile Ile Met |     |     |
|   | 115 | 120 |
| Arg Pro Val Leu Leu Met Leu Pro Ile Leu Tyr Leu Thr His Arg Leu |     |     |
|   | 130 | 135 |
| Pro Phe Cys Glu Ala Arg Ile Ile Ala His Ser Tyr Cys Glu His Met |     |     |
| 145   | 150 | 155 |
| Gly Ile Ala Lys Leu Ala Cys Ala Ser Ile His Ile Asn Ala Ile Tyr |     |     |
|   | 165 | 170 |
|   |     | 175 |

Gly Leu Phe Val Ala Ser Phe Leu Asp Val Ala Leu Val Gly Ile Ser  
 180 185 190  
 Tyr Thr Tyr Ile Leu Arg Ala Val Phe His Leu Pro Ser Gln Asp Ala  
 195 200 205  
 Arg His Lys Ala Leu Arg Thr Cys Gly Ser His Val Gly Val Met Cys  
 210 215 220  
 Val Phe Tyr Thr Pro Ser Leu Phe Ser Phe Leu Thr Tyr Arg Phe Ala  
 225 230 235 240  
 Lys Lys Ile Pro Arg Tyr Val His Ile Leu Val Ala Asn Leu Tyr Val  
 245 250 255  
 Val Ile Pro Pro Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys  
 260 265 270  
 Gln Ile His Glu His Val Val His Thr Phe Thr Ser Lys Xaa Gly Leu  
 275 280 285  
 Leu

<210> 1199  
 <211> 174  
 <212> PRT  
 <213> Unknown (H38g116 protein)

<220>  
 <223> Synthetic construct  
 <221> VARIANT  
 <222> (1)...(174)  
 <223> Xaa = Any Amino Acid

<400> 1199  
 Thr Cys Trp Val Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly  
 1 5 10 15  
 Leu Ser Gly Ala Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe  
 20 25 30  
 Cys Asp Asp Asn Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys  
 35 40 45  
 Leu Ile Xaa Asn Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Phe  
 50 55 60  
 Asp Ser Phe Leu Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr  
 65 70 75 80  
 Leu Leu Ile Ile Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Lys Ala  
 85 90 95  
 Lys Xaa Phe Tyr Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr  
 100 105 110  
 Phe Leu Trp Asp Pro His Leu Gln Tyr Met Xaa Ser Thr Ser Asp Lys  
 115 120 125  
 Ser Leu Thr Glu Asp Lys Leu Ala Ser Val Thr Cys Thr Ile Phe Ile  
 130 135 140  
 Pro Met Leu Glu Leu Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val  
 145 150 155 160  
 Ala Phe Lys Lys Ala Ile Gly Asn Phe Trp Val Phe Glu Arg  
 165 170

<210> 1200  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g117 protein)

<220>  
 <223> Synthetic construct



&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1200

```

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe
 1           5           10           15
Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser
          20           25           30
Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser
          35           40           45
Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr
 50           55           60
Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr
 65           70           75           80
Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile
          85           90           95
Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser
          100          105          110
Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile
          115          120          125
Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val
          130          135          140
Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val
          145          150          155          160
Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn
          165          170          175
Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr
          180          185          190
Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile
          195          200          205
Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu
          210          215          220
Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg
          225          230          235          240
Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr
          245          250          255
Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala
          260          265          270
Pro His Ile Val His Val Leu Met Ala Asn Val Tyr Leu Met Gly Pro
          275          280          285
Pro Leu Met Asn Pro Val Phe Tyr Ser Val Lys Thr Arg Gln Ile Arg
          290          295          300
Asp Arg Ile Phe Gln Ile Lys Phe Arg Asn Met Lys Cys Arg
          305          310          315

```

&lt;210&gt; 1201

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g118 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1201

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15

```

Phe Leu Cys Gln Gln Gly Phe Leu Trp Glu Ile Pro Leu Phe Leu Ala  
 20 25 30  
 Phe Leu Val Ile Asp Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile  
 35 40 45  
 Phe Leu Ile Trp Lys Asp Pro His Leu His Ile Ser Met Tyr Leu Phe  
 50 55 60  
 Leu Gly Ser Leu Ala Phe Val Asp Thr Trp Leu Ser Ser Thr Val Thr  
 65 70 75 80  
 Pro Lys Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu  
 85 90 95  
 Ser Glu Cys Met Val Gln Phe Phe Ser Leu Ala Ile Ser Val Thr Thr  
 100 105 110  
 Glu Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Ala Asp Ile  
 115 120 125  
 Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile  
 130 135 140  
 Trp Leu Phe Val Leu Ser Phe Leu Gly Gly Leu Phe His Ala Leu Ile  
 145 150 155 160  
 His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Met Ile  
 165 170 175  
 Gln His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr  
 180 185 190  
 Asp Ser Cys Ile Asn Phe Leu Met Phe Phe Ile Phe Ser Gly Ser Ile  
 195 200 205  
 Gln Val Leu Thr Ile Gly Ile Val Phe Val Ser Tyr Met Phe Val Leu  
 210 215 220  
 Phe Thr Ile Leu Lys Lys Lys Ser Asn Lys Gly Ile Arg Glu Ala Phe  
 225 230 235 240  
 Ser Thr Cys Gly Ala His Tyr Ile Pro Leu Ser Leu Cys Tyr Gly Leu  
 245 250 255  
 Leu Leu Phe Met Tyr Val Gly Pro Ala Ala Pro Gln Ala Asp Asn Gln  
 260 265 270  
 Asp Met Met Glu Tyr Leu Phe Tyr Pro Ile Ile Val Arg Leu Leu Asn  
 275 280 285  
 Pro Tyr Tyr Tyr Ser Leu Arg Asn Lys Gln Val Ile Gly Ser Leu Thr  
 290 295 300  
 Lys Met Leu Lys Xaa Asn Ile Cys Ile Ala Tyr  
 305 310 315

&lt;210&gt; 1202

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g119 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1202

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu  
 1 5 10 15  
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro  
 20 25 30  
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu  
 35 40 45  
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Gly Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu  
 65 70 75 80  
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Thr Ser Ser  
 85 90 95  
 Ser Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu

```

      100      105      110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
      115      120      125
His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
      130      135      140
Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
      145      150      155      160
Phe Pro Phe Thr Leu Arg Ser Leu Arg Tyr Cys Lys Lys Asn Gln Leu
      165      170      175
Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
      180      185      190
Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
      195      200      205
Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
      210      215      220
Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Glu Leu Lys Ala Leu Asn
      225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
      245      250      255
Ile Asn Leu Ala Val Val His Arg Phe Ala Gly His Val Ser Pro Leu
      260      265      270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Met
      275      280      285
Lys Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
      290      295      300
Val Ala Lys Leu Cys Gln Trp Lys Ile
      305      310

```

&lt;210&gt; 1203

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g120 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1203

```

Met Glu Glu Lys Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Leu
1      5      10      15
Phe Leu Tyr Gln Pro His Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
20      25      30
Val Ile Tyr Leu Ile Thr Ile Phe Gly Asn Leu Gly Leu Ile Ala Val
35      40      45
Val Trp Lys Asp Pro His Leu His Ile Pro Ile Tyr Leu Phe Leu Glu
50      55      60
Asn Leu Ala Phe Val Asp Asp Leu Leu Ser Ser Thr Val Thr Leu Lys
65      70      75      80
Met Leu Ile Asn Phe Phe Thr Lys Ser Lys Leu Ile Ser Leu Glu Cys
85      90      95
Trp Ile His Phe Phe Ser Phe Ala Ile Gly Val Thr Thr Glu Cys Phe
100      105      110
Ile Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
115      120      125
Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu Leu
130      135      140
Ile Leu Ser Phe Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Ala
145      150      155      160

```

Phe Ser Tyr Arg Leu Thr Phe Cys Asn Ser Asn Thr Ile His His Phe  
 165 170 175  
 Xaa Cys Asp Ile Ile Pro Leu Leu Lys Ile Phe Cys Thr Asp Ser Ser  
 180 185 190  
 Ile Asn Phe Pro Met Val Phe Ile Phe Ser Cys Ser Ile Gln Val Phe  
 195 200 205  
 Thr Ile Gly Thr Val Leu Val Ser Tyr Thr Phe Val Leu Ser Thr Ile  
 210 215 220  
 Leu Lys Lys Lys Ser Val Lys Gly Ile Arg Lys Asp Phe Ser Thr Cys  
 225 230 235 240  
 Gly Ala His Ile Leu Pro Val Ser Leu Tyr Tyr Gly Pro Leu Ala Phe  
 245 250 255  
 Met Tyr Val Gly Ser Ala Ser Gln Arg Ala Asp Asp Gln Asp Met Met  
 260 265 270  
 Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Phe Thr Lys Met Phe  
 290 295 300  
 Lys Gly Asn Asn Val Xaa Ile Ser Tyr Ser  
 305 310

<210> 1204  
 <211> 171  
 <212> PRT  
 <213> Unknown (H38g121 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(171)  
 <223> Xaa = Any Amino Acid

<400> 1204  
 Cys Xaa Val Gln Val Ser Xaa Val Ala Glu Lys Tyr Xaa Xaa Ile Leu  
 1 5 10 15  
 Phe Val Ala Leu Phe Asn Lys Thr Lys Ser Ile Cys Gln Pro Gln Asn  
 20 25 30  
 Ile Ala Thr Pro Arg Pro Trp Ala Phe Pro Gln His Ser Phe Thr Ser  
 35 40 45  
 Thr Ser Cys Phe Gly Gly Thr Ser Thr Gly Leu Ser Xaa Ala Val Lys  
 50 55 60  
 Ser Pro Ile Ser Ser Val Cys Pro Leu Leu Gln Leu Leu Leu Gln Tyr  
 65 70 75 80  
 Pro Cys Asn Asn Ile Thr Cys Leu Xaa Asn Ala Ala Asp Arg Glu Phe  
 85 90 95  
 Leu Ser Phe Xaa Asp Pro Leu Leu Ala Val Gly Ser Phe Thr Ile Ser  
 100 105 110  
 Ser Cys Leu Leu Met Leu Lys Leu Ile Ser Phe Ser Ser Ser Arg Ile  
 115 120 125  
 Ile Ala Ser Leu Leu Ser Arg Cys Pro Thr Glu Ser His Arg Ser Pro  
 130 135 140  
 Phe Xaa Tyr Ser Phe Cys His Leu Phe Cys Leu Phe Phe Phe Met Thr  
 145 150 155 160  
 Glu Asn Pro Trp Xaa Tyr Leu Xaa Phe Pro Ser  
 165 170

<210> 1205  
 <211> 308  
 <212> PRT  
 <213> Unknown (H38g122 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1205

```

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile
 1           5           10           15
Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala
          20           25           30
Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile
          35           40           45
Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile
          50           55           60
Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met
          65           70           75           80
Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys
          85           90           95
Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala
          100          105          110
Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro
          115          120          125
Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala
          130          135          140
Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu
          145          150          155          160
Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr
          165          170          175
Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg
          180          185          190
Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp
          195          200          205
Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe
          210          215          220
Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly
          225          230          235          240
Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser
          245          250          255
Phe Met Thr His Arg Phe Gly Arg Asn Ile Pro His Phe Ile His Ile
          260          265          270
Leu Leu Ala Asn Phe Tyr Val Val Ile Pro Pro Ala Leu Asn Ser Val
          275          280          285
Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Ala Gln Val Leu Lys Met
          290          295          300
Phe Phe Asn Lys
          305

```

&lt;210&gt; 1206

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g123 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1206

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Phe Leu His Gln Pro Asp Cys Lys Ile Pro Leu Phe Leu Ala Phe Leu
          20           25           30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu
          35           40           45

```

```

      100      105      110
Thr Val Met Ala Tyr Asp Cys Tyr Val Val Ile Cys Lys Pro Leu Arg
      115      120      125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
      130      135      140
Ser Arg Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe Ile
      145      150      155      160
Phe Gln Leu Pro Phe Cys Ser Ser Asn Val Ile Asp His Phe Ile Cys
      165      170      175
Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asn Thr His Thr Leu
      180      185      190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
      195      200      205
Leu Leu Leu Leu Val Ser Tyr Val Val Ile Leu Tyr Ser Leu Arg Thr
      210      215      220
His Ser Leu Glu Ala Arg His Lys Gly Leu Ser Thr Cys Val Ser His
      225      230      235      240
Asn Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
      245      250      255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
      260      265      270
Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275      280      285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
      290      295      300
Ser Ser Val Lys
305

```

&lt;210&gt; 1208

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g125 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1208

```

Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu
  1      5      10
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20      25      30
Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu
      35      40      45
Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe
      50      55      60
Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile
      65      70      75      80
Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe
      85      90      95
Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met
      100      105      110
Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro
      145      150      155      160
Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile
      165      170      175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala
      180      185      190

```

Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu  
 195 200 205  
 Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys  
 210 215 220  
 Ala Val Phe Arg Leu Pro Thr His Glu Pro Arg Leu Lys Ser Leu Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala  
 245 250 255  
 Leu Phe Ser Phe Met Thr His Cys Phe Gly Arg Asn Val Pro Arg Tyr  
 260 265 270  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu  
 275 280 285  
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val  
 290 295 300  
 Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu  
 305 310 315 320  
 Ile

&lt;210&gt; 1209

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g126 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1209

Met Arg Asn His Thr Met Val Thr Glu Phe Ile Leu Leu Gly Ile Pro  
 1 5 10 15  
 Glu Thr Glu Gly Leu Glu Thr Ala Leu Phe Leu Phe Ser Ser Phe  
 20 25 30  
 Tyr Leu Cys Thr Leu Leu Gly Asn Val Leu Ile Leu Thr Ala Ile Ile  
 35 40 45  
 Ser Ser Thr Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu  
 50 55 60  
 Ser Ile Phe Asp Leu Gly Phe Ser Ser Thr Thr Val Pro Lys Met Leu  
 65 70 75 80  
 Phe Tyr Leu Ser Gly Asn Ser His Ala Ile Ser Tyr Ala Gly Cys Val  
 85 90 95  
 Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu  
 100 105 110  
 Tyr Thr Val Met Ala Cys Asp Arg Phe Val Ala Ile Cys Phe Pro Leu  
 115 120 125  
 Arg Tyr Thr Val Ile Met Asn His Arg Val Cys Phe Met Leu Ala Thr  
 130 135 140  
 Gly Thr Trp Met Ile Gly Cys Val His Ala Met Ile Leu Thr Pro Leu  
 145 150 155 160  
 Thr Phe Gln Leu Pro Tyr Cys Gly Pro Asn Lys Val Gly Tyr Tyr Phe  
 165 170 175  
 Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu  
 180 185 190  
 Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys  
 195 200 205  
 Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile Ser  
 210 215 220  
 Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser Thr Cys Ser  
 225 230 235 240  
 Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Val Ile  
 245 250 255  
 Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser Ile Ile Gln Ile

260                      265                      270  
 Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu  
                          275                      280                      285  
 Arg Asn Lys Asp Val Lys Ser Asp Gln Pro  
                          290                      295

<210> 1210  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g127 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(324)  
 <223> Xaa = Any Amino Acid

<400> 1210  
 Met Glu Glu Glu Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly  
 1                      5                      10                      15  
 Phe Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu  
                          20                      25                      30  
 Val Ile Xaa Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu  
                          35                      40                      45  
 Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Arg Gly  
                          50                      55                      60  
 Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Thr Val Thr Pro Lys  
 65                      70                      75                      80  
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu  
                          85                      90                      95  
 Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu Cys  
                          100                      105                      110  
 Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
                          115                      120                      125  
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln Leu  
                          130                      135                      140  
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu  
 145                      150                      155                      160  
 Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His  
                          165                      170                      175  
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser  
                          180                      185                      190  
 Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln Val  
                          195                      200                      205  
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu Ile  
                          210                      215                      220  
 Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser Thr  
 225                      230                      235                      240  
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Val  
                          245                      250                      255  
 Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met  
                          260                      265                      270  
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser Met  
                          275                      280                      285  
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met  
                          290                      295                      300  
 Phe Lys Arg Asn Val Xaa Ile Ser Tyr Asn Leu Cys Ser Leu Phe Thr  
 305                      310                      315                      320  
 Lys Ile Phe Pro



<210> 1211  
 <211> 308  
 <212> PRT  
 <213> Unknown (H38g128 protein)

<220>  
 <223> Synthetic construct

<400> 1211  
 Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe  
 1 5 10 15  
 Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe  
 20 25 30  
 Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile  
 35 40 45  
 Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn  
 50 55 60  
 Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala  
 65 70 75 80  
 Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys  
 85 90 95  
 Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu  
 100 105 110  
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro  
 115 120 125  
 Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala  
 130 135 140  
 Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly  
 145 150 155 160  
 Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe  
 165 170 175  
 Phe Cys Glu Val Pro Pro Leu Leu Leu Leu Ser Cys Ser Ser Thr Tyr  
 180 185 190  
 Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val  
 195 200 205  
 Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile  
 210 215 220  
 Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr  
 245 250 255  
 Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu  
 260 265 270  
 Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe  
 290 295 300  
 Pro Phe Phe Arg  
 305

<210> 1212  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g129 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1212

```

Met Asp Asp Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1          5          10          15
Leu Thr Tyr Gln Ser Glu Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Ile Met Ala Asn Leu Gly Leu Ile Ala Val
          35          40          45
Ile Trp Lys Asp Ser His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
          50          55          60
Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Ser Val Thr Pro Lys
65          70          75          80
Met Leu Ile Ser Phe Leu Ala Lys Ser Met Ile Ile Ser Val Ser Glu
          85          90          95
Cys Lys Ile Gln Phe Phe Ser Phe Gly Ile Ser Gly Thr Thr Glu Cys
          100          105          110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu
          130          135          140
Leu Val Leu Ser Phe Ile Gly Gly Phe Leu His Ala Leu Ile His Glu
145          150          155          160
Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His
          165          170          175
Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Pro
          180          185          190
Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser Gly Ser Ile Gln Val
          195          200          205
Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Thr Phe Val Leu Phe Thr
          210          215          220
Ile Leu Lys Lys Lys Ser Ala Lys Asp Ile Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Leu
          245          250          255
Phe Met Tyr Val His Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
          260          265          270
Val Glu Ser Leu Phe Tyr Thr Val Ile Ile Pro Phe Leu Asn Pro Ile
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Leu Thr Lys Thr
          290          295          300
Leu Lys Gly Asn Val Xaa Ile Ser Tyr Trp Asn Val Phe Ser Ile
305          310          315

```

<210> 1213

<211> 311

<212> PRT

<213> Unknown (H38g130 protein)

<220>

<223> Synthetic construct

<400> 1213

```

Met Val Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly
 1          5          10          15
Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe
          20          25          30
Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu
          35          40          45
Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly
50          55          60

```

Asn Leu Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Glu Asn Phe Phe Ser Glu Gly Lys Arg Ile Ser Leu Tyr Glu  
 85 90 95  
 Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys  
 100 105 110  
 Phe Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met  
 130 135 140  
 Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val  
 145 150 155 160  
 Gly Leu Val Phe Arg Leu Val Phe Cys Gly Leu Asn His Ile Asn His  
 165 170 175  
 Phe Tyr Cys Asp Thr Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro  
 180 185 190  
 Phe Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val  
 195 200 205  
 Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr  
 210 215 220  
 Ile Phe Arg Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Phe Ser Ser Val Ser Leu Phe Tyr Gly Ser Ile Phe  
 245 250 255  
 Phe Leu Tyr Ile Arg Pro Asn Leu Leu Glu Glu Gly Gly Asn Asp Ile  
 260 265 270  
 Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Ser Val Leu Arg Lys Ile  
 290 295 300  
 Leu Leu Lys Ile Lys Ser Gln  
 305 310

&lt;210&gt; 1214

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g131 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1214

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu  
 1 5 10 15  
 Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys  
 20 25 30  
 Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala  
 35 40 45  
 Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys  
 50 55 60  
 Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu  
 100 105 110  
 Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys

```

      115      120      125
His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
 130      135      140
Leu Val Leu Leu Ser Phe Phe Ser Val Phe Xaa His Ser Gln Leu
 145      150      155      160
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Ser Lys Asp Val Glu Ile
      165      170      175
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
      180      185      190
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe
      195      200      205
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val
      210      215      220
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe
 225      230      235      240
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr
      245      250      255
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
      260      265      270
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
      275      280      285
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp
 290      295      300
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His
 305      310      315      320
Leu Phe His Ser Phe Cys Arg Met
      325

```

&lt;210&gt; 1215

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g132 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1215

```

Met Glu Pro Gln Phe Thr Thr Gln Gly Ser Met Phe Val Leu Leu Gly
 1      5      10      15
Xaa Ser Gln Thr Gln Glu Leu Gln Arg Val Met Phe Ile Leu Phe Leu
      20      25      30
Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr
      35      40      45
Val Thr Phe Asp Cys Arg Leu His Pro Met Tyr Phe Leu Leu Arg Asn
      50      55      60
Leu Ala Leu Ile Asp Val Cys Tyr Ser Thr Val Thr Ser Pro Lys Met
 65      70      75      80
Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly Cys
      85      90      95
Met Ala Gln Ile Phe Phe Phe His Leu Gly Gly Gly Thr Val Phe
      100      105      110
Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln Pro
      115      120      125
Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu Val
      130      135      140
Val Ala Ala Trp Val Gly Phe Val His Ser Ile Val Gln Leu Ala
 145      150      155      160

```

```

Val Ile Arg Pro Gln Pro Leu Cys Gly Pro Asn Ile Leu Asp Asn Phe
      165                      170                      175
Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr Ser
      180                      185                      190
Leu Leu Glu Phe Leu Met Ile Ser Asn Ser Gly Leu Leu Val Ile Ile
      195                      200                      205
Trp Phe Leu Leu Ser Leu Met Ser Tyr Thr Val Ile Leu Val Met Leu
      210                      215                      220
Arg Ser His Ser Gly Lys Ala Arg Ser Lys Ala Ala Ser Thr Cys Thr
      225                      230                      235                      240
Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr Ile
      245                      250                      255
Tyr Thr Trp Pro Phe Thr Pro Phe Ile Met Asp Lys Ala Val Ser Ile
      260                      265                      270
Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr Leu
      275                      280                      285
Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys Leu
      290                      295                      300
Val Ile Cys Arg Glu Leu Thr Leu Ser Lys Leu Thr Leu Asn Asp Lys
      305                      310                      315                      320
Leu Leu Trp Ile Cys Tyr Phe Pro
      325

```

&lt;210&gt; 1216

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g133 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1216

```

Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
  1                      5                      10                      15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
      20                      25                      30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
      35                      40                      45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
      50                      55                      60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
      65                      70                      75                      80
Leu Leu Val Asn Leu Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
      85                      90                      95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
      100                      105                      110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115                      120                      125
Pro

```

&lt;210&gt; 1217

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g134 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1217

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
          35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
          65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Phe Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Thr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Cys His Ser Ala Ser Met Asn Pro Cys Phe Cys Gly
          130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Thr Gln
          145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Asp
          165          170          175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
          180          185          190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
          195          200          205
Phe Gly Phe Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
          210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala
          225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
          290          295          300
Arg Arg Pro Gln Gly Ser Lys Val Xaa Tyr Gln Tyr Leu Leu Ile Cys
          305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys
          325          330          335

```

<210> 1218

<211> 319

<212> PRT

<213> Unknown (H38g135 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1218

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1          5          10          15

```

Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu  
 20 25 30  
 Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Leu Val Val Thr Ile Thr  
 35 40 45  
 Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu  
 50 55 60  
 Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile  
 65 70 75 80  
 Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met  
 85 90 95  
 Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu  
 100 105 110  
 Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val  
 130 135 140  
 Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe  
 145 150 155 160  
 Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met  
 165 170 175  
 Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr  
 180 185 190  
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn  
 195 200 205  
 Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys  
 210 215 220  
 Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser  
 225 230 235 240  
 His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr  
 245 250 255  
 Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe  
 260 265 270  
 Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val  
 290 295 300  
 Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg  
 305 310 315

&lt;210&gt; 1219

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g136 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1219

Met Glu Ile Gly Asn His Thr Thr Val Thr Glu Phe Ile Ile Leu Gly  
 1 5 10 15  
 Leu Thr Glu Asp Pro Thr Leu Cys Asp Ile Phe Phe Val Ile Phe Leu  
 20 25 30  
 Gly Ile Tyr Ile Val Thr Leu Ile Gly Asn Ile Ser Ile Ile Lys Lys  
 35 40 45  
 Arg Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser His Leu Ala  
 50 55 60  
 Phe Val Asp Ile Gly Leu Ala Thr Val Val Thr Pro Ile Met Leu Met

```

65          70          75          80
Gly Phe Leu Arg Arg Gly Thr Ala Leu Pro Val Thr Ser Cys Glu Ala
      85          90          95
Gln Leu Cys Ser Val Val Met Phe Gly Thr Ser Glu Cys Phe Leu Leu
      100         105         110
Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu Val
      115         120         125
Asn Ser Thr His Leu Ser Pro Ile Ile Cys Ile Leu Leu Val Gly Val
      130         135         140
Cys Tyr Leu Gly Gly Trp Val Asn Ala Ser Thr Phe Thr Ser Cys Leu
145         150         155         160
Leu Ser Leu Ser Phe Cys Gly Pro Asn Gln Ile Asp His Phe Phe Cys
      165         170         175
Asp Phe Ser Pro Leu Leu Lys Leu Ser Cys Ser Asn Ile Ser Ile Pro
      180         185         190
Glu Ile Ile Pro Ser Ile Ser Ser Gly Ser Ile Ile Val Val Thr Val
      195         200         205
Phe Ala Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys
      210         215         220
Met Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys Thr Ser
225         230         235         240
His Leu Ala Ala Val Thr Leu Tyr Tyr Gly Thr Ile Thr Phe Ile Tyr
      245         250         255
Val Met Pro Lys Ser Ser Tyr Ser Thr Ser Gln Asn Arg Leu Ile Ser
      260         265         270
Leu Ser Tyr Thr Val Val Ile Pro Ile Leu Asn Pro Phe Ile Tyr Ser
      275         280         285
Leu Arg Asn Arg Asp Val Lys Glu Ala Leu Arg Lys Ala Thr Val Arg
      290         295         300
Ile Tyr Ser Xaa Asp Gln Phe Val
305         310

```

&lt;210&gt; 1220

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g137 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1220

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20         25         30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35         40         45
Ile Pro Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Thr Tyr Phe
      50         55         60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65         70         75         80
Val Ser Lys Thr Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85         90         95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100        105        110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
      115        120        125

```



```

Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
          210          215          220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
          245          250          255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg
          260          265          270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290          295          300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305          310          315          320
Phe Phe Trp Cys

```

&lt;210&gt; 1221

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g138 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1221

```

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val
 1          5          10          15
Ser Glu Phe Leu Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His
          20          25          30
Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala
          35          40          45
Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln
          50          55          60
Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Asp Ile Val Leu
65          70          75          80
Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu
          85          90          95
Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn
          100          105          110
Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp
          115          120          125
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr
          130          135          140
Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala
145          150          155          160
Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys
          165          170          175
Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser
          180          185          190
Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val

```

```

      195              200              205
Ala Gly Trp Thr Leu Leu Gly Ser Asp Leu Phe Leu Ile Phe Leu Ser
  210              215              220
Tyr Thr Phe Ile Leu Arg Ala Val Leu Arg Phe Lys Ala Glu Gly Ala
  225              230              235              240
Ala Val Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu
      245              250              255
Phe Phe Ser Thr Ile Leu Leu Val Val Val Leu Thr Asn Val Ala Arg
  260              265              270
Lys Lys Val Pro Met Asp Ile Leu Ile Leu Leu Asn Val Leu His His
  275              280              285
Leu Ile Pro Pro Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys
  290              295              300
Glu Ile Lys Gln Gly Ile Gln Lys Leu Leu Gln Arg Gly Arg
  305              310              315

```

&lt;210&gt; 1222

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g139 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(236)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1222

```

Pro Lys Val Pro Asp Phe Phe Val Phe Gly Leu Arg Ala Ile Ser Phe
  1              5              10              15
Pro Ala Gly Phe Leu Gln Lys Tyr Ile Lys Asn Cys Phe Gln Ala Met
      20              25              30
Glu Phe Trp Pro Phe Lys Val Arg Ala Met Asp Arg Xaa Gly Thr Leu
      35              40              45
Cys His Pro Leu Lys Tyr Pro Ser Ile Ile Thr Asp Pro Phe Gly Val
      50              55              60
Lys Ala Ala Arg Phe Ile Leu Pro Arg Asn Val Leu Met Thr Leu Pro
      65              70              75              80
Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn Val Ile
      85              90              95
Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser Cys Asp
      100              105              110
Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp Thr Leu
      115              120              125
Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe Ile Leu
      130              135              140
Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys Ala Leu
      145              150              155              160
Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser Thr Ile
      165              170              175
Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val Ser Pro
      180              185              190
Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro Ala Ala
      195              200              205
Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys Gln Gly
      210              215              220
Met Gln Arg Leu Leu Lys Lys Gly Cys Xaa Gln Gly
      225              230              235

```

&lt;210&gt; 1223

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g140 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1223

```

Met Asn Ser Leu Lys Asp Gly Asn His Thr Ala Leu Thr Gly Phe Ile
 1           5           10           15
Leu Leu Gly Leu Thr Asp Asp Pro Ile Leu Arg Val Ile Leu Phe Met
          20           25           30
Ile Ile Leu Ser Gly Asn Leu Ser Ile Ile Ile Leu Ile Arg Ile Ser
          35           40           45
Ser Gln Leu His His Pro Met Tyr Phe Phe Leu Ser His Leu Ala Phe
          50           55           60
Ala Asp Met Ala Tyr Ser Ser Ser Val Thr Pro Asn Met Leu Val Asn
65           70           75           80
Phe Leu Val Glu Arg Asn Thr Val Ser Tyr Leu Gly Cys Ala Ile Gln
          85           90           95
Leu Gly Ser Ala Ala Phe Phe Ala Thr Val Glu Cys Val Leu Leu Ala
          100          105          110
Ala Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Ser Pro Leu Leu Tyr
          115          120          125
Ser Thr Lys Met Ser Thr Gln Val Ser Val Gln Leu Leu Leu Val Val
          130          135          140
Tyr Ile Ala Gly Phe Leu Ile Ala Val Ser Tyr Thr Thr Ser Phe Tyr
145           150           155           160
Phe Leu Leu Phe Cys Gly Pro Asn Gln Val Asn His Phe Phe Cys Asp
          165          170          175
Phe Ala Pro Leu Leu Glu Leu Ser Cys Ser Asp Ile Ser Val Ser Thr
          180          185          190
Val Val Leu Ser Phe Ser Ser Gly Ser Ile Ile Val Val Thr Val Cys
          195          200          205
Val Ile Ala Val Cys Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys Met
          210          215          220
Arg Ser Thr Glu Gly His His Lys Ala Phe Ser Thr Cys Thr Ser His
225           230           235           240
Leu Thr Val Val Thr Leu Phe Tyr Gly Thr Ile Thr Phe Ile Tyr Val
          245          250          255
Met Pro Asn Phe Ser Tyr Ser Thr Asp Gln Asn Lys Val Val Ser Val
          260          265          270
Leu Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
          275          280          285
Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu Leu Val Arg Lys
          290          295          300
Ile Leu Ser His
305

```

&lt;210&gt; 1224

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g141 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1224

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
20      25      30
Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu
35      40      45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly
85      90      95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
100     105     110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
115     120     125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
130     135     140
Leu Asp Leu Leu Ser Phe Phe Phe Phe Pro Arg Leu Leu Asp Ser Gln
145     150     155     160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
165     170     175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
180     185     190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
195     200     205
Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met
210     215     220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225     230     235     240
Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
245     250     255
Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
260     265     270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
275     280     285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
290     295     300
Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys
305     310     315     320
Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
325     330     335

```

&lt;210&gt; 1225

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g142 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1225

```

Met Gly Thr Gly Asn Asp Thr Thr Val Val Glu Phe Thr Leu Leu Gly
1      5      10      15
Leu Ser Glu Asp Thr Thr Val Cys Ala Ile Leu Phe Leu Val Phe Leu
20      25      30
Gly Ile Tyr Val Val Thr Leu Met Gly Asn Ile Ser Ile Ile Val Leu
35      40      45
Ile Arg Arg Ser His His Leu His Thr Pro Met Tyr Ile Phe Leu Cys
50      55      60

```

His Leu Ala Phe Val Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro Val  
 65 70 75 80  
 Met Leu Met Ser Phe Leu Arg Lys Glu Thr Ser Leu Pro Val Ala Gly  
 85 90 95  
 Cys Val Ala Gln Leu Cys Ser Val Val Thr Phe Gly Thr Ala Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser  
 115 120 125  
 Pro Leu Leu Tyr Ser Thr Cys Met Ser Pro Gly Val Cys Ile Ile Leu  
 130 135 140  
 Val Gly Met Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Thr Phe Ile  
 145 150 155 160  
 Gly Cys Leu Leu Arg Leu Ser Phe Cys Gly Pro Asn Lys Val Asn His  
 165 170 175  
 Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ala Cys Ser His Asp  
 180 185 190  
 Phe Thr Phe Glu Ile Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile Val  
 195 200 205  
 Ala Thr Val Cys Val Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr  
 210 215 220  
 Ile Leu Lys Met His Ser Thr Lys Gly Arg His Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Thr  
 245 250 255  
 Phe Ile Tyr Val Met Pro Lys Ser Ser Tyr Ser Thr Asp Gln Asn Lys  
 260 265 270  
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu  
 290 295 300  
 Leu Arg Ile Lys Ile Phe Ser  
 305 310

&lt;210&gt; 1226

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g143 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1226

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu  
 1 5 10 15  
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu  
 20 25 30  
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile  
 35 40 45  
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu  
 50 55 60  
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr  
 65 70 75 80  
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly  
 85 90 95  
 Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser  
 100 105 110  
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile  
 130 135 140  
 Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Ile

```

145          150          155          160
Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile
          165          170          175
Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
          180          185          190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu
          195          200          205
Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
          210          215          220
Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val
          245          250          255
Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
          260          265          270
His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro
          275          280          285
Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln
          290          295          300
Arg Val Leu Arg Val Phe Thr Gln Lys Asp
305          310

```

&lt;210&gt; 1227

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38gl44 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1227

```

Met Thr Lys Gly Asn Arg Thr Thr Val Thr Glu Phe Val Leu Met Gly
1          5          10          15
Phe Thr Asp Arg Pro Glu Leu Gln Leu Pro Leu Phe Val Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Leu Leu
          35          40          45
Ile Arg Ala Asp Ser Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
          50          55          60
His Leu Ala Phe Ile Asp Leu Cys Tyr Ser Ser Ser Ile Gly Pro Lys
65          70          75          80
Met Leu Gln Asn Val Leu Val Lys Lys Lys Thr Ile Ser Phe Ser Gly
          85          90          95
Cys Phe Ala Gln Leu Tyr Phe Ser Gly Ala Phe Ala Thr Thr Glu Xaa
          100          105          110
Phe Leu Leu Ala Thr Met Pro Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Ile Tyr Thr Ala Ile Met Thr Gln Arg Val Cys Arg Glu Leu
          130          135          140
Val Ile Gly Val Tyr Thr Gly Phe Arg Asn Ser Val Ile Gln Thr
145          150          155          160
Ala Leu Thr Phe Gln Leu Ser Phe Cys Asn Ser Asp Val Ile His His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
          180          185          190
His Asn Lys Glu Lys Gln Leu Met Ile Phe Ser Ala Val Asn Leu Thr
          195          200          205

```

Gly Ser Leu Leu Thr Ile Phe Ile Ser Tyr Ile Cys Ile Leu Phe Ser  
 210 215 220  
 Ile Ile Lys Ile Gln Ser Ser Glu Gly Lys Cys Arg Ala Phe Ser Thr  
 225 230 235 240  
 Arg Ala Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Thr Leu Phe  
 245 250 255  
 Phe Met Tyr Leu Gln Gln Pro Lys Ala Gly Asn Ser Trp Lys Pro Asn  
 260 265 270  
 Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Arg Leu Arg Asn Thr Glu Val Lys Asp Ala Leu Lys Lys  
 290 295 300  
 Met Leu Glu Gly Lys Glu Leu Xaa Xaa Val Ser  
 305 310 315

&lt;210&gt; 1228

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g145 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(202)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1228

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe  
 1 5 10 15  
 Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser  
 20 25 30  
 Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr  
 35 40 45  
 Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr  
 50 55 60  
 Tyr Leu Leu Ser Leu Leu Ser Lys Leu Asp Ile Val Leu Cys Leu Thr  
 65 70 75 80  
 Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile  
 85 90 95  
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu  
 100 105 110  
 Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe  
 130 135 140  
 Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr  
 145 150 155 160  
 Leu Ala Ile Pro Ile Leu Ser Ala Gln Leu Leu Leu Gly Thr Met Phe  
 165 170 175  
 Leu Lys Pro Phe Cys Gly Lys Cys Phe Val His Asn Phe Cys Gly Asp  
 180 185 190  
 Ala Pro Xaa Xaa Pro Tyr Thr Phe Leu Lys  
 195 200

&lt;210&gt; 1229

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g146 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1229

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
 20           25           30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
 35           40           45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
 50           55           60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
 65           70           75           80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
 85           90           95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
 100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
 130          135          140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
 145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
 165          170          175
Phe Phe Cys Asp Leu Pro Leu Ala Ser Lys Leu Ala Cys Ile Asp Thr
 180          185          190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser
 195          200

```

&lt;210&gt; 1230

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g147 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1230

```

Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe
 1           5           10           15
Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
 20           25           30
Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
 35           40           45
Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
 50           55           60
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr
 65           70           75           80
Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly
 85           90           95
Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser
 100          105          110
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
 115          120          125
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
 130          135          140
Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile
 145          150          155          160
Pro Phe Leu Ile Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile
 165          170          175

```



```

Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
      180                      185                      190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu
      195                      200                      205
Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
      210                      215                      220
Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala
      225                      230                      235                      240
Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile
      245                      250                      255
Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
      260                      265                      270
His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro
      275                      280                      285
Ala Leu Asn Pro Leu Val Tyr Arg Val Lys Thr Gln Lys Ile His Gln
      290                      295                      300

```

&lt;210&gt; 1231

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g148 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(110)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1231

```

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
  1      5      10      15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
      20      25      30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
      35      40      45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
      50      55      60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
      65      70      75      80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
      85      90      95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
      100      105      110

```

&lt;210&gt; 1232

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g149 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1232

```

Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
  1      5      10      15
Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe

```

```
<210> 1233
<211> 241
<212> PRT
<213> Unknown (H38a150 protein)
```

```
<221> VARIANT
<222> (1)...(241)
<223> Xaa = Any Amino Acid
```

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 1233 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu        | Arg | Gln | Leu | His | Asn | Leu | Phe | Leu | Pro | Val | Gly | Phe | Phe | Leu | Ser |
| 1          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser        | Tyr | Ser | Phe | Xaa | Val | Ile | Trp | His | Asn | Leu | Asn | Ser | Val | Thr | Lys |
|            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe        | Ser | Ser | Lys | Thr | Asp | Glu | Ser | Lys | Leu | Lys | Ser | Xaa | Cys | Lys | Val |
|            |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys        | Ser | Leu | Phe | Phe | Thr | Tyr | Ala | Gly | Cys | Cys | Glu | Lys | Leu | Leu | Leu |
|            | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu  
 65 70 75 80  
 His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val  
 85 90 95  
 Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys  
 100 105 110  
 Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu  
 115 120 125  
 Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro  
 130 135 140  
 Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro  
 145 150 155 160  
 His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser  
 165 170 175  
 Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly  
 180 185 190  
 Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val  
 195 200 205  
 Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val  
 210 215 220  
 Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly  
 225 230 235 240  
 Pro

&lt;210&gt; 1234

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g151 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1234

Met Ala Ser Pro Asn Asn Asp Ser Thr Ala Pro Val Ser Glu Phe Leu  
 1 5 10 15  
 Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Trp Leu Ser Leu  
 20 25 30  
 Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala Asn Thr Thr Leu  
 35 40 45  
 Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln Pro Leu Tyr Tyr  
 50 55 60  
 Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val  
 65 70 75 80  
 Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Ser  
 85 90 95  
 Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Thr  
 100 105 110  
 Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp Gln Phe Val  
 130 135 140  
 Ala Arg Ala Val Val Phe Val Ile Ala Arg Asn Ala Phe Val Ser Leu  
 145 150 155 160  
 Pro Val Pro Met Leu Ser Ala Arg Leu Arg Tyr Cys Ala Gly Asn Ile  
 165 170 175  
 Ile Lys Asn Cys Ile Cys Ser Asn Leu Ser Val Ser Lys Leu Ser Cys  
 180 185 190  
 Asp Asp Ile Thr Phe Asn Gln Leu Tyr Gln Phe Val Ala Gly Trp Thr  
 195 200 205  
 Leu Leu Gly Ser Asp Leu Ile Leu Ile Val Ile Ser Tyr Ser Phe Ile

```

      210              215              220
Leu Lys Val Val Leu Arg Ile Lys Ala Glu Gly Ala Val Ala Lys Ala
225              230              235              240
Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu Phe Phe Ser Thr
      245              250              255
Val Leu Leu Val Leu Val Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro
      260              265              270
Pro Asp Val Pro Ile Leu Leu Asn Ile Leu His His Leu Ile Pro Pro
      275              280              285
Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln
      290              295              300
Gly Ile Gln Asn Leu Leu Lys Arg Leu
305              310

```

<210> 1235  
 <211> 135  
 <212> PRT  
 <213> Unknown (H38g152 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(135)  
 <223> Xaa = Any Amino Acid

```

<400> 1235
Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1              5              10              15
Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
      20              25              30
Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
      35              40              45
Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
      50              55              60
His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
      65              70              75              80
Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
      85              90              95
Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
      100              105              110
Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
      115              120              125
Arg Arg Leu Xaa Lys Ile Lys
      130              135

```

<210> 1236  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g153 protein)

<220>  
 <223> Synthetic construct

```

<400> 1236
Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1              5              10              15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
      20              25              30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
      35              40              45

```

```

Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
 50          55          60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
65          70          75          80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
      85          90          95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
      100          105          110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
      115          120          125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
      130          135          140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
      145          150          155          160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
      165          170          175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
      180          185          190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
      195          200          205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
      210          215          220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
      225          230          235          240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
      245          250          255
Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
      260          265          270
Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
      275          280          285
Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
      290          295          300
Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
      305          310          315

```

&lt;210&gt; 1237

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g154 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1237

```

Met Phe Leu Pro Asn Asn Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20          25          30
Phe Cys Ala Val Tyr Ile Ile Ala Leu Ile Gly Arg Phe Thr Ile Leu
      35          40          45
Leu Val Ile Lys Thr Asp Ser Ser Leu Tyr Gln Pro Met Phe Tyr Phe
      50          55          60
Leu Ala Met Leu Ala Thr Ile Asp Leu Gly Leu Ser Thr Ala Thr Ile
      65          70          75          80
Pro Lys Met Leu Gly Ile Phe Trp Phe Ser Leu Arg Glu Ile Ile Cys
      85          90          95
Asp Ala Cys Leu Ile Gln Met Phe Phe Ile His Asn Phe Thr Gly Met

```

```

      100      105      110
Glu Ser Ala Ala Leu Val Gly Met Ala Tyr Asp His Phe Val Ala Ile
      115      120      125
Cys Asn Pro Leu Arg Tyr Ser Ile Ile Leu Thr Lys Lys Ala Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Leu Val Arg Ser Phe Met Ser Val Ile Pro
      145      150      155      160
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly Asp His Val Ile
      165      170      175
Pro His Thr Asn Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ser
      180      185      190
Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Gly Ala Ile Ser Ile Leu
      195      200      205
Val Phe Asp Ile Ile Ala Ile Ala Leu Ser Tyr Val Gln Ile Leu His
      210      215      220
Ala Val Phe His Leu Pro Ser Cys Lys Ala Xaa Leu Lys Ser Leu Ser
      225      230      235      240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
      245      250      255
Leu Phe Ser Phe Val Thr His Arg Phe Gly Gln Asn Val Pro Arg Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
      275      280      285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Val
      290      295      300
Lys Asn Ile Phe Leu Gln Lys Xaa Glu Ile Glu Lys Lys Ser His Leu
      305      310      315      320
Ile His Ile Arg Arg
      325

```

&lt;210&gt; 1238

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g155 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1238

```

Met Ser Pro Leu Asn Asp Thr Lys Met Glu Val Leu Arg Phe Leu Leu
  1      5      10      15
Ile Gly Ile Thr Gly Leu Glu Lys Ser Arg Thr Trp Ile Ser Ile Pro
      20      25      30
Phe Leu Ser Val Tyr Leu Leu Ser Trp Met Gly Asn Phe Thr Val Leu
      35      40      45
Phe Phe Ile Lys Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Leu
      50      55      60
Leu Ser Met Leu Ser Ile Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
      65      70      75      80
Pro Ile Thr Leu Gly Leu Phe Leu Phe Asp Val His Glu Ile His Ala
      85      90      95
Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser
      100      105      110
Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile
      115      120      125
His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile
      130      135      140

```

Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu  
 165 170 175  
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser  
 180 185 190  
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr  
 195 200 205  
 Met Leu Asp Leu Val Leu Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg  
 210 215 220  
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Thr  
 245 250 255  
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met  
 260 265 270  
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu  
 275 280 285  
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val  
 290 295 300  
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu  
 305 310 315

&lt;210&gt; 1239

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g156 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1239

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu  
 1 5 10 15  
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro  
 20 25 30  
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu  
 35 40 45  
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu  
 65 70 75 80  
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Ile Ser Ser  
 85 90 95  
 Asn Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu  
 100 105 110  
 Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile  
 115 120 125  
 His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala  
 130 135 140  
 Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro  
 145 150 155 160  
 Phe Pro Phe Thr Leu Arg Asn Leu Arg Tyr Cys Lys Lys Asn Gln Leu  
 165 170 175  
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser  
 180 185 190  
 Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu  
 195 200 205  
 Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys  
 210 215 220  
 Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Gln Leu Lys Ala Leu Asn

[illegible]



<210> 1241  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g158 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(321)  
 <223> Xaa = Any Amino Acid

<400> 1241  
 Met Ala Tyr His Gly Asn Arg Gly Thr Phe His Pro Ala Thr Phe Phe  
 1 5 10 15  
 Leu Ile Gly Ile Pro Gly Leu Glu Asp Val His Met Xaa Ile Ser Leu  
 20 25 30  
 His Phe Cys Ser Val Tyr Leu Leu Ala Leu Leu Gly Asn Ala Thr Ile  
 35 40 45  
 Leu Leu Val Ile Lys Ala Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr  
 50 55 60  
 Phe Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser  
 65 70 75 80  
 Val Pro Arg Thr Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn  
 85 90 95  
 Phe Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly  
 100 105 110  
 Met Glu Ala Glu Val Leu Val Ala Met Ala Phe Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys Asn Pro Leu His Tyr Thr Asn Ile Leu Thr Ser Arg Val Leu  
 130 135 140  
 Val Gly Ile Thr Met Cys Ile Val Ile Arg Pro Val Leu Phe Thr Leu  
 145 150 155 160  
 Pro Ile Ile Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Gly His Ile  
 165 170 175  
 Ile Ala His Ser Tyr Tyr Glu His Met Gly Ile Ala Lys Leu Ser Cys  
 180 185 190  
 Gly Asn Ile Arg Val Asn Ala Ile Tyr Gly Leu Phe Val Val Ser Phe  
 195 200 205  
 Tyr Leu Leu Asn Leu Val Leu Ile Val Ile Ser Tyr Val Tyr Ile Leu  
 210 215 220  
 Cys Ala Val Phe Cys Leu Ala Ser His Asp Ala Arg Leu Lys Ala Leu  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Val Gly Val Ile Cys Val Phe Tyr Ile Pro  
 245 250 255  
 Ser Asp Phe Ser Phe Leu Thr His Xaa Phe Gly His Asn Ile Pro His  
 260 265 270  
 Tyr Met His Ile Leu Val Ala Thr Leu Tyr Leu Val Ile Pro Pro Ser  
 275 280 285  
 Leu Asn Pro Ile Ile Cys Gly Val Arg Thr Lys Trp Lys Arg Glu Arg  
 290 295 300  
 Val Leu Tyr Val Leu Thr Lys Lys Xaa Asp Ser Asp His Val Leu Leu  
 305 310 315 320  
 Leu

<210> 1242  
 <211> 162  
 <212> PRT  
 <213> Unknown (H38g159 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(162)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1242

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Val | Xaa | Ile | Leu | Ser | Pro | Val | Xaa | Leu | Pro | Phe | Tyr | Asp | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Val | Ile | Ala | His | Phe | Met | Cys | Asp | Leu | Asn | Thr | Leu | Leu | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Cys | Met | Gly | Thr | Thr | Asn | Thr | Leu | Gly | Phe | Phe | Val | Ala | Ala | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Phe | Asn | Tyr | Leu | Leu | Asn | Ile | Ile | Phe | Leu | Met | Val | Ser | Xaa |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Ile | Leu | Cys | Thr | Leu | Lys | Thr | His | Ser | Leu | Glu | Glu | Arg | Cys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Ala | Leu | Ser | Thr | Cys | Ile | Ser | His | Thr | Thr | Val | Val | Ile | Leu | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gly | Phe | Cys | Ile | Ser | Val | Tyr | Leu | Cys | Pro | Val | Thr | Leu | Leu | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asn | Lys | Ala | Val | Ala | Val | Phe | Tyr | Thr | Met | Ile | Asn | Pro | Met | Leu |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Lys | Pro | Leu | Val | Tyr | Thr | Leu | Arg | Asn | Ala | Glu | Val | Lys | Ser | Ala | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Lys | Leu | Trp | Val | Lys | Arg | Xaa | Thr | Glu | Glu | Arg | Asn | Asn | Pro | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 1243

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g160 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1243

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Tyr | His | Asn | Lys | Ser | Ile | Phe | His | Pro | Val | Thr | Phe | Phe | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Gly | Ile | Pro | Gly | Leu | Glu | Asp | Phe | His | Met | Trp | Ile | Ser | Gly | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Cys | Ser | Val | Tyr | Leu | Val | Ala | Leu | Leu | Gly | Asn | Ala | Thr | Ile | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Val | Ile | Lys | Val | Glu | Gln | Thr | Leu | Arg | Glu | Pro | Met | Phe | Tyr | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Ile | Leu | Ser | Thr | Ile | Asp | Leu | Ala | Leu | Ser | Ala | Thr | Ser | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Arg | Met | Leu | Gly | Ile | Phe | Trp | Phe | Asp | Ala | His | Glu | Ile | Asn | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ala | Cys | Val | Ala | Gln | Met | Phe | Leu | Ile | His | Ala | Phe | Thr | Gly | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Glu | Val | Leu | Leu | Ala | Met | Ala | Phe | Asp | Arg | Tyr | Val | Ala | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Ala | Pro | Leu | His | Tyr | Ala | Thr | Ile | Leu | Thr | Ser | Leu | Val | Leu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ile | Ser | Met | Cys | Ile | Val | Ile | Arg | Pro | Val | Leu | Leu | Thr | Leu | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |

Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile  
                           165                          170                          175  
 Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly  
                           180                          185                          190  
 Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe  
                           195                          200                          205  
 Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg  
                           210                          215                          220  
 Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser  
 225                          230                          235                          240  
 Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser  
                           245                          250                          255  
 Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr  
                           260                          265                          270  
 Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu  
                           275                          280                          285  
 Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val  
                           290                          295                          300  
 Leu Tyr Val Phe Thr Lys Lys  
 305                          310

&lt;210&gt; 1244

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g161 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1244

Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr  
 1                          5                          10                          15  
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile  
                           20                          25                          30  
 Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile Thr  
                           35                          40                          45  
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr Leu  
                           50                          55                          60  
 Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile  
 65                          70                          75                          80  
 Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys Met  
                           85                          90                          95  
 Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile Leu  
                           100                          105                          110  
 Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
                           115                          120                          125  
 His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met Gly  
                           130                          135                          140  
 Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe  
 145                          150                          155                          160  
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met  
                           165                          170                          175  
 Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His Met  
                           180                          185                          190  
 Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn  
                           195                          200                          205  
 Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu Arg

|   |     |     |
|---|-----|-----|
| 210   | 215 | 220 |
| Thr His Ser Leu Glu Ala Arg His Lys Ala Leu Ser Thr Cys Val Ser |     |     |
| 225   | 230 | 235 |
| His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val Tyr |     | 240 |
|   | 245 | 250 |
| Met Arg Pro Ala Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Ile Phe |     | 255 |
|   | 260 | 265 |
| Tyr Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg |     | 270 |
|   | 275 | 280 |
| Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Asp |     | 285 |
|   | 290 | 295 |
| Ile Ser Gly Asn Lys Xaa Met Xaa Leu Glu Leu                     |     | 300 |
| 305   | 310 | 315 |

&lt;210&gt; 1245

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g162 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1245

|   |     |     |
|---|-----|-----|
| Ser Asn Thr Gly Met Ser Ile Leu Asn Thr Ser Glu Met Glu Ile Ser |     |     |
| 1   | 5   | 10  |
| Ile Phe Tyr Leu Val Gly Ile Pro Gly Leu Glu His Ala Asn Ile Trp |     | 15  |
|   | 20  | 25  |
| Ile Ser Ile Pro Ile Cys Leu Met Tyr Thr Val Ala Ile Leu Gly Asn |     | 30  |
|   | 35  | 40  |
| Cys Thr Ile Leu Phe Phe Ile Lys Thr Glu Pro Ser Leu His Glu Pro |     | 45  |
|   | 50  | 55  |
| Met Tyr Tyr Phe Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser |     | 60  |
|   | 65  | 70  |
| Leu Ser Ser Leu Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Ala Pro |     | 75  |
|   | 85  | 90  |
| Gly Ile Ser Pro Asp Ala Cys Ile Ala Gln Glu Phe Phe Ile His Gly |     | 95  |
|   | 100 | 105 |
| Phe Ser Ala Met Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg |     | 110 |
|   | 115 | 120 |
| Phe Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Ser |     | 125 |
|   | 130 | 135 |
| Ala Arg Val Ile Gln Ile Gly Leu Ala Phe Ser Leu Lys Asn Val Leu |     | 140 |
|   | 145 | 150 |
| Leu Ile Leu Pro Phe Pro Phe Thr Leu Lys His Leu Lys Tyr Cys Lys |     | 155 |
|   | 165 | 170 |
| Lys Asn Leu Leu Ser Gln Ser Tyr Cys Leu His Gln Asp Val Met Lys |     | 175 |
|   | 180 | 185 |
| Leu Ala Cys Thr Asp Asn Lys Val Asn Ile Ile Tyr Gly Leu Phe Val |     | 190 |
|   | 195 | 200 |
| Ala Leu Thr Gly Ile Leu Asp Leu Thr Phe Ile Phe Met Ser Tyr Met |     | 205 |
|   | 210 | 215 |
| Leu Ile Leu Lys Ala Val Leu Ser Ile Ala Ser Xaa Lys Lys Arg Leu |     | 220 |
|   | 225 | 230 |
| Lys Val Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe |     | 235 |
|   | 245 | 250 |
| Tyr Val Pro Ile Ser Leu Ala Val Ile Tyr Arg Phe Ala Lys His     |     | 255 |
|   | 260 | 265 |
|   |     | 270 |

Ser Phe Pro Ile Thr Arg Ile Leu Ile Ala Asp Ala Phe Leu Leu Val  
 275 280 285  
 Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val Lys Ser Gln Gln Ile  
 290 295 300  
 Arg Asn Leu Val Leu Glu Lys Leu Cys Gln Lys Gln Ser Xaa Ser Gly  
 305 310 315 320  
 Cys Leu

&lt;210&gt; 1246

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g163 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1246

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu  
 1 5 10 15  
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu  
 20 25 30  
 Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Ile  
 35 40 45  
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr  
 65 70 75 80  
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys  
 100 105 110  
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Leu Asp Ser Xaa Leu  
 145 150 155 160  
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp  
 180 185 190  
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser  
 210 215 220  
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val  
 260 265 270  
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu  
 290 295 300  
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser

305

310

315

&lt;210&gt; 1247

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g164 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1247

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Ile | Xaa | Asp | Glu | Glu | Met | Ser | Arg | Arg | Asn | Tyr | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Thr | Glu | Phe | Val | Leu | Leu | Gly | Leu | Thr | Ser | Arg | Pro | Glu | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ala | Phe | Leu | Ala | Leu | Phe | Leu | Phe | Val | Tyr | Ile | Ala | Thr | Val | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Asn | Leu | Gly | Met | Ile | Ile | Leu | Ile | Lys | Val | Asp | Ser | Arg | Leu | His |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Pro | Met | Xaa | Phe | Phe | Leu | Ser | Ser | Leu | Ser | Ile | Leu | Asp | Leu | Cys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Ser | Thr | Asn | Phe | Thr | Pro | Lys | Met | Leu | Glu | Asn | Phe | Leu | Ser | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Lys | Thr | Ile | Ser | Tyr | Ala | Gly | Cys | Leu | Met | Gln | Cys | Tyr | Val | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Ala | Val | Val | Leu | Ala | Glu | His | Cys | Met | Leu | Ala | Val | Met | Ala | Tyr |
|     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |
| Asp | Arg | Tyr | Met | Ala | Ile | Cys | Asn | Pro | Leu | Leu | Tyr | Ser | Ser | Lys | Met |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ser | Gln | Gly | Val | Cys | Val | His | Leu | Val | Ile | Val | Pro | Tyr | Val | Tyr | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Phe | Leu | Leu | Ser | Val | Met | Glu | Thr | Leu | Arg | Thr | Tyr | Asn | Leu | Ser | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Cys | Gly | Thr | Asn | Glu | Ile | Asn | His | Phe | Tyr | Cys | Ala | Asp | Pro | Pro | Leu |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ile | Lys | Leu | Ala | Cys | Ser | Asp | Thr | Tyr | Ser | Lys | Glu | Leu | Ser | Met | Tyr |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ile | Val | Ala | Gly | Tyr | Ser | Asn | Val | Gln | Ser | Leu | Leu | Ile | Ile | Leu | Thr |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Ser | Tyr | Met | Phe | Ile | Leu | Val | Ala | Ile | Leu | Arg | Ser | His | Ser | Ala | Glu |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Gly | Arg | Lys | Lys | Ala | Phe | Ser | Thr | Cys | Gly | Ser | His | Leu | Thr | Val | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Thr | Ile | Phe | Tyr | Gly | Thr | Leu | Phe | Cys | Met | His | Leu | Arg | Arg | Pro | Thr |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asp | Glu | Ser | Val | Glu | Gln | Gly | Lys | Met | Val | Ala | Val | Phe | Tyr | Thr | Thr |
|     | 275 |     |     |     |     | 280 |     |     |     | 285 |     |     |     |     |     |
| Val | Ile | Leu | Met | Leu | Asn | Ser | Met | Ile | Tyr | Gly | Leu | Arg | Asn | Lys | Asp |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Val | Lys | Glu | Ala | Leu | Lys | Lys | Ala | Ile | Gly | Lys | Gln | Thr | Leu | Gly | Lys |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |

&lt;210&gt; 1248

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g165 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1248

```

Arg Arg Met Gly Asn His Thr Ala Val Ser Leu Phe Leu Leu Trp Gly
 1      5      10      15
Phe Ser Ser Phe Ser Asp Leu Gln Ser Leu Leu Phe Val Val Ile Leu
 20      25      30
Leu Leu His Val Thr Ile Leu Ala Ala Asn Val Ser Ile Met Gly Ala
 35      40      45
Ile Lys Leu Ser His Asn Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50      55      60
Gly Leu Ser Phe Ser Glu Thr Cys Thr Thr Val Val Val Ile Pro Arg
 65      70      75      80
Met Leu Val Asp Phe Leu Ser Glu Ser Lys Thr Ile Ser Leu Pro Glu
 85      90      95
Cys Ala Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Ser Asn Asn Cys
 100     105     110
Phe Ile Met Ala Ala Met Ser Tyr Asp Arg Tyr Thr Ala Ile His Asn
 115     120     125
Pro Leu Gln Tyr His Thr Leu Met Thr Arg Lys Ile Cys Leu Gln Met
 130     135     140
Met Met Ala Ser Trp Met Val Gly Phe Leu Phe Ser Leu Cys Ile Ile
 145     150     155     160
Val Thr Val Phe Asn Leu Ser Leu Cys Asp Leu Asn Thr Ile Gln His
 165     170     175
Tyr Phe Cys Asp Ile Ser Pro Val Val Ser Leu Ala Cys Asn Tyr Thr
 180     185     190
Phe Tyr His Glu Met Ala Ile Phe Val Leu Ser Ala Phe Val Leu Val
 195     200     205
Gly Ser Cys Ile Leu Ile Met Ile Ser Tyr Val Phe Ile Val Phe Ile
 210     215     220
Val Ile Lys Met Pro Ser Ala Lys Gly Arg Ser Lys Ala Phe Ser Thr
 225     230     235     240
Cys Ser Ser His Leu Thr Val Val Ser Ile His Tyr Gly Phe Ala Cys
 245     250     255
Phe Val Tyr Leu Arg Pro Lys Asn Ser Asn Ser Phe Asp Glu Asp Met
 260     265     270
Leu Thr Ala Met Ile Tyr Thr Ile Leu Met Pro Leu Leu Asn Pro Ile
 275     280     285
Val Tyr Ser Leu Arg Asn Lys Glu Met Gln Ile Ala Leu Arg Lys Thr
 290     295     300
Leu Gly Ser Val Phe Gly Val Phe Pro Gln Lys Thr
 305     310     315

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&lt;210&gt; 1249

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g166 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1249

```

Met Ser Ala Tyr Asn Asn Thr Asn Ala Arg Pro Ser Thr Phe Ile Leu
 1      5      10      15
Ile Gly Ile Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro
 20      25      30
Phe Cys Val Val Tyr Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu
 35      40      45
Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe

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|   |     |     |
|---|-----|-----|
| 50  | 55  | 60  |
| Leu Cys Met Leu Ala Val Val Asp Leu Val Val Cys Ser Thr Ala Val |     |     |
| 65  | 70  | 75  |
| Pro Lys Leu Leu Ser Leu Phe Trp Phe His Asp Gly Glu Ile Arg Phe |     | 80  |
|   | 85  | 90  |
| Glu Thr Cys Leu Thr Gln Met Phe Leu Ile His Ser Cys Ser Thr Met |     | 95  |
|   | 100 | 105 |
| Glu Ser Gly Phe Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile |     | 110 |
|   | 115 | 120 |
| Cys Asn Pro Leu Arg His Ser Ala Ile Leu Thr Arg Ala Val Ile Gly |     | 125 |
|   | 130 | 135 |
| Arg Val Gly Leu Ala Ile Val Leu Arg Gly Ile Ala Leu Leu Ser Pro |     | 140 |
|   | 145 | 150 |
| His Ser Phe Leu Leu Arg Trp Leu Pro Tyr Cys Arg Thr His Ile Ile |     | 155 |
|   | 165 | 170 |
| Ser His Thr Tyr Cys Glu Phe Met Ala Leu Ile Arg Ile Ala Cys Ala |     | 175 |
|   | 180 | 185 |
| Glu Thr Lys Phe Arg Arg Ala Tyr Ser Leu Ile Val Ala Phe Leu Thr |     | 190 |
|   | 195 | 200 |
| Gly Val Val Asp Phe Ile Leu Ile Ile Tyr Ser Tyr Val Leu Ile Leu |     | 205 |
|   | 210 | 215 |
| His Thr Val Phe Gln Leu Pro Ser Lys Asp Ala Arg Leu Lys Ser Leu |     | 220 |
|   | 225 | 230 |
| Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Val Ser Tyr Thr Pro |     | 235 |
|   | 245 | 250 |
| Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Ala Pro |     | 255 |
|   | 260 | 265 |
| His Phe His Ile Phe Val Ala Asn Ile Tyr Leu Leu Val Pro Pro Met |     | 270 |
|   | 275 | 280 |
| Val Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Arg Ile Trp Asp Arg |     | 285 |
|   | 290 | 295 |
| Phe Leu Lys Val Phe Ser Phe Ser Lys Pro Leu Ser Lys Ser Phe     |     | 300 |
|   | 305 | 310 |
|   |     | 315 |

&lt;210&gt; 1250

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38gl67 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1250

|   |     |
|---|-----|
| Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu Thr |     |
| 1   | 5   |
| Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Ile Phe Leu Val Val | 10  |
|   | 15  |
|   | 20  |
| Tyr Ile Ile Thr Met Val Gly Asn Ile Gly Met Met Val Leu Ile Lys | 25  |
|   | 30  |
|   | 35  |
| Val Ser Pro Gln Leu Asn Asn Pro Met Tyr Phe Phe Leu Ser His Leu | 40  |
|   | 45  |
|   | 50  |
| Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu | 55  |
|   | 60  |
|   | 65  |
| Glu Asn Leu Leu Ser Asp Lys Lys Thr Ile Thr Tyr Ala Gly Cys Leu | 70  |
|   | 75  |
|   | 80  |
|   | 85  |
| Val Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile | 90  |
|   | 95  |
|   | 100 |
| Leu Ala Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Gly Asn Pro Leu | 105 |
|   | 110 |
|   | 115 |
| Leu Tyr Gly Ser Lys Met Ser Arg Val Val Cys Ile Arg Leu Ile Thr | 120 |
|   | 125 |
|   | 130 |
|   | 135 |
|   | 140 |



Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Ala Ala Thr Leu Trp  
 145 150 155 160  
 Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr  
 165 170 175  
 Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val  
 180 185 190  
 Lys Glu Tyr Thr Met Ile Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser  
 195 200 205  
 Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu  
 210 215 220  
 Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met  
 245 250 255  
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val  
 260 265 270  
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val Ile Ser  
 290 295 300  
 Arg Ser Cys  
 305

&lt;210&gt; 1251

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g168 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1251

Met Thr Met Thr Thr Glu Asn Pro Asn Gln Thr Val Val Ser His Phe  
 1 5 10 15  
 Phe Leu Glu Gly Leu Arg Tyr Thr Ala Lys His Ser Ser Leu Phe Phe  
 20 25 30  
 Leu Leu Phe Leu Leu Ile Tyr Ser Ile Thr Val Ala Gly Asn Leu Leu  
 35 40 45  
 Ile Leu Leu Thr Val Gly Ser Asp Ser His Leu Ser Leu Pro Met Tyr  
 50 55 60  
 His Phe Leu Gly His Leu Ser Phe Leu Asp Ala Trp Leu Ser Thr Val  
 65 70 75 80  
 Thr Val Pro Lys Val Met Ala Gly Leu Leu Thr Leu Asp Gly Lys Val  
 85 90 95  
 Ile Ser Phe Glu Gly Cys Ala Val Gln Leu Tyr Cys Phe His Phe Leu  
 100 105 110  
 Ala Ser Thr Glu Cys Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Tyr  
 115 120 125  
 Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Ala Met Asn Arg Arg  
 130 135 140  
 Met Cys Ala Glu Met Ala Gly Ile Thr Trp Ala Ile Gly Ala Thr His  
 145 150 155 160  
 Ala Ala Ile His Thr Ser Leu Thr Phe Arg Leu Leu Tyr Cys Gly Pro  
 165 170 175  
 Cys His Ile Ala Tyr Phe Phe Cys Asp Ile Pro Pro Val Leu Lys Leu  
 180 185 190  
 Ala Cys Thr Asp Thr Thr Ile Asn Glu Leu Val Met Leu Ala Ser Ile  
 195 200 205  
 Gly Ile Val Ala Ala Gly Cys Leu Ile Leu Ile Val Ile Ser Tyr Ile  
 210 215 220  
 Phe Ile Val Ala Ala Val Leu Arg Ile Arg Thr Ala Gln Gly Arg Gln

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225          230          235          240
Arg Ala Phe Ser Pro Cys Thr Ala Gln Leu Thr Gly Val Leu Leu Tyr
          245          250          255
Tyr Val Pro Pro Val Cys Ile Tyr Leu Gln Pro Arg Ser Ser Glu Ala
          260          265          270
Gly Ala Gly Ala Pro Ala Val Phe Tyr Thr Ile Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys His Ala Leu
          290          295          300
Gln Arg Leu Leu Cys Ser Ser Phe Arg Glu Ser Thr Ala Gly Ser Pro
305          310          315          320
Pro Pro

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&lt;210&gt; 1252

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g169 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1252

```

Lys Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Val Phe Leu Val
          20          25          30
Val Tyr Ile Ile Thr Val Val Gly Asn Ile Gly Met Met Leu Leu Ile
          35          40          45
Lys Val Ser Pro Gln Leu Asn Ser Pro Met Tyr Phe Phe Leu Ser His
          50          55          60
Leu Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met
          65          70          75          80
Leu Glu Asn Leu Leu Ser Asp Lys Lys Lys Thr Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Ala Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile
          100          105          110
Phe Ile Leu Ala Ala Ile Ala Phe Asp Arg Tyr Thr Val Ile Gly Asn
          115          120          125
Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Asp Val Cys Ile Arg Leu
          130          135          140
Ile Thr Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Thr Ala Thr
          145          150          155          160
Leu Trp Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr
          180          185          190
Phe Val Lys Glu Tyr Thr Met Leu Ile Leu Ala Gly Ile Asn Phe Thr
          195          200          205
Tyr Ser Leu Thr Val Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala
          210          215          220
Ile Leu Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
          225          230          235          240
Cys Gly Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile
          245          250          255
Phe Met Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys
          260          265          270

```

Met Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val  
 290 295 300  
 Ile Ser Arg Ser Cys Xaa Thr Lys Xaa Asn Gln Val Xaa Ile Asn Phe  
 305 310 315 320  
 Val Phe

&lt;210&gt; 1253

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g170 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1253

Met Ser Asn Ala Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro  
 1 5 10 15  
 His Ala Pro Gly Leu Asp Ala Leu Leu Phe Gly Ile Phe Leu Val Val  
 20 25 30  
 Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg  
 35 40 45  
 Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu  
 50 55 60  
 Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu  
 65 70 75 80  
 Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys  
 85 90 95  
 Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe  
 100 105 110  
 Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro  
 115 120 125  
 Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala  
 130 135 140  
 Thr Gly Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile  
 145 150 155 160  
 Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr  
 165 170 175  
 Phe Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser  
 180 185 190  
 Ala Asn Val Met Val Ile Phe Val Asp Ile Gly Ile Val Ala Ser Gly  
 195 200 205  
 Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile  
 210 215 220  
 Leu Arg Ile Arg Thr Ser Asp Gly Arg Arg Arg Ala Phe Gln Thr Cys  
 225 230 235 240  
 Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Val  
 245 250 255  
 Ile Tyr Leu Arg Pro Gly Ser Met Asp Ala Met Asp Gly Val Val Ala  
 260 265 270  
 Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys  
 290 295 300  
 Val Ala His Pro Gln Arg Lys  
 305 310

&lt;210&gt; 1254

&lt;211&gt; 320

<212> PRT  
 <213> Unknown (H38g171 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1254

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Gly | Leu | Xaa | Lys | Leu | Xaa | Trp | Gln | Ile | Ile | Phe | Ser | Gly | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Ser | Thr | Trp | Glu | Met | Phe | Ser | Leu | Ser | Ile | Leu | Gln | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Met | Tyr | Thr | Val | Ala | Leu | Ser | Gly | Thr | Ser | Ile | Leu | Ile | Phe | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Xaa | Thr | Asp | Phe | Xaa | Val | His | Thr | Ser | Leu | Tyr | Ser | Phe | Xaa | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ile | Asp | Ile | Ala | Ile | Ser | Val | Val | Lys | Ile | Gly | Ile | Glu | Val | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ser | Gly | Lys | Ile | Asn | Phe | Ser | His | Thr | Gly | Cys | Gly | Thr | Gln | Ile | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Phe | Leu | Thr | Ala | Gly | Ile | Phe | Lys | Tyr | Val | Leu | Leu | Thr | Tyr | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Tyr | Asp | His | Asn | Val | Ala | Ile | Cys | Asp | Leu | Arg | Xaa | Pro | Thr | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Ser | Asp | Gln | Val | Phe | Xaa | Gln | Trp | Ala | Val | Glu | Ser | Trp | Ile | Gly |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Lys | Leu | Ser | Ser | Leu | Ala | His | Thr | Ile | Tyr | Ile | Phe | His | Leu | Phe |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Ser | Tyr | Lys | Ala | Lys | Glu | Ile | Ser | His | Leu | Trp | Pro | Lys | Leu | Phe | Xaa |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Ser | Ser | Val | Gly | Ile | Pro | Tyr | Ile | Gln | Asn | Asp | Val | Phe | Phe | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ile | Thr | Phe | Leu | Phe | Thr | Leu | Leu | Pro | Leu | Thr | Leu | Thr | Leu | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Lys | Leu | Ile | Val | Phe | Thr | Ile | Leu | His | Met | Asn | Ser | Ser | Asn | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ala | Lys | Ser | Trp | His | Thr | Tyr | Cys | Phe | His | Leu | Ser | Val | Leu | Ile |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Pro | Cys | Cys | Gly | Gln | Ala | Ile | Phe | Val | Tyr | Met | Thr | Ser | Ser | Ser | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Xaa | Thr | Val | Asn | Lys | Tyr | Gln | Thr | Met | Ser | Val | Leu | Thr | Ala | Xaa | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr | Pro | Leu | Leu | Lys | Pro | Leu | Ile | Asp | Ile | Leu | Lys | Asn | Ala | Glu | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Gly | Ala | Trp | Ser | Lys | Phe | Leu | Xaa | Lys | Lys | Ala | Leu | Lys | Ser | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| His | Leu | Ile | Thr | Arg | Ser | Cys | Glu | Asn | Lys | Xaa | Thr | Thr | Glu | Gln | Ser |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |

<210> 1255

<211> 320

<212> PRT

<213> Unknown (H38g172 protein)

<220>

<223> Synthetic construct

<221> VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1255

```

Met Leu Val Pro Lys Lys Met Val Arg Gly Asn Ser Thr Leu Val Thr
 1           5           10           15
Glu Phe Ile Leu Leu Gly Leu Lys Asp Leu Pro Glu Leu Gln Pro Ile
      20           25           30
Leu Phe Val Leu Phe Leu Leu Ile Tyr Leu Ile Thr Val Gly Gly Asn
      35           40           45
Leu Gly Met Leu Val Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro
      50           55           60
Met Tyr Phe Phe Leu Ala Ser Leu Ser Cys Leu Asp Leu Tyr Tyr Ser
      65           70           75           80
Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys
      85           90           95
Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala
      100          105          110
Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg
      115          120          125
Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys
      130          135          140
Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu
      145          150          155          160
Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly
      165          170          175
Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg
      180          185          190
Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val
      195          200          205
Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr
      210          215          220
Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg
      225          230          235          240
Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val
      245          250          255
Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg
      260          265          270
Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser
      275          280          285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290          295          300
Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn
      305          310          315          320

```

&lt;210&gt; 1256

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g173 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(235)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1256

```

Met Leu Phe Ile Ser Gln Trp Gly Glu Arg Xaa Arg Val Arg Arg Asn
 1           5           10           15
Val Gln Leu Met Thr Ala Phe Ile Leu Met Asp Leu Pro His Val Pro

```

```

      20      25      30
Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val Tyr Val Leu
  35      40      45
Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg Val Tyr Ser
  50      55      60
His Leu His Thr Pro Lys Tyr Tyr Phe Leu Thr Asn Leu Ser Phe Ile
  65      70      75      80
Asp Leu Trp Phe Phe Thr Val Met Val Pro Lys Met Pro Arg Thr Leu
      85      90      95
Leu Ser Leu Cys Gly Lys Ala Val Ser Phe His Ser Cys Met Thr Gln
      100      105      110
Leu Tyr Phe Phe Tyr Phe Leu Gly Ser Thr Glu Cys Leu Leu Tyr Thr
      115      120      125
Val Met Ser Tyr Asp Arg Tyr Arg Gly Asn Thr Gln His Phe Pro Gly
      130      135      140
Ser Glu Asn Leu Pro Thr Lys Xaa Ala Lys Cys Xaa Trp Pro Gly Gly
      145      150      155      160
His Thr Gly Leu Pro Leu Ile Ile Leu Ala Asp Leu Ser Gly Xaa Leu
      165      170      175
Arg Val Asp Ser Ser Xaa Trp Ala Ile Gln Asn Xaa Xaa Tyr Asn Leu
      180      185      190
Val Ile Gln Val Lys Phe Ile Thr Cys Ile Gly Leu Ser Ile Lys His
      195      200      205
Tyr Ser Lys Gln Leu Ala Gln Leu Xaa Phe Phe His Arg Leu Ser Lys
      210      215      220
Thr Phe Leu Asn Ser Gln Leu Asp Phe Tyr Leu
      225      230      235

```

&lt;210&gt; 1257

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g174 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(307)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1257

```

Met Ile Thr Glu Phe Ile Leu Ile Gly Phe Ser Asn Leu Gly Asp Leu
  1      5      10      15
Gln Ile Leu Leu Phe Phe Ile Phe Leu Leu Val Tyr Leu Thr Thr Leu
      20      25      30
Met Ala Asn Thr Thr Ile Met Thr Val Ile His Leu Asp Arg Ala Leu
      35      40      45
His Thr Pro Met Tyr Phe Phe Leu Phe Val Leu Ser Cys Ser Glu Thr
      50      55      60
Cys Tyr Thr Leu Val Ile Val Pro Lys Met Leu Thr Asn Leu Leu Ser
      65      70      75      80
Ala Ile Pro Thr Ile Ser Phe Ser Gly Cys Val Val Gln Leu Tyr Leu
      85      90      95
Phe Val Gly Leu Ala Cys Thr Asn Cys Phe Leu Ile Ala Val Met Gly
      100      105      110
Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Asn Tyr Thr Leu Ile
      115      120      125
Val Ser Xaa Ala Thr Cys Met Gln Leu Val Leu Ala Ser Ser Phe Cys
      130      135      140
Gly Phe Leu Thr Ser Val Ile Val Asn Ile Leu Val Phe Ser Val Leu
      145      150      155      160

```

Leu Cys Ala Ser Asn Arg Ile Asn His Phe Phe Cys Asp Ile Ser Pro  
                   165                  170                  175  
 Val Ile Lys Leu Gly Cys Thr Asp Thr Asn Leu Lys Glu Met Val Ile  
                   180                  185                  190  
 Phe Phe Leu Ser Ile Leu Val Leu Leu Val Pro Leu Val Leu Ile Phe  
                   195                  200                  205  
 Ile Ser Tyr Ile Phe Ile Val Ser Thr Ile Leu Lys Ile Ser Ser Val  
                   210                  215                  220  
 Glu Gly Gln Cys Lys Ala Phe Ala Thr Cys Ala Ser His Leu Thr Val  
 225                  230                  235                  240  
 Val Val Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr  
                   245                  250                  255  
 Ser Leu Tyr Ser Ser Asp Lys Asp Arg Leu Val Ala Val Thr Tyr Thr  
                   260                  265                  270  
 Val Ile Thr Pro Leu Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys  
                   275                  280                  285  
 Glu Val Lys Met Ala Leu Arg Lys Val Leu Gly Arg Cys Leu Asn Ser  
 290                  295                  300  
 Lys Thr Val  
 305

&lt;210&gt; 1258

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g175 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1258

Ile Cys His Asn Arg Lys Val Ile Pro Ala Ser Met Xaa Asn Met Cys  
 1                  5                  10                  15  
 Xaa Phe Leu Leu Lys Val Ala Xaa Asp Asn Phe Leu His Val Leu Phe  
                   20                  25                  30  
 Ile Leu Ala Lys Thr Ala Pro Pro Leu Leu Phe Leu Xaa Glu Ile Pro  
                   35                  40                  45  
 Ser Tyr Phe Ser Ser Pro Ser Xaa Ile Ile Val Leu Xaa Cys Leu Pro  
 50                  55                  60  
 Xaa Phe Leu Lys Gln Leu Val Ile Leu Phe Val Phe Leu Leu Leu Asn  
 65                  70                  75                  80  
 Xaa Ser Tyr Leu Thr Leu Ile Phe Met Leu Leu Thr Met Lys Ile Thr  
                   85                  90                  95  
 Ser Ser Phe Lys Ala Ser Thr Val Ile Ser Cys Leu Gln Phe Pro Ser  
                   100                  105                  110  
 Lys Ala Thr Cys Met His Gly Val Phe Ser Ala Val Cys Ala Gln Met  
                   115                  120                  125  
 Xaa Pro Tyr Tyr Asn Gly Xaa Ile Ile Xaa His Pro Glu Ser Ile Thr  
 130                  135                  140  
 Glu Ser Lys Xaa Leu Thr Cys Val Asn Pro Xaa Phe Asn  
 145                  150                  155

&lt;210&gt; 1259

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g176 protein)

&lt;220&gt;

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1259

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Lys | Ser | Ile | Lys | Leu | Thr | Ser | Leu | Ser | Glu | Phe | Leu | Leu | Leu | 1   | 5   | 10  | 15  |
| Glu | Phe | Ser | Ser | Leu | Glu | Glu | Ile | Gln | Gln | Ile | Leu | Phe | Leu | Val | Cys | 20  | 25  | 30  |     |
| Leu | Trp | Leu | Tyr | Leu | Ile | Val | Leu | Ser | Gly | Asn | Ile | Thr | Thr | Val | Thr | 35  | 40  | 45  |     |
| Val | Ile | Arg | Leu | Asp | Gln | Ser | Leu | His | Ile | Pro | Val | Tyr | Leu | Phe | Leu | 50  | 55  | 60  |     |
| Gly | Ile | Leu | Ser | Ile | Ser | Gly | Thr | Cys | Tyr | Thr | Phe | Val | Ile | Leu | Pro | 65  | 70  | 75  | 80  |
| Lys | Met | Leu | Ile | Asp | Leu | Leu | Ser | Leu | Leu | Arg | Thr | Ile | Ser | Phe | Ile | 85  | 90  | 95  |     |
| Asn | Cys | Ala | Leu | Gln | Met | Phe | Phe | Phe | Leu | Gly | Phe | Ala | Val | Thr | Asn | 100 | 105 | 110 |     |
| Phe | Met | Phe | Leu | Gly | Met | Thr | Val | Tyr | Asp | Ser | Tyr | Val | Ala | Ile | Cys | 115 | 120 | 125 |     |
| His | Pro | Leu | His | Tyr | Pro | Val | Leu | Thr | Ser | Trp | Gln | Ile | Cys | Lys | Gln | 130 | 135 | 140 |     |
| Leu | Ala | Ala | Thr | Cys | Ala | Val | Ile | Val | Phe | Phe | Cys | Leu | Phe | Val | Phe | 145 | 150 | 155 | 160 |
| Thr | Asp | Arg | Leu | Leu | Leu | Arg | Phe | Ser | Leu | Leu | Phe | Cys | Gly | Pro | Asn | 165 | 170 | 175 |     |
| Lys | Ile | Asn | His | Tyr | Phe | Cys | Asp | Ile | Ser | Leu | Leu | Ile | Gln | Leu | Ala | 180 | 185 | 190 |     |
| Cys | Thr | Asp | Thr | Tyr | Ile | Arg | Glu | Leu | Val | Ile | Phe | Ile | Gly | Gly | Ile | 195 | 200 | 205 |     |
| Leu | Ala | Leu | Thr | Val | Pro | Leu | Met | Phe | Ile | Cys | Ile | Ser | Tyr | Gly | Phe | 210 | 215 | 220 |     |
| Ile | Val | His | Thr | Ile | Leu | Arg | Ile | Pro | Ser | Cys | Glu | Ser | Lys | Gln | Lys | 225 | 230 | 235 | 240 |
| Ala | Ile | Ser | Thr | Cys | Ala | Ser | His | Leu | Ile | Met | Val | Val | Val | His | Tyr | 245 | 250 | 255 |     |
| Gly | Cys | Ala | Ser | Phe | Val | Asn | Leu | Xaa | Pro | Ser | Ala | Lys | Xaa | Ser | Ser | 260 | 265 | 270 |     |
| Ser | Lys | Xaa | Pro | Ser | Ser | Lys | Asn | Arg | Leu | Val | Thr | Val | Thr | Tyr | Thr | 275 | 280 | 285 |     |
| Val | Val | Thr | Pro | Leu | Leu | Asn | Pro | Met | Val | Tyr | Ser | Phe | Lys | Asn | Lys | 290 | 295 | 300 |     |
| Asn | Val | Gln | Met | Ala | Ile | Trp | Lys | Val | Ile | Cys | Gln | Gly | Gly | Phe | Pro | 305 | 310 | 315 | 320 |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 1260

<211> 317

<212> PRT

<213> Unknown (H38g177 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid



<400> 1260  
 Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu  
 1 5 10 15  
 Ala Asn His Arg Glu Leu Gln Ile Phe Leu Phe Thr Leu Phe Leu Thr  
 20 25 30  
 Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Ala Leu Ile  
 35 40 45  
 Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn  
 50 55 60  
 Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Arg Met  
 65 70 75 80  
 Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Arg  
 85 90 95  
 Leu Val Gln Cys Tyr Leu Phe Ile Thr Leu Val His Val Glu Leu Tyr  
 100 105 110  
 Ile Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Asn Pro  
 115 120 125  
 Leu Leu Tyr Gly Ser Arg Met Ser Lys Ser Val Cys Ser Phe Leu Ile  
 130 135 140  
 Thr Val Leu Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met  
 145 150 155 160  
 Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Ser Glu Ile Asn His Phe  
 165 170 175  
 Tyr Cys Val Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr  
 180 185 190  
 Asn Lys Glu Val Ser Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr  
 195 200 205  
 Pro Leu Leu Ile Ile Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr  
 210 215 220  
 Leu Arg Ile Cys Ser Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe  
 245 250 255  
 Met Tyr Leu Arg Arg Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met  
 260 265 270  
 Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Cys Lys Glu Leu  
 290 295 300  
 Phe Lys Arg Lys Leu Phe Ser Lys Xaa Thr Leu Leu Leu  
 305 310 315

<210> 1261

<211> 317

<212> PRT

<213> Unknown (H38g178 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1261

Thr Asp Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu  
 1 5 10 15  
 Leu Gln Pro Val Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu  
 20 25 30  
 Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp

```

      35      40      45
Ser Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp
  50      55      60
Pro Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp
  65      70      75      80
Thr Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln
      85      90      95
Met Ser Phe Leu Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr
      100      105      110
Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr
      115      120      125
Pro Ile Ile Val Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser
      130      135      140
Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu
      145      150      155      160
Gln Leu Thr Ile Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp
      165      170      175
Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Asn
      180      185      190
Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile Ser
      195      200      205
Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
      210      215      220
Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His
      225      230      235      240
Leu Ala Val Val Cys Trp Phe Tyr Gly Thr Gly Ile Gly Leu Tyr Leu
      245      250      255
Thr Ser Ala Gly Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser Val
      260      265      270
Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Cys Ser Leu
      275      280      285
Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Arg Ser Arg Ala
      290      295      300
Val Glu Tyr Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys
      305      310      315

```

&lt;210&gt; 1262

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g179 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1262

```

Met Arg Gly Phe Asn Lys Thr Thr Val Val Thr Gln Phe Ile Leu Val
  1      5      10      15
Gly Phe Ser Ser Leu Gly Glu Leu Gln Leu Leu Leu Phe Val Ile Phe
      20      25      30
Leu Leu Leu Tyr Leu Thr Ile Leu Val Ala Asn Val Thr Ile Met Ala
      35      40      45
Val Ile Arg Phe Ser Trp Thr Leu His Thr Pro Met Tyr Gly Phe Leu
      50      55      60
Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile Ile Pro
      65      70      75      80
Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser Phe Met
      85      90      95
Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys Thr Asn
      100      105      110
Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
      115      120      125

```

His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu  
 130 135 140  
 Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala  
 145 150 155 160  
 Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn  
 165 170 175  
 His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp  
 180 185 190  
 Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile  
 195 200 205  
 Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn  
 210 215 220  
 Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser  
 245 250 255  
 Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln  
 260 265 270  
 Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu  
 275 280 285  
 Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys Arg Val  
 290 295 300  
 Leu Gly Met Pro Val Ala Thr Lys Met Ser  
 305 310

&lt;210&gt; 1263

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g180 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1263

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu  
 130 135 140  
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr  
 180 185 190  
 Arg Val Asn Glu Trp Val Ile Phe Met Gly Gly Leu Ile Leu Val  
 195 200 205  
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser

```

      210              215              220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
225              230              235              240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
      245              250              255
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
      260              265              270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val
      290              295              300
Ile His Gln Lys Lys Thr Phe Phe Ser Leu
305              310

```

&lt;210&gt; 1264

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g181 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(275)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1264

```

Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe
1              5              10              15
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val
      20              25              30
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile
      35              40              45
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His
      50              55              60
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met
      65              70              75              80
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala
      85              90              95
Ser Pro Ser Phe Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu
      100              105              110
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val
      115              120              125
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg
      130              135              140
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe
      145              150              155              160
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg
      165              170              175
Cys Lys Leu Pro Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val
      180              185              190
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr
      195              200              205
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu
      210              215              220
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro
      225              230              235              240
Ser His Leu Ala Val Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg
      245              250              255
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val
      260              265              270

```

Gln Tyr Ser  
275

<210> 1265  
<211> 312  
<212> PRT  
<213> Unknown (H38g182 protein)

<220>  
<223> Synthetic construct

<221> VARIANT  
<222> (1)...(312)  
<223> Xaa = Any Amino Acid

<400> 1265  
Met Arg Arg Asn Phe Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu  
1 5 10 15  
Thr Asn His Gln Glu Leu Gln Ile Leu Leu Phe Met Leu Phe Leu Ala  
20 25 30  
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Ser Met Ile Ala Leu Ile  
35 40 45  
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His  
50 55 60  
Leu Ser Phe Leu Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met  
65 70 75 80  
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys  
85 90 95  
Leu Val Gln Cys Tyr Leu Tyr Ile Ile Leu Val His Val Glu Ile Tyr  
100 105 110  
Ile Leu Ala Val Met Ala Phe Asp Xaa Tyr Met Ala Ile Xaa Asn Pro  
115 120 125  
Leu Leu Tyr Gly Ser Lys Met Ser Lys Ser Val Cys Ser Phe Leu Ile  
130 135 140  
Thr Val Pro Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met  
145 150 155 160  
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Asn Glu Ile Asn His Phe  
165 170 175  
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr  
180 185 190  
Asn Lys Glu Leu Ser Met Phe Val Val Ala Gly Trp Asn Leu Ser Phe  
195 200 205  
Ser Leu Phe Ile Ile Phe Ile Ser Tyr Phe Tyr Ile Phe Pro Ala Ile  
210 215 220  
Leu Arg Ile Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys  
225 230 235 240  
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ala Thr Leu Phe Phe  
245 250 255  
Met Cys Leu Arg Pro Pro Ser Glu Glu Ser Met Glu Gln Gly Gln Met  
260 265 270  
Val Ala Val Leu Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile  
275 280 285  
Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ser Lys Glu Leu  
290 295 300  
Phe Lys Arg Lys Leu Phe Pro Lys  
305 310

<210> 1266  
<211> 315  
<212> PRT  
<213> Unknown (H38g183 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1266

```

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
 1          5          10          15
Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val
 20          25          30
Leu Leu Leu Phe Ala Tyr Leu Val Thr Ile Gly Gly Asn Leu Ser Ile
 35          40          45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe
 50          55          60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
 65          70          75          80
Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser
 85          90          95
Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe His Leu Leu Ala Gly
 100          105          110
Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala
 115          120          125
Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
 130          135          140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
 145          150          155          160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
 165          170          175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
 180          185          190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Val Ala Ala Ala Phe
 195          200          205
Met Ala Val Ala Pro Leu Val Phe Ile Ser Val Ser Tyr Ala His Val
 210          215          220
Val Ala Ala Val Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala
 225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
 245          250          255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
 260          265          270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
 275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
 290          295          300
Trp Gln Leu Leu Val Gly Glu Arg Ser Leu Thr
 305          310          315

```

&lt;210&gt; 1267

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g184 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1267

```

Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
 20          25          30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Ile Phe Ile
 35          40          45

```

Thr Ser Trp Thr Asp Pro Lys Leu Asn Ser Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro  
 65 70 75 80  
 Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val  
 85 90 95  
 Cys Cys Met Thr Gln Thr Tyr Phe Val Phe Cys Val Gly Val Ala Glu  
 100 105 110  
 Cys Ile Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Tyr Pro Leu Asn Tyr Val Pro Ile Ile Ser Gln Lys Val Cys Val Arg  
 130 135 140  
 Leu Val Gly Thr Ala Trp Phe Phe Gly Leu Ile Asn Gly Ile Phe Leu  
 145 150 155 160  
 Glu Tyr Ile Ser Phe Arg Glu Pro Phe Arg Arg Asp Asn His Ile Glu  
 165 170 175  
 Ser Phe Phe Cys Glu Ala Pro Ile Val Ile Gly Leu Ser Cys Gly Asp  
 180 185 190  
 Pro Gln Phe Ser Leu Trp Ala Ile Phe Ala Asp Ala Ile Val Val Ile  
 195 200 205  
 Leu Ser Pro Met Val Leu Thr Val Thr Ser Tyr Val His Ile Leu Ala  
 210 215 220  
 Thr Ile Leu Ser Lys Ala Ser Ser Ser Gly Arg Gly Lys Thr Phe Ser  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Val Val Ile Phe Leu Tyr Thr Ser Ala  
 245 250 255  
 Met Phe Ser Tyr Met Asn Pro His Ser Thr His Gly Pro Asp Lys Asp  
 260 265 270  
 Lys Pro Phe Ser Leu Leu Tyr Thr Ile Ile Thr Pro Met Cys Asn Pro  
 275 280 285  
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Glu Ala Met Val Arg  
 290 295 300  
 Ala Leu Gly Arg Thr Arg Leu Ala Gln Pro Gln Ser Val  
 305 310 315

&lt;210&gt; 1268

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g185 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1268

Met Phe Tyr Phe Phe Pro Pro Leu Gln Ile Leu Ala Glu Asn Leu Thr  
 1 5 10 15  
 Met Val Thr Glu Phe Leu Leu Leu Gly Phe Ser Ser Leu Gly Glu Ile  
 20 25 30  
 Gln Leu Ala Leu Phe Val Val Phe Leu Phe Leu Tyr Leu Val Ile Leu  
 35 40 45  
 Ser Gly Asn Val Thr Ile Ile Ser Val Ile His Leu Asp Lys Ser Leu  
 50 55 60  
 His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu Ser Thr Ser Glu Thr  
 65 70 75 80  
 Phe Tyr Thr Phe Val Ile Leu Pro Lys Met Leu Ile Asn Leu Leu Ser  
 85 90 95  
 Val Ala Arg Thr Ile Ser Phe Asn Cys Cys Ala Leu Gln Met Phe Phe  
 100 105 110  
 Phe Leu Gly Phe Ala Ile Thr Asn Cys Leu Leu Leu Gly Val Met Gly  
 115 120 125  
 Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu His Tyr Pro Thr Leu

```

      130              135              140
Met Ser Trp Gln Val Cys Gly Lys Leu Ala Ala Cys Ala Ile Gly
145              150              155              160
Gly Phe Leu Ala Ser Leu Thr Val Val Asn Leu Val Phe Ser Leu Pro
      165              170              175
Phe Cys Ser Ala Asn Lys Val Asn His Tyr Phe Cys Asp Ile Ser Ala
      180              185              190
Val Ile Leu Leu Ala Cys Thr Asn Thr Asp Val Asn Glu Phe Val Ile
      195              200              205
Phe Ile Cys Gly Val Leu Val Leu Val Val Pro Phe Leu Phe Ile Cys
      210              215              220
Val Ser Tyr Leu Cys Ile Leu Arg Thr Ile Leu Lys Ile Pro Ser Ala
225              230              235              240
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val
      245              250              255
Val Ile Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      260              265              270
Ala Asn Tyr Val Ser Asn Lys Asp Arg Leu Val Thr Val Thr Tyr Thr
      275              280              285
Ile Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Leu Arg Asn Lys
      290              295              300
Asp Val Gln Leu Ala Ile Arg Lys Val Leu Gly Lys Lys Gly Ser Leu
305              310              315              320
Lys Leu Tyr Asn

```

&lt;210&gt; 1269

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g186 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1269

```

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile
1      5      10      15
Ser Phe Thr Glu Glu Phe Asp Val Gln Val Phe Leu Phe Leu Leu Phe
      20      25      30
Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val
      35      40      45
Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu
      50      55      60
Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro
      65      70      75      80
Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu
      85      90      95
Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu
      100      105      110
Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr
      115      120      125
Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro
      130      135      140
Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His
      145      150      155      160
Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg
      165      170      175

```



```

His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp
      180                      185                      190
Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe Val Gly Ser Ile Glu
      195                      200                      205
Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
      210                      215                      220
Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
      225                      230                      235                      240
Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
      245                      250                      255
Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp
      260                      265                      270
Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
      275                      280                      285
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
      290                      295                      300
Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa
      305                      310                      315                      320
Val Lys Leu Gln Ile Ile Leu
      325

```

&lt;210&gt; 1270

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g187 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1270

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
  1          5          10          15
Leu Ser Lys Pro Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe
      20          25          30
Ser Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe
      35          40          45
Thr Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu
      50          55          60
Ala Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe
      65          70          75          80
Phe Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Ile Ile Gln Ile
      85          90          95
Phe Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr
      100         105         110
Met Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu
      115         120         125
Thr Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp
      130         135         140
Ile Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn
      145         150         155         160
Leu Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe
      165         170         175
Pro Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val
      180         185         190
Val Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu
      195         200         205
Leu Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser

```

|                     |                             |                     |
|---------------------|-----------------------------|---------------------|
| 210                 | 215                         | 220                 |
| Ser Gly Asp Leu Ser | Lys Ala Phe Val Ser Cys     | Ser Asp His Ile Thr |
| 225                 | 230                         | 235                 |
| Val Gly Ile Leu Phe | Met Pro Cys Ile Phe         | Leu Tyr Val Xaa Pro |
| 245                 | 250                         | 255                 |
| Leu Pro Lys Thr Thr | His Asp Xaa Tyr Leu Phe     | Ile Val Pro Leu Leu |
| 260                 | 265                         | 270                 |
| Ser Pro Leu Ser Arg | Ile Tyr Thr Leu Arg Asn Lys | Asp Met Asn Val     |
| 275                 | 280                         | 285                 |
| Ser Met Glu Arg Leu | Gly Lys Trp Ile Ala Gly     | Ser Ser Arg Met Ser |
| 290                 | 295                         | 300                 |
| Xaa Xaa Met Val Leu | Ser Arg Val Gln Asp Asp     | Ser Val Ser Pro     |
| 305                 | 310                         | 315                 |

&lt;210&gt; 1271

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g188 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1271

|                 |                 |                 |                 |
|-----------------|-----------------|-----------------|-----------------|
| Met Thr Thr Ile | Ile Leu Glu Val | Asp Asn His Thr | Val Thr Thr Arg |
| 1               | 5               | 10              | 15              |
| Phe Ile Leu Leu | Gly Phe Pro Thr | Arg Pro Ala Phe | Gln Leu Leu Phe |
| 20              | 25              | 30              |                 |
| Phe Ser Ile Phe | Leu Ala Thr Tyr | Leu Leu Thr Leu | Leu Glu Asn Leu |
| 35              | 40              | 45              |                 |
| Leu Ile Ile Leu | Ala Ile His Ser | Asp Gly Gln Leu | His Lys Pro Met |
| 50              | 55              | 60              |                 |
| Tyr Phe Phe Leu | Ser His Leu Ser | Phe Leu Glu Met | Trp Tyr Val Thr |
| 65              | 70              | 75              | 80              |
| Val Ile Ser Pro | Lys Met Leu Val | Asp Phe Leu Ser | His Asp Lys Ser |
| 85              | 90              | 95              |                 |
| Ile Ser Phe Asn | Gly Cys Met Thr | Gln Leu Tyr Phe | Phe Val Thr Phe |
| 100             | 105             | 110             |                 |
| Val Cys Thr Glu | Tyr Ile Leu Leu | Ala Ile Met Ala | Phe Asp Arg Tyr |
| 115             | 120             | 125             |                 |
| Val Ala Ile Cys | Asn Pro Leu Arg | Tyr Pro Val Ile | Met Thr Asn Gln |
| 130             | 135             | 140             |                 |
| Leu Cys Gly Thr | Leu Ala Gly Gly | Cys Trp Phe Cys | Gly Leu Met Thr |
| 145             | 150             | 155             | 160             |
| Ala Met Ile Lys | Met Val Phe Ile | Ala Gln Leu His | Tyr Cys Gly Met |
| 165             | 170             | 175             |                 |
| Pro Gln Ile Asn | His Tyr Phe Cys | Asp Ile Ser Pro | Leu Leu Asn Val |
| 180             | 185             | 190             |                 |
| Ser Cys Glu Asp | Ala Ser Gln Ala | Glu Met Val Asp | Phe Phe Leu Ala |
| 195             | 200             | 205             |                 |
| Leu Met Val Ile | Ala Ile Pro Leu | Cys Val Val Val | Ala Ser Tyr Ala |
| 210             | 215             | 220             |                 |
| Ala Ile Leu Ala | Thr Ile Leu Arg | Ile Pro Ser Ala | Gln Gly Arg Gln |
| 225             | 230             | 235             | 240             |
| Lys Ala Phe Ser | Thr Cys Ala Ser | His Leu Thr Val | Val Ile Leu Phe |
| 245             | 250             | 255             |                 |
| Tyr Ser Met Thr | Leu Phe Thr Tyr | Ala Arg Pro Lys | Leu Met Tyr Ala |
| 260             | 265             | 270             |                 |
| Tyr Asn Ser Asn | Lys Val Val Ser | Val Leu Tyr Thr | Val Ile Val Pro |
| 275             | 280             | 285             |                 |
| Leu Leu Asn Pro | Ile Ile Tyr Cys | Leu Arg Asn His | Glu Val Lys Ala |
| 290             | 295             | 300             |                 |

Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn  
 305 310 315 320  
 Gly Ala Phe Ser

<210> 1272

<211> 323

<212> PRT

<213> Unknown (H38g189 protein)

<220>

<223> Synthetic construct

<400> 1272

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile  
 130 135 140  
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu  
 145 150 155 160  
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys  
 165 170 175  
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala  
 180 185 190  
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile  
 195 200 205  
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu  
 210 215 220  
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser  
 225 230 235 240  
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val  
 245 250 255  
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser  
 260 265 270  
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr  
 275 280 285  
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg  
 290 295 300  
 Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro  
 305 310 315 320  
 Phe Leu Leu

<210> 1273

<211> 311

<212> PRT

<213> Unknown (H38g190 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1273

```

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1           5           10           15
Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
      20           25           30
Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
      35           40           45
Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50           55           60
His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
65           70           75           80
Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
      85           90           95
Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
      100          105          110
Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
      115          120          125
Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
      130          135          140
Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
145          150          155          160
Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
      165          170          175
Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
      180          185          190
Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
      195          200          205
Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
      210          215          220
Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
      245          250          255
Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
      260          265          270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
      290          295          300
Gln Arg Arg Gln Asp Ser Arg
305          310

```

&lt;210&gt; 1274

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g191 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1274

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1           5           10           15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
      20           25           30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
      35           40           45

```

His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu  
 50 55 60  
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser  
 65 70 75 80  
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu  
 85 90 95  
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly  
 100 105 110  
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile  
 115 120 125  
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Thr Trp Gly Fle  
 130 135 140  
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Leu  
 145 150 155 160  
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
 165 170 175  
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val  
 180 185 190  
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile  
 195 200 205  
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp  
 210 215 220  
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val  
 225 230 235 240  
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro  
 245 250 255  
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr  
 260 265 270  
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys  
 275 280 285  
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys  
 290 295 300  
 Phe  
 305

&lt;210&gt; 1275

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g192 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1275

Met Glu Arg Val Asn Glu Thr Val Val Arg Glu Val Ile Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu  
 20 25 30  
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr  
 35 40 45  
 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly  
 85 90 95  
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser  
 100 105 110  
 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu

|                     |                         |                             |
|---------------------|-------------------------|-----------------------------|
| 130                 | 135                     | 140                         |
| Val Ala Ala Ala Cys | Ala Cys Gly Phe Thr     | Val Ala Gln Ile Ile Thr     |
| 145                 | 150                     | 155                         |
| Ser Leu Val Phe His | Leu Pro Phe Tyr Ser     | Ser Asn Gln Leu His His     |
| 165                 | 170                     | 175                         |
| Phe Phe Cys Asp Ile | Ala Pro Val Leu Lys Leu | Ala Ser His His Asn         |
| 180                 | 185                     | 190                         |
| His Phe Ser Gln Ile | Val Ile Phe Met Leu     | Cys Thr Leu Val Leu Ala     |
| 195                 | 200                     | 205                         |
| Ile Pro Leu Leu Leu | Ile Leu Val Ser Tyr     | Val His Ile Leu Ser Ala     |
| 210                 | 215                     | 220                         |
| Ile Leu Gln Phe Pro | Ser Thr Leu Gly Arg     | Cys Lys Ala Phe Ser Thr     |
| 225                 | 230                     | 235                         |
| Cys Val Ser His Leu | Ile Ile Val Thr         | Val His Tyr Gly Cys Ala Ser |
| 245                 | 250                     | 255                         |
| Phe Ile Tyr Leu Arg | Pro Gln Ser Asn         | Tyr Ser Ser Ser Gln Asp Ala |
| 260                 | 265                     | 270                         |
| Leu Ile Ser Val Ser | Tyr Thr Ile Thr         | Pro Leu Phe Asn Pro Met     |
| 275                 | 280                     | 285                         |
| Ile Tyr Ser Leu Arg | Asn Lys Glu Phe         | Lys Ser Ala Leu Cys Lys Ile |
| 290                 | 295                     | 300                         |
| Val Arg Arg Thr Ile | Ser Leu Leu             |                             |
| 305                 | 310                     |                             |

&lt;210&gt; 1276

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g193 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(244)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1276

|                     |                 |                 |             |
|---------------------|-----------------|-----------------|-------------|
| Met Met Ile Ser Ser | Asp Glu Glu Asn | Asp Thr Asn Met | Met Glu Phe |
| 1                   | 5               | 10              | 15          |
| Ile Leu Val Gly Leu | Ser Arg Gln Pro | Ala Ser Gln Leu | Leu Phe Phe |
| 20                  | 25              | 30              |             |
| Xaa Ala Ile Leu Phe | Ile Tyr Ser Val | Thr Leu Val Gly | Asn Ile Leu |
| 35                  | 40              | 45              |             |
| Ile Ile Val Ile Ile | Gln Ile Asp Ser | His Leu Gln Thr | Pro Met Tyr |
| 50                  | 55              | 60              |             |
| Phe Phe Leu Ile Gln | Val Ser Phe Leu | Asp Ile Cys Ser | Thr Pro Thr |
| 65                  | 70              | 75              | 80          |
| Val Leu Val Asn Cys | Xaa Lys Asp Phe | Pro Ser Val Ser | Tyr Ser Gly |
| 85                  | 90              | 95              |             |
| Cys Leu Phe Xaa Met | Thr Ile Phe Leu | Tyr Leu Gly Val | Thr Glu Cys |
| 100                 | 105             | 110             |             |
| Val Phe Phe Leu Phe | Cys Phe Glu Cys | Phe Leu Ile Ala | Val Met Ala |
| 115                 | 120             | 125             |             |
| Tyr Asp Arg Phe Val | Ala Ile Ser Lys | Pro Leu Cys Tyr | Pro Phe Ile |
| 130                 | 135             | 140             |             |
| Ile Asn Ser Asn Val | Cys Ile Trp Met | Val Ala Gly Val | Trp Ala His |
| 145                 | 150             | 155             | 160         |
| Pro Gly Arg Thr Asn | Pro Ile Leu Trp | Pro Gln Cys Ser | Gln His Phe |
| 165                 | 170             | 175             |             |
| Thr Cys Glu Leu Gln | Val Ile Phe Lys | Leu Thr Cys Ser | Pro Val Leu |
| 180                 | 185             | 190             |             |

Val Lys Glu Ile Gln Xaa Phe Met Ile Pro Gly Cys Thr Leu Xaa Ala  
 195 200 205  
 Leu Tyr Gln His Xaa Val Cys Ser Tyr Ser Xaa Ala Arg Gln Gln Thr  
 210 215 220  
 His Pro Arg Ser Xaa Glu Ala Tyr Asn Xaa Gly Ile Arg Xaa Gly Ile  
 225 230 235 240  
 Ile Gly Val His

&lt;210&gt; 1277

&lt;211&gt; 306

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g194 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(306)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1277

Thr Ala Gly Ser Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly  
 1 5 10 15  
 Tyr Ala Asn His Pro Glu Leu Gln Val Ser Phe Phe Leu Met Phe Leu  
 20 25 30  
 Phe Ile Tyr Leu Phe Thr Ile Leu Gly Asn Leu Gly Leu Ile Met Leu  
 35 40 45  
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Val Thr Pro Lys  
 65 70 75 80  
 Thr Leu Ala Asn Phe Gln Ser Asn Gln Arg Ser Ile Ser Phe Val Gly  
 85 90 95  
 Cys Phe Val Gln Met Tyr Phe Ser Val Gly Leu Val Cys Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Gly Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Trp Asn  
 115 120 125  
 Pro Tyr Ser Val Val Ile Ser Xaa Lys Ala Cys Asn Trp Leu Gly Val  
 130 135 140  
 Met Ser Tyr Thr Ile Gly Phe Thr Asn Ser Leu Val Ser Val Trp Val  
 145 150 155 160  
 Ile Ser Gly Leu Phe Cys Asp Ser Ser Ile Asn Phe Phe Phe Cys Asp  
 165 170 175  
 Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Ala Phe Ser Thr Glu  
 180 185 190  
 Met Val Ser Phe Ala Leu Ala Gly Phe Thr Leu Leu Gly Ser Ile Leu  
 195 200 205  
 Ile Ile Thr Val Thr Tyr Ile Ala Ile Thr Ser Ala Ile Leu Lys Asn  
 210 215 220  
 Gln Trp Ala Ala Gly Trp Gln Lys Ala Phe Ser Thr Cys Ala Phe His  
 225 230 235 240  
 Leu Met Ala Leu Thr Ile Phe Tyr Gly Ser Leu Ile Phe Thr Tyr Leu  
 245 250 255  
 Gln Leu Asp Lys Thr Ser Ser Leu Ile His Ala Gln Leu Ala Phe Val  
 260 265 270  
 Phe Tyr Met Thr Val Ile Pro Met Leu Asn Pro Leu Ile Xaa Ser Leu  
 275 280 285  
 Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile His Arg Lys  
 290 295 300  
 Leu Phe

305

&lt;210&gt; 1278

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g195 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1278

```

Met Ala Asn Ser Ser Ser Val Thr Glu Phe Leu Val Leu Gly Phe Ser
 1          5          10          15
Ser Leu Gly Glu Leu Gln Leu Val Leu Phe Ala Val Phe Leu Cys Leu
          20          25          30
Tyr Leu Ile Ile Leu Ser Gly Asn Ile Ile Ile Ile Ser Val Ile His
          35          40          45
Leu Asp His Ser Leu His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu
          50          55          60
Ser Ile Ser Glu Ile Phe Tyr Thr Thr Val Ile Leu Pro Lys Met Leu
          65          70          75          80
Ile Asn Leu Phe Ser Val Phe Arg Thr Leu Ser Phe Val Ser Cys Ala
          85          90          95
Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn Cys Leu Leu
          100          105          110
Leu Gly Val Met Gly Tyr Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu
          115          120          125
Gln Tyr Ala Val Leu Met Ser Trp Arg Val Cys Gly Gln Leu Ile Ala
          130          135          140
Thr Cys Ile Ile Ser Gly Phe Leu Ile Ser Leu Val Gly Thr Thr Phe
          145          150          155          160
Val Phe Ser Leu Pro Phe Cys Gly Ser Asn Lys Val Asn His Tyr Phe
          165          170          175
Cys Asp Ile Ser Pro Val Ile Arg Leu Ala Cys Ala Asp Ser Tyr Ile
          180          185          190
Ser Glu Leu Val Ile Phe Ile Phe Gly Val Leu Val Leu Val Val Pro
          195          200          205
Leu Ile Phe Ile Cys Ile Ser Tyr Gly Phe Ile Val Arg Thr Ile Leu
          210          215          220
Lys Ile Pro Ser Ala Glu Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
          225          230          235          240
Ser His Leu Ile Val Val Ile Val His Tyr Gly
          245          250

```

&lt;210&gt; 1279

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g196 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1279

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1          5          10          15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
          20          25          30

```



Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile  
                   35                                  40                                  45  
 Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe  
                   50                                  55                                  60  
 Phe Phe Leu Ser Thr Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser  
 65                                  70                                  75                                  80  
 Trp Glu Leu Xaa Val Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile  
                                   85                                  90                                  95  
 Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly  
                                   100                                  105                                  110  
 Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val  
                                   115                                  120                                  125  
 Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val  
 130                                  135                                  140  
 Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala  
 145                                  150                                  155                                  160  
 Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val  
                                   165                                  170                                  175  
 Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys  
                                   180                                  185                                  190  
 Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe  
 195                                  200                                  205  
 Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile  
 210                                  215                                  220  
 Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly  
 225                                  230                                  235                                  240  
 Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met  
                                   245                                  250                                  255  
 Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val  
                                   260                                  265                                  270  
 Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr  
                                   275                                  280                                  285  
 Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys  
 290                                  295                                  300  
 Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn  
 305                                  310                                  315

&lt;210&gt; 1280

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g197 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1280

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr  
 1                                  5                                  10                                  15  
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro  
                                   20                                  25                                  30  
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn  
                                   35                                  40                                  45  
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro  
                                   50                                  55                                  60  
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser  
 65                                  70                                  75                                  80  
 Thr Val Ile Ala Pro Lys Met Leu Val Asn Phe Ile Val His Lys Asn  
                                   85                                  90                                  95  
 Thr Ile Ser Tyr Asn Trp Tyr Ala Thr Gln Leu Ala Phe Phe Glu Ile  
                                   100                                  105                                  110  
 Phe Ile Ile Ser Glu Leu Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg

```

      115              120              125
Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Val Ile Ile Met Ala Glu
  130              135              140
Lys Val Leu Trp Val Leu Val Ile Val Pro Tyr Leu Tyr Ser Thr Phe
  145              150              155              160
Val Ser Leu Phe Leu Thr Ile Lys Leu Phe Lys Leu Ser Phe Cys Gly
      165              170              175
Ser Asn Ile Ile Ser Tyr Phe Tyr Cys Asp Cys Ile Pro Leu Met Ser
      180              185              190
Ile Leu Cys Ser Asp Thr Asn Glu Leu Glu Leu Ile Ile Leu Ile Phe
      195              200              205
Ser Gly Cys Asn Leu Leu Phe Ser Leu Ser Ile Val Leu Ile Ser Tyr
      210              215              220
Met Phe Ile Leu Val Ala Ile Leu Arg Met Asn Ser Arg Lys Gly Arg
      225              230              235              240
Tyr Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met
      245              250              255
Phe Tyr Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His
      260              265              270
Thr Leu Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile
      275              280              285
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
      290              295              300
Asp Ala Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile
      305              310              315

```

&lt;210&gt; 1281

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g198 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1281

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
  1           5           10           15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
      20           25           30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
      35           40           45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
      50           55           60
Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu
      65           70           75           80
Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg
      85           90           95
Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His
      100          105          110
Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln
      115          120          125
Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu
      130          135          140
Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu
      145          150          155

```

&lt;210&gt; 1282

<211> 317  
 <212> PRT  
 <213> Unknown (H38g199 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(317)  
 <223> Xaa = Any Amino Acid

<400> 1282

```

Met Gly Gln Lys Asn Leu Thr Val Leu Thr Glu Leu Ile Leu Met Glu
 1      5      10      15
Ile Thr Arg Arg Leu Glu Leu Gln Leu Ser Leu Phe Trp Val Phe Leu
      20      25      30
Ile Ile Cys Thr Phe Thr Val Val Ser Lys Glu Cys Ile Ile Leu
      35      40      45
Asn Asn Val Asp Leu Gly Leu Gln Thr Phe Val Tyr Phe Leu Ile Arg
      50      55      60
Tyr Leu Asn Phe Ile Asn Leu Gly Asn Ser Met Val Ile Tyr Pro Lys
      65      70      75      80
Ile Leu Val Asn Phe Val Val Ala Gln Asn Ala Ile Pro Cys Tyr Ala
      85      90      95
Cys Thr Met Gln Met Ala Phe Phe Ile Met Phe Ile Ile Cys Glu Leu
      100     105     110
Phe Val Ser Ser Ala Met Ala Tyr Asp His Tyr Val Asp Ile His Ser
      115     120     125
Leu Leu Pro Xaa Asn Val Met Ser Gln Glu Leu Cys His Val Leu Val
      130     135     140
Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile
      145     150     155     160
Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe
      165     170     175
Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa
      180     185     190
Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe
      195     200     205
Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val
      210     215     220
Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr
      225     230     235     240
Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe
      245     250     255
Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys
      260     265     270
Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu
      275     280     285
Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser
      290     295     300
Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val
      305     310     315

```

<210> 1283  
 <211> 302  
 <212> PRT  
 <213> Unknown (H38g200 protein)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1283

```

Met Thr Asn Leu Asn Ala Ser Gln Ala Asn His Arg Asn Phe Ile Leu
 1           5           10           15
Thr Gly Ile Pro Gly Thr Pro Asp Lys Asn Pro Trp Leu Ala Phe Pro
          20           25           30
Leu Gly Phe Leu Tyr Thr Leu Thr Leu Leu Gly Asn Gly Thr Ile Leu
          35           40           45
Ala Val Ile Lys Val Glu Pro Ser Leu His Glu Pro Thr Tyr Tyr Phe
          50           55           60
Leu Ser Ile Leu Ala Leu Thr Asp Val Ser Leu Ser Met Ser Thr Leu
65           70           75           80
Pro Ser Met Leu Ser Ile Tyr Trp Phe Asn Ala Pro Gln Ile Val Phe
          85           90           95
Asp Ala Cys Ile Met Gln Met Phe Phe Ile His Val Phe Gly Ile Val
          100          105          110
Glu Ser Gly Val Leu Val Ser Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Arg Asn Pro Leu His Tyr Val Ser Ile Leu Thr His Asp Val Ile Arg
          130          135          140
Lys Thr Gly Ile Ser Val Leu Thr Arg Ala Val Cys Val Val Phe Pro
145           150           155           160
Val Pro Phe Leu Ile Lys Cys Leu Pro Phe Cys His Ser Asn Val Leu
          165          170          175
Ser His Ser Tyr Cys Leu His Gln Asn Met Met Arg Leu Ala Cys Ala
          180          185          190
Ser Thr Arg Ile Asn Ser Leu Tyr Gly Leu Ile Val Val Ile Phe Thr
          195          200          205
Leu Gly Leu Asp Val Leu Leu Thr Leu Leu Ser Tyr Val Leu Thr Leu
          210          215          220
Lys Thr Val Leu Gly Ile Val Ser Arg Gly Glu Arg Leu Lys Thr Leu
225           230           235           240
Ser Thr Cys Leu Ser His Met Ser Thr Val Leu Leu Phe Tyr Val Pro
          245          250          255
Phe Met Gly Ala Ala Ser Met Ile His Arg Phe Trp Glu His Leu Ser
          260          265          270
Pro Val Val His Met Val Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro
          275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
          290          295          300

```

&lt;210&gt; 1284

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g201 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1284

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Pro Ala Val Ser Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe
          50           55           60

```

```

Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65          70          75          80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Arg Val Ile Ser
          85          90          95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100         105         110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
          115         120         125
Ile Tyr Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130         135         140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150         155         160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165         170         175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Ser
          180         185         190
Tyr Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
          195         200         205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Ser Ser Tyr Tyr Lys Ile
          210         215         220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Thr
225          230         235         240
Phe Ser Thr Tyr Gly Ser His Leu Ala Phe Val Cys Xaa Phe Tyr Gly
          245         250         255
Thr Gly Ile Asp Met Tyr Leu Ala Ser Ala Met Ser Pro Thr Pro Arg
          260         265         270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
          275         280         285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290         295         300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305          310         315         320
Phe Phe Trp Cys

```

&lt;210&gt; 1285

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g202 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(144)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1285

```

Phe Ser Val Thr Gly Ile Ser Val Val Asp Cys Cys Phe Xaa Ser Thr
1          5          10         15
Val Ile Pro Glu Met Leu Phe Ser Cys Gln Val Gln His Leu Val His
          20         25         30
Asn Pro Lys Gly Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
          35         40         45
Leu Leu Thr Phe Phe Xaa Lys Ile Ser Phe His Arg Met His Phe Cys
          50         55         60
Ile Arg Asp Ser Ser Ser Gly Lys Ile Thr Val Tyr Tyr Leu Xaa Phe
65          70         75         80
Tyr Ile Cys Gly Gln Ile Val Leu Glu Gln Val Lys His Ile Xaa Glu
          85         90         95
Xaa Ser Leu Ser Leu Glu Phe Val Ile Phe Xaa Tyr Phe Tyr Lys Gly

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |     |     |
| Asp | Leu | Ala | Leu | Lys | Gln | Asn | Phe | Ala | Ile | Leu | Arg | Ser | Ile | Pro | Ser |
|     | 115 |     | 120 |     | 125 |     |     |     |     |     |     |     |     |     |     |
| Phe | Ser | Ser | Xaa | Asp | Leu | Glu | Ile | His | Asn | Val | Arg | Tyr | Gln | His | Phe |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |

&lt;210&gt; 1286

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g203 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1286

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | His | Gly | Tyr | Thr | Phe | Ser | Leu | Arg | Leu | Phe | Leu | His | Cys | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Tyr | Val | Xaa | Val | Ser | His | Cys | Leu | Leu | Ile | Trp | Leu | Ile | Thr | Phe | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Phe | Asn | Leu | Leu | Phe | Lys | Xaa | Asn | Leu | Xaa | Phe | Thr | Ile | Xaa | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ile | Thr | Xaa | Ile | Glu | Ser | Arg | Tyr | Ser | Lys | His | Trp | Pro | Phe | Phe | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Xaa | Cys | Phe | Cys | Asn | Val | Leu | Phe | His | Leu | Asp | Cys | Asp | Ser | Pro |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Val | Cys | Asn | Thr | Lys | Arg | Ile | Arg | Ser | Phe | Phe | Val | Leu | Glu | Arg | Xaa |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Lys | Ser | Ser | Xaa | Lys | Ser | Glu | Lys | Ile | His | Phe | Xaa | Thr | Arg | Asn | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Ser | Cys | Phe | Xaa | Asp | Phe | Gly | Ile | Lys | Tyr | Thr | Val | Tyr | Leu | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Leu | Lys | His | Phe | Leu | Leu | Ile | His | Ser | Ile | Leu | Arg | Tyr | Leu | Xaa |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Val | Ala | Gly | Tyr | Gly | Thr | Ser | Xaa | Phe | Leu | Ser | Arg | Ile | Ser | Ser | Ile |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Leu | Lys | Thr | Ile | Ile | Cys | Ile | Leu | Lys | Lys | Ser | Tyr | His | Phe | Phe |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Ser | Val | Gln | Tyr | Thr | Ile | Ser | Tyr | Ile | Asp | Pro | Phe | Ile | Asn | Ser | Leu |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| Val | Met | Phe | Val | Val | Phe | Thr | Ala | Phe | Ile | Gln | Ala | Phe | Ala | Phe | Met |
|     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |
| Ile | Ile | Ile | Val | Ser | Tyr | Thr | Gln | Val | Leu | Phe | Ala | Leu | Leu | Lys | Lys |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Asn | Ser | Glu | Lys | Gly | Arg | Ser | Lys | Ser | Phe | Leu | Met | Cys | Ser | Ala | His |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Leu | Ser | Val | Ser | Leu | Phe | Tyr | Ser | Ser | Val | Phe | Phe | Met | Tyr | Gly |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Cys | Pro | Arg | Ser | Gly | Pro | Asp | Xaa | Gln | Trp | Asn | Glu | Met | Tyr | Phe | Pro |
|     |     |     | 260 |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| Phe | Tyr | Met | Ile | Ile | Ile | Pro | Leu | Gln | Thr | Pro | Phe | Ile | Tyr | Ser | Met |
|     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |     |
| Lys | Asn | Lys | Glu | Val | Leu | Gly | Thr | Leu | Arg | Thr | Met | Ile | Lys | Lys | Tyr |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Phe | Trp | Arg | Thr | Leu | Ser | Xaa | Phe | Phe | Pro |     |     |     |     |     |     |
| 305 |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 1287

<211> 253  
 <212> PRT  
 <213> Unknown (H38g204 protein)

<220>  
 <223> Synthetic construct

<400> 1287  
 Met Cys Leu Phe Leu Cys His Leu Ser Phe Leu Asp Met Thr Ile Ser  
 1 5 10 15  
 Cys Ala Ile Val Pro Lys Met Leu Ala Gly Phe Leu Leu Gly Ser Arg  
 20 25 30  
 Ile Ile Ser Phe Gly Gly Cys Val Ile Gln Leu Phe Ser Phe His Phe  
 35 40 45  
 Leu Gly Cys Thr Glu Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg  
 50 55 60  
 Phe Leu Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Thr His  
 65 70 75 80  
 Arg Val Cys Asn Ser Leu Ala Leu Gly Thr Trp Leu Gly Gly Thr Ile  
 85 90 95  
 His Ser Leu Phe Gln Thr Ser Phe Val Phe Arg Leu Pro Phe Cys Gly  
 100 105 110  
 Pro Asn Arg Val Asp Tyr Ile Phe Cys Asp Ile Pro Ala Met Leu Arg  
 115 120 125  
 Leu Ala Cys Ala Asp Thr Ala Ile Asn Glu Leu Val Thr Phe Ala Asp  
 130 135 140  
 Ile Gly Phe Leu Ala Leu Thr Cys Phe Met Leu Ile Leu Thr Ser Tyr  
 145 150 155 160  
 Gly Tyr Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Asp Gly Arg  
 165 170 175  
 Arg Asn Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile Val  
 180 185 190  
 Tyr Tyr Val Pro Cys Thr Phe Ile Tyr Leu Arg Pro Cys Ser Gln Glu  
 195 200 205  
 Pro Leu Asp Gly Val Val Ala Val Phe Tyr Thr Val Ile Thr Pro Leu  
 210 215 220  
 Leu Asn Ser Ile Ile Tyr Thr Leu Cys Asn Lys Glu Met Lys Ala Ala  
 225 230 235 240  
 Leu Gln Arg Leu Gly Gly His Lys Glu Val Gln Pro His  
 245 250

<210> 1288  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g205 protein)

<220>  
 <223> Synthetic construct

<400> 1288  
 Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly  
 1 5 10 15  
 Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe  
 20 25 30  
 Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu  
 35 40 45  
 Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln  
 65 70 75 80  
 Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly

```

      85              90              95
Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys
      100              105              110
Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
      115              120              125
Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu
      130              135              140
Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr
      145              150              155              160
Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe
      165              170              175
Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu
      180              185              190
Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val
      195              200              205
Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val
      210              215              220
Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys
      225              230              235              240
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
      245              250              255
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
      260              265              270
Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile
      275              280              285
Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu
      290              295              300
Trp Arg Gly Arg Asp Ser Gly
      305              310

```

&lt;210&gt; 1289

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g206 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1289

```

Met Lys Ile Lys Asn His Thr Pro Val Thr Glu Val Pro Leu Met Gly
  1              5              10              15
Ile Pro His Thr Lys Gly Met Glu Asn Val Leu Phe Val Leu Phe Leu
      20              25              30
Ala Phe Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Leu Ala
      35              40              45
Val Leu Thr Phe Ser Asn Leu His Thr Pro Met Tyr Phe Phe Leu Gly
      50              55              60
Asn Leu Ser Val Phe Asp Ile Phe Phe Pro Ser Val Ser Ser Pro Lys
      65              70              75              80
Met Met Leu Cys Leu Val Gly Gln Ser Cys Thr Ile Ser Phe Gln Gly
      85              90              95
Cys Ala Ser Gln Leu Phe Phe His His Phe Leu Gly Cys Thr Glu Cys
      100              105              110
Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His
      115              120              125
Pro Leu Pro Tyr Thr Val Ile Met Lys Arg Arg Val Cys Ala Leu Leu
      130              135              140
Thr Leu Gly Thr Trp Thr Gly Ser Cys Leu His Ala Ser Val Leu Thr
      145              150              155              160
Leu Leu Ile Phe Lys Leu Ser Tyr Cys Gly Pro Asn Glu Val Asp Asn
      165              170              175

```



Phe Phe Cys Asp Ile Pro Val Val Leu Pro Leu Ala Cys Ala Asp Thr  
 180 185 190  
 Ser Leu Ala Arg Thr Val Ser Phe Ile Asn Val Gly Val Val Ala Leu  
 195 200 205  
 Met Cys Phe Leu Leu Ile Leu Thr Ser Tyr Ala Cys Ile Val Ile Ser  
 210 215 220  
 Ile Leu Lys Ile Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Leu Thr Ser Ile Leu Leu Phe Tyr Gly Pro Ile Val  
 245 250 255  
 Leu Ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val Val  
 260 265 270  
 Gln Val Leu Asn Asn Ile Val Ile Pro Ser Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu Ile  
 290 295 300  
 Gln Gly Val His Asn Cys Gly  
 305 310

&lt;210&gt; 1290

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g207 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(298)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1290

Val Arg Gly Ser Lys Gln Leu Arg Asn Gly Thr Leu Val Ser Gln Phe  
 1 5 10 15  
 Leu Leu Lys Gly Leu Arg Asp Ser Lys Ala Trp Arg Pro Leu Leu Phe  
 20 25 30  
 Thr Thr Phe Leu Leu Ile Tyr Ile Val Val Val Gly Ser His Met  
 35 40 45  
 Phe Thr Val Asp Tyr Arg Arg His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Gly His Ser Leu Met Asp Ala Ala Cys Ile Ser Asn Met Val Thr Gln  
 65 70 75 80  
 Val Leu Val His Leu Leu Ala Pro Val Gly Pro Val Leu Tyr Cys Ala  
 85 90 95  
 Cys Leu Ile Gln Ile Cys Phe Leu His Phe Leu Ala Pro Xaa Glu Ser  
 100 105 110  
 Phe Leu Leu Thr Ala Val Ala Tyr Asp Ser Met Leu Ala Ile Cys Gln  
 115 120 125  
 Pro Leu His Tyr Phe Val Leu Val Gly Arg Leu Thr His Thr Gly Leu  
 130 135 140  
 Thr Ser Ile Ser Cys Leu Leu Ala Leu Ala Asn Ala Phe Thr Tyr Ser  
 145 150 155 160  
 Ile Leu Thr Ala Leu Pro Lys Phe Cys Arg Pro Cys Leu Ile Thr His  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Ser Leu Leu Arg Leu Ser Cys Phe Ser Thr  
 180 185 190  
 Arg Thr Asn Glu Leu Ala Leu Phe Phe Ser Phe Leu Val Ala Leu Ala  
 195 200 205  
 His Cys Val Leu Val Val Val Ser Tyr Gly His Val Val Ala Ala Val  
 210 215 220  
 Gln Ile His Ser Thr Gln Gly Xaa Arg Lys Ala Phe Ser Thr Cys Val

225                      230                      235                      240  
 Ala His Leu Ala Met Ile Gly Leu Phe Tyr Val Thr Ser Val Pro Cys  
                                  245                      250                      255  
 Tyr Ile Leu Pro Asn Ser Ala Tyr Ser Gly Leu Gly Asp Trp Val Leu  
                                  260                      265                      270  
 Ser Val Leu Cys Val Val Leu Thr His Met Leu Asn Pro Ile Phe Pro  
                                  275                      280                      285  
 Ser Met Leu Gly Xaa Gln Cys Met Ser His  
                                  290                      295

&lt;210&gt; 1291

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g208 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1291

Met Gly Val Lys Asn His Ser Thr Val Thr Glu Phe Leu Leu Ser Gly  
 1                      5                      10                      15  
 Leu Thr Glu Gln Ala Glu Leu Gln Leu Pro Leu Phe Cys Leu Phe Leu  
                                  20                      25                      30  
 Gly Ile Tyr Thr Val Thr Val Val Gly Asn Leu Ser Met Ile Ser Ile  
                                  35                      40                      45  
 Ile Arg Leu Asn Arg Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
                                  50                      55                      60  
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys  
 65                      70                      75                      80  
 Met Leu Ser Gly Phe Leu Cys Arg Asp Arg Ser Ile Ser Tyr Ser Gly  
                                  85                      90                      95  
 Cys Met Ile Gln Leu Phe Phe Phe Cys Val Cys Val Ile Ser Glu Cys  
                                  100                      105                      110  
 Tyr Met Leu Ala Ala Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Ser  
                                  115                      120                      125  
 Pro Leu Leu Tyr Arg Val Ile Met Ser Pro Arg Val Cys Ser Leu Leu  
                                  130                      135                      140  
 Val Ala Ala Val Phe Ser Val Gly Phe Thr Asp Ala Val Ile His Gly  
 145                      150                      155                      160  
 Gly Cys Ile Leu Arg Leu Ser Phe Cys Gly Ser Asn Ile Ile Lys His  
                                  165                      170                      175  
 Tyr Phe Cys Asp Ile Val Pro Leu Ile Lys Leu Ser Cys Ser Ser Thr  
                                  180                      185                      190  
 Tyr Ile Asp Glu Leu Leu Ile Phe Val Ile Gly Gly Phe Asn Met Val  
                                  195                      200                      205  
 Ala Thr Ser Leu Thr Ile Ile Ser Tyr Ala Phe Ile Leu Thr Ser  
                                  210                      215                      220  
 Ile Leu Arg Ile His Ser Lys Lys Gly Arg Cys Lys Ala Phe Ser Thr  
 225                      230                      235                      240  
 Cys Ser Ser His Leu Thr Ala Val Leu Met Phe Tyr Gly Ser Leu Met  
                                  245                      250                      255  
 Ser Met Tyr Leu Lys Pro Ala Ser Ser Ser Leu Thr Gln Glu Lys  
                                  260                      265                      270  
 Val Ser Ser Val Phe Tyr Thr Thr Val Ile Leu Met Leu Asn Pro Leu  
                                  275                      280                      285  
 Ile Tyr Ser Leu Arg Asn Asn Glu Val Arg Asn Ala Leu Met Lys Leu  
                                  290                      295                      300  
 Leu Arg Arg Lys Ile Ser Leu Ser  
 305                      310

&lt;210&gt; 1292

<211> 251  
 <212> PRT  
 <213> Unknown (H38g209 protein)

<220>  
 <223> Synthetic construct

<400> 1292

```

Met Tyr Tyr Phe Leu Ser His Leu Ala Phe Val Asp Leu Cys Tyr Ser
 1           5           10           15
Ser Ala Ile Thr Pro Lys Met Met Val Asn Phe Val Val Glu Arg Asn
           20           25           30
Thr Ile Pro Phe His Ala Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr
           35           40           45
Phe Met Ile Thr Glu Cys Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys
           50           55           60
Tyr Val Ala Ile Cys Ser Pro Leu His Tyr Ser Thr Leu Met Ser Arg
           65           70           75           80
Arg Val Cys Ile Gln Leu Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu
           85           90           95
Val Ala Leu Phe His Thr Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly
           100          105          110
Pro Asn Leu Ile Asn His Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala
           115          120          125
Leu Ser Cys Ser Asp Thr His Met Lys Glu Ile Leu Ile Phe Ala Phe
           130          135          140
Ala Gly Phe Asp Met Ile Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr
           145          150          155          160
Ile Phe Ile Ile Ala Ala Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln
           165          170          175
His Lys Ala Ile Ser Thr Cys Gly Ser His Met Val Thr Val Thr Ile
           180          185          190
Phe Tyr Gly Thr Leu Ile Phe Met Tyr Leu Gln Pro Lys Ser Asn His
           195          200          205
Ser Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile
           210          215          220
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
           225          230          235          240
Asp Ala Ser Lys Lys Ala Leu Asp Lys Gly Cys
           245          250

```

<210> 1293  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g210 protein)

<220>  
 <223> Synthetic construct

<400> 1293

```

Met Ser Asn Ala Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1           5           10           15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
           20           25           30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
           35           40           45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
           50           55           60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
           65           70           75           80
Met Thr Leu Val Ser Pro Ser Gly Arg Thr Ile Ser Phe His Ser Cys

```

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 1294 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| His        | Ser | Ser | Leu | Leu | Phe | Ala | Val | Phe | Leu | Leu | Thr | Tyr | Ser | Val | Thr |
| 1          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu        | Val | Gly | Asn | Leu | Gly | Met | Thr | Asp | Leu | Ile | Cys | Gln | Ser | Arg | Thr |
|            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser        | Ser | Ala | Leu | His | Thr | Pro | Met | Cys | Phe | Leu | Leu | Ser | Val | Phe | Ser |
|            |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe        | Leu | Asp | Ile | Cys | Ser | Ser | Ser | Ile | Val | His | Pro | Arg | Leu | Leu | Ile |
|            | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His        | Phe | Leu | Thr | Thr | Arg | Pro | Ser | Ile | Ser | Phe | Ala | Gly | Gly | Ile | Ile |
| 65         |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln        | Met | Ala | Leu | Met | Thr | Phe | Tyr | Gly | Thr | Gly | Glu | Cys | Leu | Leu | Leu |
|            |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala        | Ile | Val | Ala | Tyr | Asp | Xaa | Val | Val | Ala | Ile | Cys | His | Pro | Phe | Pro |
|            |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Xaa        | His | Ile | Ile | Met | Ser | Lys | Gly | Leu | Cys | Ala | Gln | Leu | Val | Val | Val |
|            |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr        | Ser | Ala | Val | Gly | Val | Leu | Ile | Ser | Ala | His | Arg | Gln | Asp | Ala | Phe |
|            | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

Ile Ser Pro Tyr Arg Gly Leu Asn Ile Ile Asp His Tyr Tyr Cys Ser  
 145 150 155 160  
 Val Thr Phe Pro Thr Pro Met Leu Gln Leu Ala Cys Ser Asp Ala Thr  
 165 170 175  
 Val Ala Asn Met Ile Leu Phe Val Ser Ser Ala Leu Ile Thr Ile Pro  
 180 185 190  
 Thr Ile Ser Val Ile Leu Val Ser Tyr Thr Tyr Ile Leu Val Asn Leu  
 195 200 205  
 Val Arg Met Arg Ser Leu Asp Ala Gln Cys Lys Ala Phe Ser Thr Arg  
 210 215 220  
 Ala Ser His Leu Thr Ala His Cys Leu Phe Tyr Gly Phe Val Phe Leu  
 225 230 235 240  
 Val Tyr Ile Pro Pro Asn Pro Glu Met Ala Ser Ala Tyr Asn Lys Ile  
 245 250 255  
 Leu Phe Thr Val Val Ile Pro Met Leu Asn Leu Leu Val Xaa Gly Leu  
 260 265 270  
 Arg Asn Lys Asp Val Lys  
 275

&lt;210&gt; 1295

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g212 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1295

Ser Val Ala Lys Gly Asn His Ser Thr Val Tyr Glu Phe Ile Leu Leu  
 1 5 10 15  
 Gly Leu Thr Asp Asn Ala Glu Leu Gln Val Thr Leu Phe Gly Ile Phe  
 20 25 30  
 Leu Val Val Tyr Leu Ala Ser Phe Met Gly Asn Phe Gly Leu Ile Met  
 35 40 45  
 Leu Ile Gln Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser His Leu Ala Phe Val Asp Phe Ser Phe Thr Ser Ser Val Ala Pro  
 65 70 75 80  
 Asn Thr Leu Val Asn Phe Leu Cys Glu Val Lys Ser Ile Thr Phe Tyr  
 85 90 95  
 Ala Cys Ala Ile Gln Val Cys Cys Phe Ile Thr Phe Val Val Cys Glu  
 100 105 110  
 Leu Tyr Leu Leu Ser Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Leu Tyr Val Ile Leu Ile Pro Arg Lys Cys Ile Lys Leu  
 130 135 140  
 Ile Ala Ser Thr Tyr Val Tyr Gly Phe Thr Val Gly Leu Val Gln Thr  
 145 150 155 160  
 Val Ala Thr Ser Tyr Leu Ser Phe Cys Asp Ser Asn Val Ile Asn His  
 165 170 175  
 Phe Tyr His Asp Asp Val Pro Leu Val Ala Leu Ala Cys Ser Asp Thr  
 180 185 190  
 His Val Lys Glu Leu Met Leu Leu Ile Ile Ala Gly Phe Asn Thr Leu  
 195 200 205  
 Cys Ser Leu Val Ile Val Leu Ile Ser Tyr Gly Phe Ile Phe Phe Ala  
 210 215 220  
 Ile Leu Arg Ile His Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr  
 225 230 235 240  
 Ser Ala Ser His Leu Thr Ser Ile Thr Ile Phe Tyr Gly Thr Ile Ile  
 245 250 255  
 Phe Met Tyr Pro Gln Pro Lys Ser Ser His Ser Leu Asn Met Asp Lys

260 265 270  
 Val Ala Ser Val Phe Asn Val Val Val Ile Pro Thr Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Leu Lys Arg Ile  
 290 295 300  
 Ile Glu Lys Leu Cys Leu Ala Val  
 305 310

&lt;210&gt; 1296

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g213 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(232)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1296

Ser Gly Leu Val Pro Lys Ser Phe Pro Gly Cys Leu Thr Gln Leu Phe  
 1 5 10 15  
 Phe Leu His Tyr Ser Phe Val Leu Asp Ser Ala Ile Leu Leu Ala Met  
 20 25 30  
 Ala Phe Asp Arg Tyr Met Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr  
 35 40 45  
 Ile Leu Thr Pro Lys Thr Ile Val Lys Ile Ala Val Gly Ile Cys Phe  
 50 55 60  
 Arg Ser Phe Cys Val Phe Val Pro Cys Val Phe Leu Val Asn Arg Leu  
 65 70 75 80  
 Pro Phe Cys Arg Thr His Ile Ile Ser His Thr Tyr Cys Glu His Ile  
 85 90 95  
 Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Ile Trp Cys  
 100 105 110  
 Gly Phe Cys Val Pro Ile Met Thr Val Met Thr Asp Val Ile Leu Ile  
 115 120 125  
 Ala Val Ser Tyr Thr Leu Ile Leu Cys Ala Val Phe Cys Leu Pro Ser  
 130 135 140  
 Gln Asp Ala Arg Gln Lys Ala Leu Cys Ser Cys Gly Ser His Val Cys  
 145 150 155 160  
 Val Ile Leu Ile Phe Tyr Ile Pro Ala Phe Phe Ser Ile Leu Ala His  
 165 170 175  
 Cys Phe Gly His Asn Val Pro His Thr Phe His Ile Met Phe Ala Asn  
 180 185 190  
 Leu Tyr Val Ile Ile Pro Pro Ala Leu Asn Ser Ile Val Tyr Arg Ile  
 195 200 205  
 Lys Thr Lys Gln Ile Gln Asn Arg Ile Leu Leu Leu Phe Pro Lys Gly  
 210 215 220  
 Ser Gln Xaa Xaa Val Pro Glu Leu  
 225 230

&lt;210&gt; 1297

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g214 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1297

```

Met Ser Asn Ala Ser Leu Leu Thr Ala Phe Ile Leu Met Gly Leu Pro
1      5      10      15
His Ala Pro Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val
20      25      30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
35      40      45
Val Asp Ser His Leu His Thr Thr Met Tyr Tyr Phe Leu Thr Asn Leu
50      55      60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Leu Leu
65      70      75      80
Met Thr Leu Val Phe Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
85      90      95
Met Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Gly Thr Glu Cys Phe
100     105     110
Leu Tyr Arg Val Met Ser Cys Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
115     120     125
Leu Arg Tyr Thr Ser Met Met Thr Gly Arg Ser Cys Thr Leu Leu Ala
130     135     140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Ala Ile
145     150     155     160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Trp Ile Gln His Tyr
165     170     175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
180     185     190
Ala Ile Glu Thr Val Ile Phe Val Thr Val Gly Ile Val Ala Ser Gly
195     200     205
Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
210     215     220
Leu Arg Ile Arg Thr Ser Glu Gly Lys His Arg Ala Phe Gln Thr Cys
225     230     235     240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Gly Pro Gly Leu Phe
245     250     255
Ile Tyr Leu Arg Pro Gly Ser Arg Lys Ala Val Asp Gly Val Val Ala
260     265     270
Val Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
275     280     285
Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Leu Lys Leu Lys Asp Lys
290     295     300
Val Ala His Ser Gln Ser
305     310

```

&lt;210&gt; 1298

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g215 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1298

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
1      5      10      15
Thr Ser Arg Arg Glu Leu Gln Ile Leu Leu Phe Thr Leu Phe Leu Ala
20      25      30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Val Leu Ile
35      40      45
Gln Ala Asn Ala Trp Leu His Met Pro Met Tyr Phe Phe Leu Ser His
50      55      60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
65      70      75      80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys

```

|            |            |            |           |            |     |            |            |           |            |            |            |     |     |           |            |
|------------|------------|------------|-----------|------------|-----|------------|------------|-----------|------------|------------|------------|-----|-----|-----------|------------|
| Met<br>1   | Leu        | Leu        | Ser       | Asn<br>5   | Ile | Thr        | Gln        | Phe       | Ser<br>10  | Pro        | Ile        | Phe | Tyr | Leu<br>15 | Thr        |
| Ser        | Phe        | Pro        | Gly<br>20 | Leu        | Glu | Gly        | Ile        | Lys<br>25 | His        | Trp        | Ile        | Phe | Ile | Pro       | Phe        |
| Phe        | Phe        | Met<br>35  | Tyr       | Met        | Val | Ala        | Ile<br>40  | Ser       | Gly        | Asn        | Cys        | Phe | Ile | Leu       | Ile        |
| Ile        | Ile<br>50  | Lys        | Thr       | Asn        | Pro | Arg<br>55  | Leu        | His       | Thr        | Pro        | Met<br>60  | Tyr | Tyr | Leu       | Leu        |
| Ser<br>65  | Leu        | Leu        | Ala       | Leu<br>70  | Thr | Asp        | Leu        | Gly       | Leu        | Cys<br>75  | Val        | Ser | Thr | Leu       | Pro<br>80  |
| Thr        | Thr        | Met        | Gly<br>85 | Ile        | Phe | Trp        | Phe        | Asn<br>90 | Ser        | Gln        | Ser        | Ile | Tyr | Phe       | Gly        |
| Ala        | Cys        | Gln<br>100 | Ile       | Gln        | Met | Phe        | Cys<br>105 | Ile       | His        | Ser        | Phe        | Ser | Phe | Met       | Glu        |
| Ser        | Ser        | Val<br>115 | Leu       | Leu        | Met | Met        | Ser<br>120 | Phe       | Asp        | Arg        | Phe        | Val | Ala | Ile       | Cys        |
| His        | Pro<br>130 | Leu        | Arg       | Tyr        | Ser | Val<br>135 | Ile        | Ile       | Thr        | Gly        | Gln<br>140 | Gln | Val | Val       | Arg        |
| Ala<br>145 | Gly        | Leu        | Ile       | Val<br>150 | Ile | Phe        | Arg        | Gly       | Pro        | Val<br>155 | Ala        | Thr | Ile | Pro       | Ile<br>160 |
| Val        | Leu        | Leu        | Leu       | Lys<br>165 | Ala | Phe        | Pro        | Tyr       | Cys<br>170 | Gly        | Ser        | Val | Val | Leu       | Ser        |



His Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp  
 180 185 190  
 Thr Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val  
 195 200 205  
 Met Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His  
 210 215 220  
 Thr Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln  
 225 230 235 240  
 Thr Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met  
 245 250 255  
 Met Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala  
 260 265 270  
 Ile His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile  
 290 295 300  
 Ile Lys Leu Leu Gly Leu Lys Lys Ala Ser Lys  
 305 310 315

&lt;210&gt; 1300

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g217 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1300

Met Asn Pro Glu Asn Trp Thr Gln Val Thr Ser Phe Val Leu Leu Gly  
 1 5 10 15  
 Phe Pro Ser Ser His Leu Ile Gln Phe Leu Val Phe Leu Gly Leu Met  
 20 25 30  
 Val Thr Tyr Ile Val Thr Ala Thr Gly Lys Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ser Trp Ile Asp Gln Arg Leu His Ile Gln Met Tyr Phe Phe Leu Arg  
 50 55 60  
 Asn Phe Ser Phe Leu Glu Leu Leu Val Thr Val Val Val Pro Lys  
 65 70 75 80  
 Met Leu Val Val Ile Leu Thr Gly Asp His Thr Ile Ser Phe Val Ser  
 85 90 95  
 Cys Ile Ile Gln Ser Tyr Leu Tyr Phe Phe Leu Gly Thr Thr Asp Phe  
 100 105 110  
 Phe Leu Leu Ala Val Met Ser Leu Asp Arg Tyr Leu Ala Ile Cys Arg  
 115 120 125  
 Pro Leu Arg Tyr Glu Thr Leu Met Asn Gly His Val Cys Ser Gln Leu  
 130 135 140  
 Val Leu Ala Ser Trp Leu Ala Gly Phe Leu Trp Val Leu Cys Pro Thr  
 145 150 155 160  
 Val Leu Met Ala Ser Leu Pro Phe Cys Gly Pro Asn Gly Ile Asp His  
 165 170 175  
 Phe Phe Arg Asp Ser Trp Pro Leu Leu Arg Leu Ser Cys Gly Asp Thr  
 180 185 190  
 His Leu Leu Lys Leu Val Ala Phe Met Leu Ser Thr Leu Val Leu Leu  
 195 200 205  
 Gly Ser Leu Ala Leu Thr Ser Val Ser Tyr Ala Cys Ile Leu Ala Thr  
 210 215 220  
 Val Leu Arg Ala Pro Thr Ala Ala Glu Arg Arg Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Val Ile Ile Tyr Gly Ser Ser Ile  
 245 250 255  
 Phe Leu Tyr Ile Arg Met Ser Glu Ala Gln Ser Lys Leu Leu Asn Lys

|            |         |         |         |         |         |         |         |         |         |         |         |         |         |     |     |
|------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----|-----|
| <400> 1301 |         |         |         |         |         |         |         |         |         |         |         |         |         |     |     |
| Met 1      | Met     | Gly     | Glu     | Ala 5   | Arg     | Asn     | Arg     | Thr     | Val 10  | Val     | Gln     | Glu     | Phe 15  | Ile | Leu |
| Glu        | Gly     | Phe     | Pro 20  | Ala     | Val     | Gln     | His     | Leu 25  | Gly     | Asn     | Val     | Leu     | Phe 30  | Leu | Val |
| His        | Leu     | Leu 35  | Ala     | Tyr     | Leu     | Ala     | Ser 40  | Ile     | Met     | Ala     | Asn     | Met 45  | Leu     | Ile | Ile |
| Thr        | Ile 50  | Thr     | Trp     | Ala     | Asp     | His 55  | His     | Leu     | Gln     | Thr     | Pro 60  | Met     | Tyr     | Phe | Phe |
| Leu 65     | Asn     | Ser     | Phe     | Ser     | Phe 70  | Cys     | Glu     | Cys     | Cys     | Phe 75  | Ile     | Thr     | Thr     | Val | Ile |
| Pro        | Lys     | Leu     | Leu     | Val 85  | Ile     | Phe     | Leu     | Ser     | Gly 90  | Arg     | Gln     | Ile     | Ile     | Pro | Phe |
| Thr        | Thr     | Cys     | Leu 100 | Met     | Gln     | Ser     | Phe     | Ser 105 | Phe     | Leu     | Phe     | Leu     | Gly 110 | Ser | Thr |
| Val        | Phe 115 | Phe     | Leu     | Met     | Ala     | Val     | Met 120 | Ser     | Leu     | Asp     | Xaa     | Tyr     | Leu     | Ala | Ile |
| Cys        | Lys 130 | Pro     | Leu     | His     | Tyr     | Ser 135 | Thr     | Ile     | Met     | Ser     | Leu 140 | Arg     | Thr     | Ser | Phe |
| His 145    | Leu     | Val     | Thr     | Val     | Cys 150 | Phe     | Val     | Val     | Gly     | Phe 155 | Thr     | Leu     | Ile     | Thr | Gly |
| Leu        | Met     | Val     | Lys     | Val 165 | Ser     | Gln     | Leu     | Ser     | Phe 170 | Cys     | Gly     | Pro     | His     | Val | Ile |
| Pro        | His     | Phe     | Phe 180 | Arg     | Asp     | Leu     | Gly     | Pro 185 | Leu     | Ile     | Gln     | Leu     | Ser 190 | Cys | Ser |
| Asp        | Thr 195 | Arg     | Ser     | Thr     | Glu     | Thr     | Leu 200 | Ala     | Phe     | Val     | Leu     | Val 205 | Ser     | Phe | Val |
| Leu        | Phe 210 | Thr     | Ser     | Leu     | Ile     | Ile 215 | Thr     | Ile     | Ile     | Ala     | Tyr     | Gly 220 | Asn     | Ile | Val |
| Val 225    | Thr     | Ile     | Val     | Arg     | Leu     | Pro     | Ser     | Ala     | Lys     | Glu 235 | Arg     | Gln     | Lys     | Ala | Phe |
| Ser        | Thr     | Cys     | Ser     | Ser 245 | His     | Leu     | Ile     | Val     | Leu 250 | Ser     | Leu     | Val     | Tyr     | Gly | Ser |
| Cys        | Val     | Phe     | Ile 260 | Tyr     | Val     | Lys     | Pro     | Lys 265 | Gln     | Met     | Asp     | Arg     | Leu 270 | Asp | Ser |
| Asn        | Arg     | Met 275 | Ala     | Ala     | Leu     | Val     | Asn 280 | Thr     | Val     | Val     | Thr     | Pro 285 | Leu     | Leu | Asn |
| Pro        | Ile 290 | Ile     | Tyr     | Thr     | Leu     | Arg 295 | Asn     | Lys     | Gln     | Val     | His     | Gln     | Ala     | Leu | Arg |

Asp Ala Gln Ser Arg Met Lys Leu Xaa Lys Gln Asn His Asn Leu Gln  
 305 310 315 320  
 Xaa Arg Asn Ala Pro Phe Leu Asp Leu Ile Gln Ser Phe Ser Cys Phe  
 325 330 335  
 Trp Asn

<210> 1302

<211> 309

<212> PRT

<213> Unknown (H38g219 protein)

<220>

<223> Synthetic construct

<400> 1302

Met Ala Ser Thr Ser Asn Val Thr Glu Leu Ile Phe Thr Gly Leu Phe  
 1 5 10 15  
 Gln Asp Pro Ala Val Gln Ser Val Cys Phe Val Val Phe Leu Pro Val  
 20 25 30  
 Tyr Leu Ala Thr Val Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser  
 35 40 45  
 Ile Ser Lys Ser Leu Asp Ser Pro Met Tyr Phe Phe Leu Ser Cys Leu  
 50 55 60  
 Ser Leu Val Glu Ile Ser Tyr Ser Ser Thr Ile Ala Pro Lys Phe Ile  
 65 70 75 80  
 Ile Asp Leu Leu Ala Lys Ile Lys Thr Ile Ser Leu Glu Gly Cys Leu  
 85 90 95  
 Thr Gln Ile Phe Phe Phe His Phe Phe Gly Val Ala Glu Ile Leu Leu  
 100 105 110  
 Ile Val Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Met Asn Ile Ile Ser Arg Gln Leu Cys His Leu Leu Val Ala  
 130 135 140  
 Gly Ser Trp Leu Gly Gly Phe Cys His Ser Ile Ile Gln Ile Leu Val  
 145 150 155 160  
 Ile Ile Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Tyr Phe  
 165 170 175  
 Cys Asp Leu Gln Pro Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Met  
 180 185 190  
 Glu Gly Val Ile Val Leu Ala Asn Ser Gly Leu Phe Ser Val Phe Ser  
 195 200 205  
 Phe Leu Ile Leu Val Ser Ser Tyr Ile Val Ile Leu Val Asn Leu Arg  
 210 215 220  
 Asn His Ser Ala Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ala Ser  
 225 230 235 240  
 His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Ala Ile Phe Leu Tyr  
 245 250 255  
 Met Arg Pro Ser Ser Thr Phe Thr Glu Asp Lys Leu Val Ala Val Phe  
 260 265 270  
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Ala Glu Val Lys Ile Ala Ile Arg Arg Leu Trp Ser Lys Lys Glu  
 290 295 300  
 Asn Pro Gly Arg Glu  
 305

<210> 1303

<211> 322

<212> PRT

<213> Unknown (H38g220 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1303

```

Met Ala Lys Gly Asn His Ser Ser Val Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Thr Asp Asn Gln Glu Leu Gln Val Ile Leu Phe Gly Val Phe Leu
 20          25          30
Leu Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Val Leu
 35          40          45
Ile His Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
His Leu Ala Phe Val Asp Phe Tyr Gly Thr Ser Ala Ile Thr Pro Asn
 65          70          75          80
Thr Leu Val Asn Ser Leu His Glu Ile Lys Ser Met Ser Phe Tyr Ala
 85          90          95
Cys Ala Thr Gln Val Cys Cys Phe Ile Thr Leu Ser Val Trp Glu Val
 100          105          110
Ile Val Ala Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115          120          125
Leu Leu Tyr Val Val Leu Met Pro Arg Arg Leu Cys Ile Gln Met Val
 130          135          140
Thr Gly Leu Tyr Ile Tyr Gly Phe Thr Met Gly Leu Ile Gln Ala Val
 145          150          155          160
Ala Thr Phe His Met Ser Phe Cys Asp Ser Asn Val Val Asn Gln Phe
 165          170          175
Tyr Cys Asp Asp Val Pro Leu Ile Ala Leu Ala Cys Ser Asp Thr Gln
 180          185          190
Val Lys Glu Leu Met Leu Phe Ile Ile Ala Ala Phe Asn Val Phe Cys
 195          200          205
Ser Leu Ile Ile Val Leu Ile Ser Tyr Val Phe Ile Val Phe Ala Ile
 210          215          220
Leu Arg Ile His Ser Ala Val Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225          230          235          240
Ala Ser His Met Phe Ser Ile Ser Ile Tyr Tyr Gly Thr Leu Ser Phe
 245          250          255
Met Tyr Leu Gln Pro Lys Ser Ser His Ser Leu Asp Lys Asp Lys Phe
 260          265          270
Ala Ser Val Phe Tyr Ala Val Val Ile Pro Met Leu Asn Pro Leu Ile
 275          280          285
Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Met Lys Lys Ile Ile
 290          295          300
Glu Lys Met Cys Ser Ser Asn Gln Gln Xaa Asn Leu Leu Val Leu Lys
 305          310          315          320
Glu Ile

```

&lt;210&gt; 1304

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g221 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1304

```

Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
 1           5           10           15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
          20           25           30
Val Cys Cys Leu Tyr Thr Ile Ser Ile Met Gly Asn Thr Thr Ile Leu
          35           40           45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
          50           55           60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
65           70           75           80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
          85           90           95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
          115          120          125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly
          130          135          140
Arg Thr Gly Leu Ala Ile Ile Cys Cys Cys Val Leu Ala Val Leu Pro
145           150           155           160
Ser Leu Phe Leu Leu Lys Arg Leu Pro Phe Cys His Ser His Leu Leu
          165          170          175
Ser Arg Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Val Cys Ala
          180          185          190
Asp Ile Arg Leu Asn Ser Trp Tyr Gly Phe Ala Leu Ala Leu Ile
          195          200          205
Ile Ile Val Asp Pro Leu Leu Ile Val Ile Ser Tyr Thr Leu Ile Leu
          210          215          220
Lys Asn Ile Leu Gly Thr Ala Thr Trp Ala Glu Arg Leu Arg Ala Leu
225           230           235           240
Asn Asn Cys Leu Ser His Ile Leu Ala Val Leu Val Leu Tyr Ile Pro
          245          250          255
Met Val Gly Val Ser Met Thr His Arg Phe Ala Lys His Ala Ser Pro
          260          265          270
Leu Val His Val Ile Met Ala Asn Ile Tyr Leu Leu Ala Pro Pro Val
          275          280          285
Met Asn Pro Ile Ile Tyr Ser Val Lys Asn Lys Gln Ile Gln Trp Gly
          290          295          300
Met Leu Asn Phe Leu Ser Leu Lys Asn Met His Ser Arg
305           310           315

```

&lt;210&gt; 1305

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g222 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1305

```

Met Asn Pro Ala Asn His Ser Gln Val Ala Gly Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Gln Val Trp Glu Leu Arg Phe Val Phe Phe Thr Val Phe Ser
          20           25           30
Ala Val Tyr Phe Met Thr Val Val Gly Asn Leu Leu Ile Val Val Ile
          35           40           45
Val Thr Ser Asp Pro His Leu His Thr Thr Met Tyr Phe Leu Leu Gly
          50           55           60
Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Ile Thr Ala Pro Arg
65           70           75           80
Met Leu Val Asp Leu Leu Ser Gly Asn Pro Thr Ile Ser Phe Gly Gly

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Leu | Thr | Gln | Leu | Phe | Phe | Phe | His | Phe | Ile | Gly | Gly | Ile | Lys | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Leu | Leu | Thr | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Ile | Ala | Ile | Ser | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | His | Tyr | Thr | Leu | Ile | Met | Asn | Gln | Thr | Val | Cys | Ala | Leu | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Ala | Ala | Ser | Trp | Val | Gly | Gly | Phe | Ile | His | Ser | Ile | Val | Gln | Ile |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Leu | Thr | Ile | Gln | Leu | Pro | Phe | Cys | Gly | Pro | Asp | Lys | Leu | Asp | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Tyr | Cys | Asp | Val | Pro | Gln | Leu | Ile | Lys | Leu | Ala | Cys | Thr | Asp | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Val | Leu | Glu | Leu | Leu | Met | Val | Ser | Asn | Asn | Gly | Leu | Val | Thr | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Met | Trp | Phe | Leu | Val | Leu | Leu | Gly | Ser | Tyr | Thr | Ala | Leu | Leu | Val | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Arg | Ser | His | Ser | Arg | Glu | Gly | Arg | Ser | Lys | Ala | Leu | Ser | Thr | Cys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Ser | His | Ile | Ala | Val | Val | Thr | Leu | Ile | Phe | Val | Pro | Cys | Ile | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Tyr | Thr | Arg | Pro | Phe | Arg | Thr | Phe | Pro | Met | Asp | Lys | Ala | Val | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Leu | Tyr | Thr | Ile | Val | Thr | Pro | Met | Leu | Asn | Pro | Ala | Ile | Tyr | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Arg | Asn | Lys | Glu | Val | Ile | Met | Ala | Met | Lys | Lys | Leu | Trp | Arg | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Lys | Asp | Pro | Ile | Gly | Pro | Leu | Glu | His | Arg |     |     |     |     |     |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     |     |

<210> 1306

<211> 320

<212> PRT

<213> Unknown (H38g223 protein)

**<220>**

<223> Synthetic construct

&lt;400&gt; 1306

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Phe | Leu | Asn | Gly | Thr | Ser | Leu | Thr | Pro | Ala | Ser | Phe | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Gly | Ile | Pro | Gly | Leu | Glu | Asp | Val | His | Leu | Trp | Ile | Ser | Phe | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Cys | Thr | Met | Tyr | Ser | Ile | Ala | Ile | Thr | Gly | Asn | Phe | Gly | Leu | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Leu | Ile | Tyr | Cys | Asp | Glu | Ala | Leu | His | Arg | Pro | Met | Tyr | Val | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Leu | Leu | Ser | Phe | Thr | Asp | Val | Leu | Met | Cys | Thr | Ser | Thr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Asn | Thr | Leu | Phe | Ile | Leu | Trp | Phe | Asn | Leu | Lys | Glu | Ile | Asp | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Ala | Cys | Leu | Ala | Gln | Met | Phe | Phe | Val | His | Thr | Phe | Thr | Gly | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ser | Gly | Val | Leu | Met | Leu | Met | Ala | Leu | Asp | His | Cys | Val | Ala | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Phe | Pro | Leu | Arg | Tyr | Ala | Thr | Ile | Leu | Thr | Asn | Ser | Val | Ile | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ala | Gly | Phe | Leu | Thr | Phe | Leu | Arg | Gly | Val | Met | Leu | Val | Ile | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Thr | Phe | Leu | Thr | Lys | Arg | Leu | Pro | Tyr | Cys | Lys | Gly | Asn | Val | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Ile Ser Cys Gly  
 180 185 190  
 Asn Val Arg Val Asn Ala Ile Tyr Gly Leu Ile Val Ala Leu Leu Ile  
 195 200 205  
 Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu  
 210 215 220  
 Gln Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe  
 225 230 235 240  
 Ser Thr Cys Thr Ala His Phe Cys Ala Ile Val Leu Thr Tyr Val Pro  
 245 250 255  
 Ala Phe Phe Thr Phe Phe Thr His His Phe Gly Gly His Thr Ile Pro  
 260 265 270  
 Leu His Ile His Ile Ile Met Ala Asn Leu Tyr Leu Leu Met Pro Pro  
 275 280 285  
 Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Arg Gln Val Arg Glu  
 290 295 300  
 Ser Val Ile Arg Phe Phe Leu Lys Gly Lys Asp Asn Ser His Asn Phe  
 305 310 315 320

&lt;210&gt; 1307

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g224 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1307

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser  
 1 5 10 15  
 Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met  
 20 25 30  
 Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu  
 35 40 45  
 Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu  
 50 55 60  
 Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile  
 65 70 75 80  
 Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu  
 85 90 95  
 Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu  
 100 105 110  
 Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg  
 130 135 140  
 Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu  
 145 150 155 160  
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe  
 165 170 175  
 Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe  
 180 185 190  
 Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser  
 195 200 205  
 Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg  
 210 215 220  
 Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser  
 225 230 235 240  
 His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr  
 245 250 255  
 Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe

260 265 270  
 Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg  
 275 280 285  
 Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val  
 290 295 300  
 Ile  
 305

<210> 1308  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g225 protein)

<220>  
 <223> Synthetic construct

<400> 1308  
 Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly  
 1 5 10 15  
 Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu  
 20 25 30  
 Val Leu Tyr Gly Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu  
 35 40 45  
 Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln  
 50 55 60  
 His Leu Ala Leu Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys  
 65 70 75 80  
 Met Leu Ile Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu  
 85 90 95  
 Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val  
 100 105 110  
 Ile Met Leu Ala Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu  
 130 135 140  
 Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser  
 145 150 155 160  
 Ser Tyr Val Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His  
 165 170 175  
 Phe Tyr Cys Asp Asn Val Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr  
 180 185 190  
 Tyr Leu Pro Glu Thr Val Val Phe Ile Ser Ala Ala Thr Asn Val Val  
 195 200 205  
 Gly Ser Leu Ile Ile Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser  
 210 215 220  
 Ile Leu Lys Ile Cys Ser Ser Glu Gly Arg Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Met Met Ala Val Thr Ile Phe Tyr Gly Thr Leu Leu  
 245 250 255  
 Phe Met Tyr Val Gln Pro Arg Ser Asn His Ser Leu Asp Thr Asp Asp  
 260 265 270  
 Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Thr Ala Leu Gln Arg  
 290 295 300  
 Phe Met Thr Asn Leu Cys Tyr Ser Phe  
 305 310

<210> 1309  
 <211> 326  
 <212> PRT



<213> Unknown (H38g226 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1309

```

Met Lys Ile Ser Asn Asn Ser Leu Gly Phe Leu Pro Thr Thr Phe Ile
 1           5           10          15
Leu Val Gly Ile Pro Gly Leu Glu Ser Glu His Leu Trp Ile Ser Val
           20           25           30
Pro Phe Ser Leu Ile Tyr Ile Ile Phe Leu Gly Asn Gly Ile Ile
 35           40           45
Leu His Val Ile Arg Thr Asp Ile Ala Leu His Gln Pro Met Tyr Leu
 50           55           60
Phe Leu Ala Met Leu Ala Leu Ala Glu Val Arg Val Ser Ala Ser Thr
 65           70           75           80
Leu Pro Thr Val Leu Gly Ile Phe Leu Phe Gly Asn Thr Glu Ile Ser
           85           90           95
Leu Glu Ala Phe Phe Phe Gln Met Phe Ser Ile His Ser Leu Ser Met
           100          105          110
Met Glu Ser Ala Val Leu Leu Ala Met Ser Leu Asp Arg Phe Ile Ala
 115          120          125
Ile Tyr Ser Pro Leu Ser Tyr Thr Ala Ile Leu Thr Leu Pro Arg Val
 130          135          140
Phe Gly Thr Gly Ala Ile Ile Val Leu Lys Ser Ile Met Leu Met Ala
 145          150          155          160
Pro Leu Pro Ile Leu Leu Trp Arg Leu Pro Phe Cys Gly His Asn Ala
           165          170          175
Leu Ser His Ser Tyr Cys Leu His Pro Asn Leu Ile Tyr Leu Ser Cys
           180          185          190
Gly Asn Ile Ser Val Asn Asn Ile Tyr Gly Ile Phe Ile Val Thr Ser
 195          200          205
Thr Phe Gly Leu Asp Ser Leu Leu Ile Val Ile Ser Tyr Gly Leu Ile
 210          215          220
Leu His Thr Val Leu Gly Ile Ala Thr Gly Glu Gly Arg Lys Lys Ala
 225          230          235          240
Leu Asn Thr Cys Gly Ser His Val Cys Ala Val Leu Ala Tyr Tyr Val
           245          250          255
Pro Met Ile Gly Leu Ser Ile Val His Arg Leu Gly His Arg Val Ser
           260          265          270
Pro Leu Leu Gln Ala Met Met Ala Asn Ala Tyr Leu Phe Phe Pro Pro
           275          280          285
Val Val Asn Pro Ile Val Tyr Ser Ile Lys Thr Lys Glu Ile His Gly
 290          295          300
Ala Ile Val Arg Met Leu Leu Glu Lys Arg Arg Arg Val Xaa Pro Lys
 305          310          315          320
Thr Ile Val Gly Arg Asn
           325

```

<210> 1310

<211> 311

<212> PRT

<213> Unknown (H38g227 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1310

```

Met Ser Lys Thr Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1           5           10           15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
          20           25           30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35           40           45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
          50           55           60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
          65           70           75           80
Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
          85           90           95
Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
          100          105          110
Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
          115          120          125
Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
          130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
          145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
          165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
          180          185          190
Ala Asn Glu Met Val Ile Phe Val Asp Ile Gly Leu Val Ala Ser Gly
          195          200          205
Cys Phe Leu Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
          210          215          220
Leu Arg Ile His Thr Ser Glu Gly Arg His Arg Ala Phe Gln Thr Cys
          225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Phe
          245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Asp Val Val Asp Gly Val Val Ala
          260          265          270
Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
          275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
          290          295          300
Val Ala His Ser Gln Gly Glu
          305          310

```

&lt;210&gt; 1311

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g228 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1311

```

Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
          20           25           30
Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu
          35           40           45
Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe
          50           55           60
Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile
          65           70           75           80

```

Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gln Glu Ile Ser Phe  
                             85                            90                            95  
 Gly Gly Cys Leu Leu Gln Met Phe Phe Ile His Met Phe Thr Gly Met  
                             100                            105                            110  
 Glu Thr Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Val Ala Ile  
                             115                            120                            125  
 Cys Asn Pro Leu Gln Tyr Thr Met Ile Leu Thr Asn Lys Thr Ile Ser  
                             130                            135                            140  
 Ile Leu Ala Ser Val Val Val Gly Arg Asn Leu Val Leu Val Thr Pro  
 145                            150                            155                            160  
 Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly His Asn Ile Val  
                             165                            170                            175  
 Pro His Thr Tyr Cys Glu His Arg Gly Leu Ala Gly Leu Ala Cys Ala  
                             180                            185                            190  
 Pro Ile Lys Ile Asn Ile Ile Tyr Gly Leu Met Val Ile Ser Tyr Ile  
                             195                            200                            205  
 Ile Val Asp Val Ile Leu Ile Ala Ser Ser Tyr Val Leu Ile Leu Arg  
                             210                            215                            220  
 Ala Val Phe Arg Leu Pro Ser Gln Asp Val Arg Leu Lys Ala Phe Asn  
 225                            230                            235                            240  
 Thr Cys Gly Ser His Val Cys Val Met Leu Cys Phe Tyr Thr Pro Ala  
                             245                            250                            255  
 Phe Phe Ser Phe Met Thr His Arg Phe Gly Gln Asn Ile Pro His Tyr  
                             260                            265                            270  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu  
                             275                            280                            285  
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Gln Ile  
                             290                            295                            300  
 Val Lys Ile Phe Val Gln Lys Glu  
 305                            310

&lt;210&gt; 1312

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g229 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1312

Met Thr Glu Phe Ile Phe Leu Val Leu Ser Pro Asn Gln Glu Val Gln  
   1                            5                            10                            15  
 Arg Val Cys Phe Val Ile Phe Leu Phe Leu Tyr Thr Ala Ile Val Leu  
                             20                            25                            30  
 Gly Asn Phe Leu Ile Val Leu Thr Val Met Thr Ser Arg Ser Leu Gly  
                             35                            40                            45  
 Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu Ser Phe Met Glu Ile Cys  
                             50                            55                            60  
 Tyr Ser Ser Ala Thr Ala Pro Lys Leu Ile Ser Asp Leu Leu Ala Glu  
 65                            70                            75                            80  
 Arg Lys Val Ile Ser Trp Trp Gly Cys Met Ala Gln Leu Phe Phe Leu  
                             85                            90                            95  
 His Phe Phe Gly Gly Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr  
                             100                            105                            110  
 Asp His Tyr Val Ala Ile Cys Lys Pro Leu Ser Tyr Thr Thr Ile Met  
                             115                            120                            125  
 Asn Trp Gln Val Cys Thr Val Leu Val Gly Ile Ala Trp Val Gly Gly  
                             130                            135                            140  
 Phe Met His Ser Phe Ala Gln Ile Leu Leu Ile Phe His Leu Leu Phe  
 145                            150                            155                            160  
 Cys Gly Pro Asn Val Ile Asn His Tyr Phe Cys Asp Leu Val Pro Leu

```

      165      170      175
Leu Lys Leu Ala Cys Ser Asp Thr Phe Leu Ile Gly Leu Leu Ile Val
      180      185      190
Ala Asn Gly Gly Thr Leu Ser Val Ile Ser Phe Gly Val Leu Leu Ala
      195      200      205
Ser Tyr Met Val Ile Leu Leu His Leu Arg Thr Trp Ser Ser Glu Gly
      210      215      220
Trp Cys Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ala Val Val Ile
      225      230      235      240
Leu Phe Phe Gly Pro Cys Val Phe Asn Ser Leu Arg Pro Ser Thr Thr
      245      250      255
Leu Pro Ile Asp Lys Met Val Ala Val Phe Tyr Thr Val Ile Thr Ala
      260      265      270
Ile Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Ala Glu Met Arg Lys
      275      280      285
Ala Met Lys Arg Leu Trp Ile Arg Thr Leu Arg Leu Asn Glu Lys
      290      295      300

```

&lt;210&gt; 1313

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g230 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1313

```

Leu Ile Ala Thr Gly Asn Trp Thr Arg Ile Ser Glu Phe Ile Leu Met
 1      5      10      15
Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu Phe Leu Thr
      20      25      30
Phe Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Cys Leu Ile Ile
      35      40      45
Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met Tyr Phe Phe
      50      55      60
Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val
      65      70      75      80
Pro Lys Met Leu Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe
      85      90      95
Leu Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Gly Val Ala
      100      105      110
Glu Cys Phe Leu Gln Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala
      130      135      140
Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val
      145      150      155      160
Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val
      165      170      175
Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala
      180      185      190
Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val
      195      200      205
Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala
      210      215      220
Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe
      225      230      235      240
Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser
      245      250      255
Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly
      260      265      270

```

Thr Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn  
 275 280 285  
 Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser  
 290 295 300  
 Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu  
 305 310 315

&lt;210&gt; 1314

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g231 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1314

Met Pro Asn Phe Thr Asp Val Thr Glu Phe Thr Leu Leu Gly Leu Thr  
 1 5 10 15  
 Cys Arg Gln Glu Leu Gln Val Leu Phe Phe Val Val Phe Leu Ala Val  
 20 25 30  
 Tyr Met Ile Thr Leu Leu Gly Asn Ile Gly Met Ile Ile Leu Ile Ser  
 35 40 45  
 Ile Ser Pro Gln Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His Leu  
 50 55 60  
 Ser Phe Ala Asp Val Cys Phe Ser Ser Asn Val Thr Pro Lys Met Leu  
 65 70 75 80  
 Glu Asn Leu Leu Ser Glu Thr Lys Thr Ile Ser Tyr Val Gly Cys Leu  
 85 90 95  
 Val Gln Cys Tyr Phe Phe Ile Ala Val Val His Val Glu Val Tyr Ile  
 100 105 110  
 Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Gly Cys Asn Pro Leu  
 115 120 125  
 Leu Tyr Gly Ser Lys Met Ser Arg Thr Val Cys Val Arg Leu Ile Ser  
 130 135 140  
 Val Pro Tyr Val Tyr Gly Phe Ser Val Ser Leu Ile Cys Thr Leu Trp  
 145 150 155 160  
 Thr Tyr Gly Leu Tyr Phe Cys Gly Asn Phe Glu Ile Asn His Phe Tyr  
 165 170 175  
 Cys Ala Asp Pro Pro Leu Ile Gln Ile Ala Cys Gly Arg Val His Ile  
 180 185 190  
 Lys Glu Ile Thr Met Ile Val Ile Ala Gly Ile Asn Phe Thr Tyr Ser  
 195 200 205  
 Leu Ser Val Val Leu Ile Ser Tyr Thr Leu Ile Val Val Ala Val Leu  
 210 215 220  
 Arg Met Arg Ser Ala Asp Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Ala Val Ser Met Phe Tyr Gly Thr Pro Ile Phe Met  
 245 250 255  
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val  
 260 265 270  
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Val Asn Lys Ala Ile Thr  
 290 295 300  
 Lys Thr Tyr Val Arg  
 305

&lt;210&gt; 1315

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g232 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1315

```

Met Leu His Thr Asn Asn Thr Gln Phe His Pro Ser Thr Phe Leu Val
 1           5           10           15
Val Gly Val Pro Gly Leu Glu Asp Val His Val Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ala Val Tyr Leu Thr Ala Leu Leu Gly Asn Ile Ile Ile Leu
          35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Gln Pro Met Phe Tyr Phe
          50           55           60
Leu Ala Met Leu Ala Gly Thr Asp Leu Gly Leu Ser Thr Ala Thr Ile
65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gly Glu Ile Ala Phe
          85           90           95
Gly Ala Cys Ile Thr Gln Met Tyr Thr Ile His Ile Cys Thr Gly Leu
          100          105          110
Glu Ser Val Val Leu Thr Val Thr Gly Ile Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Met Ile Leu Thr Asn Lys Val Ile Ala
          130          135          140
Ile Leu Gly Ile Val Ile Ile Val Arg Thr Leu Val Phe Val Thr Pro
145          150          155          160
Phe Thr Phe Leu Thr Leu Arg Leu Pro Phe Cys Gly Val Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala Lys Leu Ala Cys Ala
          180          185          190
Ser Ile Asn Val Ile Tyr Gly Leu Ile Ala Phe Ser Val Gly Tyr Ile
          195          200          205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val
          210          215          220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys
225          230          235          240
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe
          245          250          255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His
          260          265          270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser
          275          280          285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg
          290          295          300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe
305          310          315          320

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&lt;210&gt; 1316

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g233 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1316

```

Met Glu Gln His Asn Leu Thr Thr Val Asn Glu Phe Ile Leu Thr Gly
 1           5           10           15
Ile Thr Asp Ile Ala Glu Leu Gln Ala Pro Leu Phe Ala Leu Phe Leu
          20           25           30
Met Ile Tyr Val Ile Ser Val Met Gly Asn Leu Gly Met Ile Val Leu
          35           40           45

```

Thr Lys Leu Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg  
 50 55 60  
 His Leu Ala Phe Met Asp Leu Gly Tyr Ser Thr Thr Val Gly Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Val Val Asp Lys Asn Ile Ile Ser Tyr Tyr Phe  
 85 90 95  
 Cys Ala Thr Gln Leu Ala Phe Phe Leu Val Phe Ile Gly Ser Glu Leu  
 100 105 110  
 Phe Ile Leu Ser Ala Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Val Ile Met Ser Arg Arg Val Cys Gln Val Leu  
 130 135 140  
 Val Ala Ile Pro Tyr Leu Tyr Cys Thr Phe Ile Ser Leu Leu Val Thr  
 145 150 155 160  
 Ile Lys Ile Phe Thr Leu Ser Phe Cys Gly Tyr Asn Val Ile Ser His  
 165 170 175  
 Phe Tyr Cys Asp Ser Leu Pro Leu Leu Pro Leu Leu Cys Ser Asn Thr  
 180 185 190  
 His Glu Ile Glu Leu Ile Ile Leu Ile Phe Ala Ala Ile Asp Leu Ile  
 195 200 205  
 Ser Ser Leu Leu Ile Val Leu Leu Ser Tyr Leu Leu Ile Leu Val Ala  
 210 215 220  
 Ile Leu Arg Met Asn Ser Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Gly Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu Leu Phe  
 245 250 255  
 Met Tyr Val Gln Pro Lys Ser Ser His Ser Phe Asp Thr Asp Lys Val  
 260 265 270  
 Ala Ser Ile Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Arg Arg Thr Trp  
 290 295 300  
 Asn Asn Leu Cys Asn Ile Phe Val  
 305 310

&lt;210&gt; 1317

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g234 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1317

Met Met Trp Glu Asn Trp Thr Ile Val Ser Glu Phe Val Leu Val Ser  
 1 5 10 15  
 Phe Ser Ala Leu Ser Thr Glu Leu Gln Ala Leu Leu Phe Leu Leu Phe  
 20 25 30  
 Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Val Leu Ile Ile Leu  
 35 40 45  
 Val Thr Ile Ala Asp Ser Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro  
 65 70 75 80  
 Lys Met Leu Gly Thr Leu Ile Ile Gln Asp Thr Thr Ile Ser Phe Leu  
 85 90 95  
 Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Gly Ala Ala Glu  
 100 105 110  
 Cys Cys Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Asp Pro Leu His Tyr Pro Val Ile Met Gly His Ile Ser Cys Ala Gln

```

      130              135              140
Leu Ala Ala Ala Ser Trp Phe Ser Gly Phe Ser Val Ala Thr Val Gln
145              150              155              160
Thr Thr Trp Ile Phe Ser Phe Pro Phe Cys Gly Pro Asn Arg Val Asn
      165              170              175
His Phe Phe Cys Asp Ser Pro Pro Val Ile Ala Leu Val Cys Ala Asp
      180              185              190
Thr Ser Val Phe Glu Leu Glu Ala Leu Thr Ala Thr Val Pro Phe Ile
      195              200              205
Leu Phe Pro Phe Leu Leu Ile Leu Gly Ser Tyr Val Arg Ile Leu Ser
210              215              220
Thr Ile Phe Arg Met Pro Ser Ala Glu Gly Lys His Gln Ala Phe Ser
225              230              235              240
Thr Cys Ser Ala His Leu Leu Val Val Ser Leu Phe Tyr Ser Thr Ala
      245              250              255
Ile Leu Thr Tyr Phe Arg Pro Gln Ser Ser Ala Ser Ser Glu Ser Lys
260              265              270
Lys Leu Leu Ser Leu Ser Ser Thr Val Val Thr Pro Met Leu Asn Pro
275              280              285
Ile Ile Tyr Ser Ser Arg Asn Lys Glu Val Lys Ala Ala Leu Lys Arg
290              295              300
Leu Ile His Arg Thr Leu Gly Ser Gln Lys Leu
305              310              315

```

&lt;210&gt; 1318

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g235 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1318

```

Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly
 1              5              10              15
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu
      20              25              30
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu
      35              40              45
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser
      50              55              60
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ser Ile Thr Pro Asn
65              70              75              80
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr
      85              90              95
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met
      100              105              110
Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115              120              125
Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met
      130              135              140
Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala
145              150              155              160
Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn
      165              170              175
Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn
      180              185              190

```



His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Phe  
 195 200 205  
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val  
 210 215 220  
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Ile Phe Tyr Gly  
 245 250 255  
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp  
 260 265 270  
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met  
 290 295 300  
 Glu Asn Leu Cys Leu Thr  
 305 310

&lt;210&gt; 1319

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g236 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(184)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1319

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr  
 1 5 10 15  
 His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile  
 20 25 30  
 Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser  
 35 40 45  
 His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu  
 50 55 60  
 Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys  
 65 70 75 80  
 Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His  
 85 90 95  
 Phe Phe Cys Asn Lys Ser Leu Gly Leu Gly Leu Ser Cys Tyr Asn Ile  
 100 105 110  
 Tyr Ile Ser Thr Ala Val Pro Ala Phe Val Gly Val Xaa Val Leu His  
 115 120 125  
 Ser Leu Pro Tyr Leu Val Ile Met Phe Ser Trp Thr Tyr Ile Leu Val  
 130 135 140  
 Ala Ile Lys Arg Met Ser Ser Val Gly Arg Lys Glu Leu Ser Ile Cys  
 145 150 155 160  
 Val Ser His Leu Lys Thr Ser Thr Ile Phe His Thr Ala Leu Phe Tyr  
 165 170 175  
 Val Tyr Leu Gln Pro Asp Phe Phe  
 180

&lt;210&gt; 1320

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g237 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1320

```

Met Ser Gly Asp Asn Ser Ser Ser Leu Thr Pro Gly Phe Phe Ile Leu
 1           5           10           15
Asn Gly Val Pro Gly Leu Glu Ala Thr His Ile Trp Ile Ser Leu Pro
          20           25           30
Phe Cys Phe Met Tyr Ile Ile Ala Val Val Gly Asn Cys Gly Leu Ile
          35           40           45
Cys Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe
          50           55           60
Leu Ala Leu Leu Ser Phe Thr Asp Val Thr Leu Cys Thr Thr Met Val
65           70           75           80
Pro Asn Met Leu Cys Ile Phe Trp Phe Asn Leu Lys Glu Ile Asp Phe
          85           90           95
Asn Ala Cys Leu Ala Gln Met Phe Phe Val His Met Leu Thr Gly Met
          100          105          110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala
          130          135          140
Lys Ala Gly Leu Ala Thr Phe Leu Arg Asn Val Met Leu Ile Ile Pro
145          150          155          160
Phe Thr Leu Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Phe Ile
          165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Val Ser Cys Gly
          180          185          190
Asn Phe Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
          195          200          205
Gly Val Phe Asp Ile Cys Cys Ile Ser Val Ser Tyr Thr Met Ile Leu
          210          215          220
Gln Ala Val Met Ser Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
225          230          235          240
Ser Thr Cys Thr Ser His Met Cys Ser Ile Val Ile Thr Tyr Val Ala
          245          250          255
Ala Phe Phe Thr Phe Phe Thr His Arg Phe Val Gly His Asn Ile Pro
          260          265          270
Asn His Ile His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro
          275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Glu
          290          295          300
Gly Val Ile Lys Phe Leu Leu Gly Asp Lys Val Ser Phe Thr Tyr Asp
305          310          315          320
Lys

```

&lt;210&gt; 1321

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g238 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(134)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1321

```

Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr
 1           5           10           15

```

Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg  
 20 25 30  
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln  
 35 40 45  
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser  
 50 55 60  
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly  
 65 70 75 80  
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln  
 85 90 95  
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser  
 100 105 110  
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Gly Lys Xaa Ser Gly Glu Arg  
 115 120 125  
 Ser Ser Phe Pro Arg Glu  
 130

&lt;210&gt; 1322

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g239 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1322

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr  
 1 5 10 15  
 Glu Phe Ile Leu Val Gly Val Ser Asp Asp Pro Glu Leu Gln Ile Pro  
 20 25 30  
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn  
 35 40 45  
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro  
 50 55 60  
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser  
 65 70 75 80  
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys  
 85 90 95  
 Thr Ile Ser Tyr Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val  
 100 105 110  
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg  
 115 120 125  
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Val Ser Pro  
 130 135 140  
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile  
 145 150 155 160  
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser  
 165 170 175  
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala  
 180 185 190  
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe  
 195 200 205  
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr  
 210 215 220  
 Phe Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg  
 225 230 235 240  
 Gln Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val

```
<210> 1323
<211> 315
<212> PRT
<213> Unknown (H38g240 protein)
```

|                    |             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <b>&lt;400&gt;</b> | <b>1323</b> |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met                | Leu         | Ser | Pro | Asn | His | Thr | Ile | Val | Thr | Glu | Phe | Ile | Leu | Leu | Gly |
| 1                  |             |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu                | Thr         | Asp | Asp | Pro | Val | Leu | Glu | Lys | Ile | Leu | Phe | Gly | Val | Phe | Leu |
|                    |             |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala                | Ile         | Tyr | Leu | Ile | Thr | Leu | Ala | Gly | Asn | Leu | Cys | Met | Ile | Leu | Leu |
|                    |             | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile                | Arg         | Thr | Asn | Ser | Gln | Leu | Gln | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Gly |
|                    | 50          |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His                | Leu         | Ser | Phe | Val | Asp | Ile | Cys | Tyr | Ser | Ser | Asn | Val | Thr | Pro | Asn |
| 65                 |             |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met                | Leu         | His | Asn | Phe | Leu | Ser | Glu | Gln | Lys | Thr | Ile | Ser | Tyr | Ala | Gly |
|                    |             |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys                | Phe         | Thr | Gln | Cys | Leu | Leu | Phe | Ile | Ala | Leu | Val | Ile | Thr | Glu | Phe |
|                    |             |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr                | Phe         | Leu | Ala | Ser | Met | Ala | Leu | Asp | Arg | Tyr | Val | Ala | Ile | Cys | Ser |
|                    |             | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro                | Leu         | His | Tyr | Ser | Ser | Arg | Met | Ser | Lys | Asn | Ile | Cys | Ile | Ser | Leu |
|                    | 130         |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val                | Thr         | Val | Pro | Tyr | Met | Tyr | Gly | Phe | Leu | Asn | Gly | Leu | Ser | Gln | Thr |
| 145                |             |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu                | Leu         | Thr | Phe | His | Leu | Ser | Phe | Cys | Gly | Ser | Leu | Glu | Ile | Asn | His |
|                    |             |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe                | Tyr         | Cys | Ala | Asp | Pro | Pro | Leu | Ile | Met | Leu | Ala | Cys | Ser | Asp | Thr |
|                    |             |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg                | Val         | Lys | Lys | Met | Ala | Met | Phe | Val | Val | Ala | Gly | Phe | Thr | Leu | Ser |
|                    |             | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser                | Ser         | Leu | Phe | Ile | Ile | Leu | Leu | Ser | Tyr | Leu | Phe | Ile | Phe | Ala | Ala |
|                    | 210         |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile                | Phe         | Arg | Ile | Arg | Ser | Ala | Glu | Gly | Arg | His | Lys | Ala | Phe | Ser | Thr |
| 225                |             |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys                | Ala         | Ser | His | Leu | Thr | Ile | Val | Thr | Leu | Phe | Tyr | Gly | Thr | Leu | Phe |
|                    |             |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Cys                | Met         | Tyr | Val | Arg | Pro | Pro | Ser | Glu | Lys | Ser | Val | Glu | Glu | Ser | Lys |
|                    |             |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile                | Ile         | Ala | Val | Phe | Tyr | Thr | Phe | Leu | Ser | Pro | Met | Leu | Asn | Pro | Leu |
|                    |             | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile                | Tyr         | Ser | Leu | Arg | Asn | Arg | Asp | Val | Ile | Leu | Ala | Ile | Gln | Gln | Met |
|                    | 290         |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile                | Arg         | Gly | Lys | Ser | Phe | Cys | Lys | Ile | Ala | Val |     |     |     |     |     |
| 305                |             |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |

<210> 1324

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g241 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1324

```

Met Pro Ile Ala Asn Asp Thr Gln Phe His Thr Ser Ser Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ser Val Tyr Leu Ile Ala Leu Leu Gly Asn Ala Ala Ile Phe
          35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Cys
          50           55           60
Leu Ala Met Leu Asp Ser Ile Asp Leu Ser Leu Ser Thr Ala Thr Ile
65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Ile Lys Glu Ile Ser Phe
          85           90           95
Gly Gly Tyr Leu Ser Gln Met Phe Phe Ile His Phe Phe Thr Val Met
          100          105          110
Glu Ser Ile Val Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Lys Pro Leu Trp Tyr Thr Met Ile Leu Thr Ser Lys Ile Ile Ser
          130          135          140
Leu Ile Ala Gly Ile Ala Val Leu Arg Ser Leu Tyr Met Val Ile Pro
145          150          155          160
Leu Val Phe Leu Leu Arg Leu Pro Phe Cys Gly His Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Ala
          180          185          190
Ser Ile Lys Val Asn Ile Met Phe Gly Leu Gly Ser Ile Ser Leu Leu
          195          200          205
Leu Leu Asp Val Leu Leu Ile Ile Leu Ser His Ile Arg Ile Leu Tyr
210          215          220
Ala Val Phe Cys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
225          230          235          240
Thr Cys Gly Ser His Ile Gly Val Ile Leu Ala Phe Ser Thr Pro Ala
          245          250          255
Phe Phe Ser Phe Phe Thr His Cys Phe Gly His Asp Ile Pro Gln Tyr
          260          265          270
Ile His Ile Phe Leu Ala Asn Leu Tyr Val Val Val Pro Pro Thr Leu
          275          280          285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys His Ile Arg Glu Thr Val
290          295          300
Leu Arg Ile Phe Phe Lys Thr Asp His
305          310

```

&lt;210&gt; 1325

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g242 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1325

```

Met His Ile Phe Lys Phe Val Leu Asp Phe Asn Met Lys Asn Val Thr
 1           5           10           15
Glu Val Thr Leu Phe Val Leu Lys Gly Phe Thr Asp Asn Leu Glu Leu

```

```

      20      25      30
Gln Thr Ile Phe Phe Phe Leu Phe Leu Ala Ile Tyr Leu Phe Thr Leu
      35      40      45
Met Gly Asn Leu Gly Leu Ile Leu Val Val Ile Arg Asp Ser Gln Leu
      50      55      60
His Lys Pro Met Tyr Tyr Phe Leu Ser Met Leu Ser Ser Val Asp Ala
      65      70      75      80
Cys Tyr Ser Ser Val Ile Thr Pro Asn Met Leu Val Asp Phe Thr Thr
      85      90      95
Lys Asn Lys Val Ile Ser Phe Leu Gly Cys Val Ala Gln Val Phe Leu
      100      105      110
Ala Cys Ser Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala
      115      120      125
Tyr Asp Arg Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser
      130      135      140
Met Ser Pro Arg Val Tyr Met Pro Leu Ile Asn Ala Ser Tyr Val Ala
      145      150      155      160
Gly Ile Leu His Ala Thr Ile His Thr Val Ala Thr Phe Ser Leu Ser
      165      170      175
Phe Cys Gly Ala Asn Glu Ile Arg Arg Val Phe Cys Asp Ile Pro Pro
      180      185      190
Leu Leu Ala Ile Ser Tyr Ser Asp Thr His Thr Asn Gln Leu Leu Leu
      195      200      205
Phe Tyr Phe Val Gly Ser Ile Glu Leu Val Thr Ile Leu Ile Val Leu
      210      215      220
Ile Ser Tyr Gly Leu Ile Leu Leu Ala Ile Leu Lys Met Tyr Ser Ala
      225      230      235      240
Glu Gly Arg Arg Lys Val Phe Ser Thr Cys Gly Ala His Leu Thr Gly
      245      250      255
Val Ser Ile Tyr Tyr Gly Thr Ile Leu Phe Met Tyr Val Arg Pro Ser
      260      265      270
Ser Ser Tyr Ala Ser Asp His Asp Met Ile Val Ser Ile Phe Tyr Thr
      275      280      285
Ile Val Ile Pro Leu Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys
      290      295      300
Asp Val Lys Asp Ser Met Lys Lys Met Phe Gly Lys Asn Gln Val Ile
      305      310      315      320
Asn Lys Val Tyr Phe His Thr Lys
      325

```

&lt;210&gt; 1326

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g243 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1326

```

Met Asn Gly Ala Asn Ser Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu
  1          5          10          15
Ser Gly Val Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro
      20      25      30
Phe Cys Phe Met Tyr Ile Ile Val Val Leu Gly Asn Cys Gly Leu Ile
      35      40      45
Tyr Leu Ile Ser His Glu Glu Ala Leu His Gln Pro Thr Tyr Tyr Phe
      50      55      60

```

Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val  
 65 70 75 80  
 Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe  
 85 90 95  
 Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met  
 100 105 110  
 Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr  
 130 135 140  
 Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro  
 145 150 155 160  
 Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile  
 165 170 175  
 His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly  
 180 185 190  
 Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile  
 195 200 205  
 Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile  
 210 215 220  
 Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe  
 225 230 235 240  
 Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro  
 245 250 255  
 Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro  
 260 265 270  
 His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro  
 275 280 285  
 Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu  
 290 295 300  
 Gly Val Ile Lys Leu Phe Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp  
 305 310 315 320  
 Ile Asn Leu Xaa Tyr Arg Ser Leu Asn  
 325

&lt;210&gt; 1327

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g244 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(301)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1327

Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe  
 1 5 10 15  
 Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val  
 20 25 30  
 Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser  
 35 40 45  
 Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu  
 50 55 60  
 Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr  
 65 70 75 80  
 Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala  
 85 90 95  
 Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro

|   |     |     |
|---|-----|-----|
| 100   | 105 | 110 |
| Leu Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr |     |     |
| 115   | 120 | 125 |
| Thr Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe |     |     |
| 130   | 135 | 140 |
| Trp Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val |     |     |
| 145   | 150 | 155 |
| Gln Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp |     |     |
| 165   | 170 | 175 |
| Leu Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly |     |     |
| 180   | 185 | 190 |
| Val Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile |     |     |
| 195   | 200 | 205 |
| Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser |     |     |
| 210   | 215 | 220 |
| Ala Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val |     |     |
| 225   | 230 | 235 |
| Phe Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr |     |     |
| 245   | 250 | 255 |
| Lys Asp Lys Leu Val Ala Val Phe Tyr Val Val Ile Thr Pro Met Leu |     |     |
| 260   | 265 | 270 |
| Asn Pro Phe Ile Tyr Thr Leu Gly Asn Ala Glu Met Lys Ile Thr Met |     |     |
| 275   | 280 | 285 |
| Arg Arg Leu Leu Gly Arg Thr Val Asn Ser Gly Met Glu             |     |     |
| 290   | 295 | 300 |

&lt;210&gt; 1328

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g245 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1328

|   |  |
|---|--|
| Gly Ser Xaa Lys Gln Xaa Lys Ser Xaa Pro Pro Ile Phe Phe Leu Thr |  |
| 1 5 10 15   |  |
| Gly Ile Pro Gly Leu Glu Ala Gln His Gly Trp Leu Ser Ile Pro Phe |  |
| 20 25 30  |  |
| Phe Thr Met Tyr Ile Val Ala Ile Val Gly Asn Ile Leu Ile Met Ala |  |
| 35 40 45  |  |
| Ala Val Gln Glu Asp Ser Ala Leu His Glu Pro Met Tyr Leu Phe Leu |  |
| 50 55 60  |  |
| Ser Met Leu Ala Val Thr Glu Val Gly Val Ser Val Ser Thr Leu Pro |  |
| 65 70 75 80   |  |
| Thr Val Thr Gly Ile Leu Trp Phe Asp Ala His Arg Val Asp Phe Asp |  |
| 85 90 95  |  |
| Gly Cys Leu Ala Gln Met Phe Phe Ile His Thr Phe Ser Cys Met Glu |  |
| 100 105 110   |  |
| Ser Gly Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Tyr |  |
| 115 120 125   |  |
| Asn Leu Leu Arg Tyr Thr Ala Ile Leu Thr Leu Pro Arg Ile Ile Cys |  |
| 130 135 140   |  |
| Met Gly Leu Gly Ile Thr Leu Lys Ser Val Ala Leu Met Ala Pro Leu |  |
| 145 150 155 160   |  |
| Pro Ile Leu Leu Arg Gln Leu Pro Tyr Cys His Thr Asn Val Leu Ser |  |
| 165 170 175   |  |



His Ser Tyr Cys Leu His Ser Asp Leu Ile Gln Leu Pro Cys Ala Asp  
 180 185 190  
 Thr Lys Leu Asn Ser Ile Leu Gly Leu Ala Ile Val Leu Ala Asn Phe  
 195 200 205  
 Gly Leu Asp Ser Leu Leu Ile Val Val Ser Tyr Val Leu Ile Leu Tyr  
 210 215 220  
 Thr Val Met Gly Ile Ala Ser Gly Glu Gly Arg Trp Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Tyr Tyr Val Pro Met  
 245 250 255  
 Ile Gly Val Ser Val Met His Arg Ala Ala Lys His Ala Ser Pro Ile  
 260 265 270  
 Val His Thr Leu Met Ser Ser Ile Cys Leu Leu Val Pro Pro Val Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Ser Val Lys Thr Gln Thr Ile Arg Gln Gly Ile  
 290 295 300  
 Leu Thr Leu Phe Ser Cys Lys Arg Glu Leu Leu Xaa Ile Thr Ala Arg  
 305 310 315 320  
 Ser Gln Glu Leu

&lt;210&gt; 1329

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g246 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(292)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1329

Thr Leu Phe Ile Ile Ser Lys Phe Gln Gly Cys Xaa Lys Val Gly Leu  
 1 5 10 15  
 Tyr Thr Gln Ser Leu Tyr Leu Leu Ala Glu Tyr Phe His Arg Gly Gln  
 20 25 30  
 Leu Met Lys Met Leu Thr Ser Thr Asn Leu Ser Leu Ser Val Val Thr  
 35 40 45  
 Ile Gly Ile Phe Gln Phe Asn Val Arg Glu Ile Val Phe Gly Ala Phe  
 50 55 60  
 Leu Val Tyr Ile Gln Met Phe Met Thr Tyr Leu Cys Thr Gly Leu Glu  
 65 70 75 80  
 Ser Gly Val Leu Ile Ile Leu Ala Ile Asp His Tyr Val Val Ile Arg  
 85 90 95  
 Asn Pro Leu Arg Tyr Thr Met Ile Leu Met Asn Asn Val Val Ala Ile  
 100 105 110  
 Leu Gly Val Met Ile Ile Arg Ser Leu Ile Phe Ile Ile Pro Phe Glu  
 115 120 125  
 Phe Leu Ile Leu Leu Leu Ser Phe Cys Ala Ala His Ile Ile Pro His  
 130 135 140  
 Thr Lys Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ala Ser Val  
 145 150 155 160  
 Arg Ala Asn Asn Met Phe Gly Met Val Ala Phe Ser Val Gly Phe Ile  
 165 170 175  
 Asp Leu Ile Ala Ile Gly Phe Ser Tyr Val Lys Lys Leu Arg Ala Leu  
 180 185 190  
 Phe His Leu Pro Pro Trp Asn Gly Gln Phe Glu Ala Leu Asn Thr Cys  
 195 200 205  
 Gly Ser His Val Cys Met Leu Ile Phe Tyr Ile Pro Val Phe Phe Phe

|                     |                                     |                     |
|---------------------|-------------------------------------|---------------------|
| 210                 | 215                                 | 220                 |
| Xaa Tyr Thr Ala Trp | Xaa Lys His Pro Cys Tyr             | Ile Arg Ile Phe Leu |
| 225                 | 230                                 | 235                 |
| Ala Asn Val Tyr Thr | Val Val Leu Pro Val Phe Asn Pro Val | Ile Tyr             |
| 245                 | 250                                 | 255                 |
| Gly Ile Arg Lys Lys | Gln Ile Pro Asp Xaa Gly Ile Asp     | Leu Lys Thr         |
| 260                 | 265                                 | 270                 |
| Phe Asp Asp Gln Ser | Leu Leu Val Met Met Ile Tyr Ile     | Leu Gly Tyr         |
| 275                 | 280                                 | 285                 |
| Ile Cys Lys Tyr     |                                     |                     |
| 290                 |                                     |                     |

&lt;210&gt; 1330

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g247 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1330

|   |     |
|---|-----|
| Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly |     |
| 1   | 5   |
| Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Leu Phe Leu Phe Ser     | 10  |
| 20  | 25  |
| Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr | 30  |
| 35  | 40  |
| Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala | 45  |
| 50  | 55  |
| Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys | 60  |
| 65  | 70  |
| Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly | 75  |
| 85  | 90  |
| Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met | 95  |
| 100   | 105 |
| Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys | 110 |
| 115   | 120 |
| Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe | 125 |
| 130   | 135 |
| Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu | 140 |
| 145   | 150 |
| Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser | 155 |
| 165   | 170 |
| Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr | 175 |
| 180   | 185 |
| Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu | 190 |
| 195   | 200 |
| Ala Ser Phe Leu Ile Leu Ile Ile Ser Tyr Ile Phe Ile Leu Val Thr | 205 |
| 210   | 215 |
| Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu | 220 |
| 225   | 230 |
| Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe | 235 |
| 245   | 250 |
| Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala | 255 |
| 260   | 265 |
| Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr | 270 |
| 275   | 280 |
| Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Arg Cys Ser Gln | 285 |
| 290   | 295 |
| Phe Val Asn Tyr Ser Lys Ile Phe                                 | 300 |
| 305   | 310 |

<210> 1331  
 <211> 168  
 <212> PRT  
 <213> Unknown (H38g248 protein)

<220>  
 <223> Synthetic construct

<400> 1331  
 Lys Gln Ser Ser Gly Asp Ser Gly Asn Gln Thr Thr Trp Leu Ile Leu  
 1 5 10 15  
 Val Gly Phe Gly Glu Leu Gln Tyr Leu Gly Phe Leu Pro Phe Thr Leu  
 20 25 30  
 Phe Leu Ala Ile Tyr Val Val Thr Val Val Gly Asn Ala Leu Ile Met  
 35 40 45  
 Leu Ala Val Ala Ser Ser Arg Thr Leu His Pro Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Cys His Phe Ser Leu Leu Glu Ile Gly Tyr Thr Ser Asn Val Ile  
 65 70 75 80  
 Leu Trp Leu Leu Gln Ser Phe Leu Glu Gly Lys Glu Val Ile Ser Leu  
 85 90 95  
 Val Ser Cys Leu Ala Gln Phe Tyr Val Phe Ser Ser Leu Ala Ala Ala  
 100 105 110  
 Glu Cys Leu Leu Leu Ser Ala Val Ser Tyr Asp Cys Tyr Leu Ala Ile  
 115 120 125  
 Cys Cys Pro Leu His Tyr Pro Ala Leu Met Ser Thr Trp Phe Cys His  
 130 135 140  
 Cys Leu Ala Ala Gly Ala Trp Phe Ser Gly Phe Phe Ser Ser Ala Phe  
 145 150 155 160  
 Thr Met Ala Leu Ala Ala Pro Leu  
 165

<210> 1332  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g249 protein)

<220>  
 <223> Synthetic construct

<400> 1332  
 Met Leu Thr Leu Asn Lys Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu  
 1 5 10 15  
 Asn Gly Val Pro Gly Leu Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro  
 20 25 30  
 Phe Cys Ser Met Tyr Val Val Ala Met Val Gly Asn Cys Gly Leu Leu  
 35 40 45  
 Tyr Leu Ile His Tyr Glu Asp Ala Leu His Lys Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ala Met Leu Ser Phe Thr Asp Leu Val Met Cys Ser Ser Thr Ile  
 65 70 75 80  
 Pro Lys Ala Leu Cys Ile Phe Trp Phe His Leu Lys Asp Ile Gly Phe  
 85 90 95  
 Asp Glu Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Thr Gly Met  
 100 105 110  
 Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Thr Asn Pro Val Ile Ala  
 130 135 140  
 Lys Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Phe | Thr | Phe | Leu | Thr | Lys | Arg | Leu | Pro | Tyr | Cys | Arg | Gly | Asn | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Pro | His | Thr | Tyr | Cys | Asp | His | Met | Ser | Val | Ala | Lys | Leu | Ser | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Asn | Val | Lys | Val | Asn | Ala | Ile | Tyr | Gly | Leu | Met | Val | Ala | Leu | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Gly | Gly | Phe | Asp | Ile | Leu | Cys | Ile | Thr | Ile | Ser | Tyr | Thr | Met | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Arg | Ala | Val | Val | Ser | Leu | Ser | Ser | Ala | Asp | Ala | Arg | Gln | Lys | Ala |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Thr | Cys | Thr | Ala | His | Ile | Cys | Ala | Ile | Val | Phe | Ser | Tyr | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Ala | Phe | Phe | Ser | Phe | Phe | Ser | His | Arg | Phe | Gly | Glu | His | Ile | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Pro | Ser | Cys | His | Ile | Ile | Val | Ala | Asn | Ile | Tyr | Leu | Leu | Leu | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Thr | Met | Asn | Pro | Ile | Val | Tyr | Gly | Val | Lys | Thr | Lys | Gln | Ile | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Cys | Val | Ile | Arg | Ile | Leu | Ser | Gly | Ser | Lys | Asp | Thr | Lys | Ser | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Met |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 1333

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g250 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1333

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | His | Arg | Asn | Asp | Thr | Leu | Ser | Thr | Glu | Ala | Ser | Asp | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Asn | Cys | Phe | Val | Arg | Ser | Pro | Ser | Trp | Gln | His | Trp | Leu | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Pro | Leu | Ser | Leu | Leu | Phe | Leu | Leu | Ala | Val | Gly | Ala | Asn | Thr | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Met | Thr | Ile | Trp | Leu | Glu | Ala | Ser | Leu | His | Gln | Pro | Leu | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Leu | Leu | Ser | Leu | Leu | Ser | Leu | Leu | Asp | Ile | Val | Leu | Cys | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Ile | Pro | Lys | Val | Leu | Thr | Ile | Phe | Trp | Phe | Asp | Leu | Arg | Pro | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Phe | Pro | Ala | Cys | Phe | Leu | Gln | Met | Tyr | Ile | Met | Asn | Cys | Phe | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Met | Glu | Ser | Cys | Thr | Phe | Met | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ile | Cys | His | Pro | Leu | Arg | Tyr | Pro | Ser | Ile | Ile | Thr | Asp | His | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Val | Lys | Ala | Ala | Met | Phe | Ile | Leu | Thr | Arg | Asn | Val | Leu | Met | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Pro | Ile | Pro | Ile | Leu | Ser | Ala | Gln | Leu | Arg | Tyr | Cys | Gly | Arg | Asn |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Ile | Glu | Asn | Cys | Ile | Cys | Ala | Asn | Met | Ser | Val | Ser | Arg | Leu | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Cys | Asp | Asp | Val | Thr | Ile | Asn | His | Leu | Tyr | Gln | Phe | Ala | Gly | Gly | Trp |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Thr | Leu | Leu | Gly | Ser | Asp | Leu | Ile | Leu | Ile | Phe | Leu | Ser | Tyr | Thr | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

Ile Leu Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys  
 225 230 235 240  
 Ala Leu Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser  
 245 250 255  
 Thr Ile Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val  
 260 265 270  
 Ser Pro Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro  
 275 280 285  
 Ala Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys  
 290 295 300  
 Gln Gly Met Gln Arg Leu Leu Lys Lys Gly Cys  
 305 310 315

&lt;210&gt; 1334

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g251 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(302)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1334

Leu Ser Ser Met Cys Leu Thr Ile Val Met His Cys Glu Phe Phe Leu  
 1 5 10 15  
 Met Asp Leu Thr Asp Asp Pro Gln Leu His Pro Thr Phe Ser Ala Leu  
 20 25 30  
 Phe Leu Pro Ile Tyr Val Val Met Val Met Ala Asn Leu Gly Leu Leu  
 35 40 45  
 Ala Phe Ile Val Val Ser Pro Gln Phe Leu Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Trp Ser Ser Val Asp Phe Cys Tyr Ser Ser Val Thr Val  
 65 70 75 80  
 Pro Lys Ile Ser Met Gly Phe Phe Ser Asp Cys Gln Val Phe Ser Phe  
 85 90 95  
 Ser Gly Cys Met Ala Gln Leu Ser Cys Phe Xaa Ile Phe Ala Asp Thr  
 100 105 110  
 Glu Phe Phe Leu Leu Ala Ser Met Val Tyr Tyr Arg Xaa Glu Ala Val  
 115 120 125  
 Cys Asn Pro Leu Leu Tyr His Ile Thr Met Ser Pro Lys Leu Cys Leu  
 130 135 140  
 Gln Leu Val Ala Thr Ser Met Asn Met Val Leu Pro Ser Ser Thr Ile  
 145 150 155 160  
 Phe His Leu Ile Phe Cys Lys Ser Arg Ala Ile Ile His Xaa Phe Cys  
 165 170 175  
 Tyr Phe Ser Pro Pro Pro Arg Leu Xaa Lys Leu Ser Cys Ser Asp Met  
 180 185 190  
 Gln Gly Leu Gln Leu Leu Thr Phe Ala Ser Ser Ser Phe Asn Val Ser  
 195 200 205  
 Val Ser Arg Thr Ile Phe Leu Val Ser Tyr Leu Ile Met Arg Met Pro  
 210 215 220  
 Ser Val Xaa Gly Lys His Cys Ala Ser His Leu Thr Ala Val Ser Leu  
 225 230 235 240  
 Cys Tyr Gly Thr Thr Val Phe Leu His Leu His Leu Ser Leu Lys Cys  
 245 250 255  
 Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu  
 260 265 270  
 Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys

275                      280                      285  
 Thr Phe Gly Thr Ser Ser Xaa Arg Phe Thr Ile Pro Leu Leu  
 290                      295                      300

<210> 1335  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g252 protein)

<220>  
 <223> Synthetic construct

<400> 1335  
 Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr  
 1                      5                      10                      15  
 Pro Pro Ser Phe Ile Leu Asn Gly Ile Pro Gly Leu Glu Arg Val His  
 20                      25                      30  
 Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val  
 35                      40                      45  
 Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His  
 50                      55                      60  
 His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu  
 65                      70                      75                      80  
 Leu Thr Cys Thr Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe  
 85                      90                      95  
 Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe  
 100                      105                      110  
 Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala  
 115                      120                      125  
 Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr  
 130                      135                      140  
 Leu Thr Asn Pro Ile Ile Ala Lys Ala Glu Leu Ala Thr Phe Leu Arg  
 145                      150                      155                      160  
 Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro  
 165                      170                      175  
 Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser  
 180                      185                      190  
 Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly  
 195                      200                      205  
 Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser  
 210                      215                      220  
 Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser  
 225                      230                      235                      240  
 Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala  
 245                      250                      255  
 Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg  
 260                      265                      270  
 Phe Gly Gly His Thr Ile Pro Pro Ser Leu His Ile Ile Val Ala Asn  
 275                      280                      285  
 Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val  
 290                      295                      300  
 Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp  
 305                      310                      315                      320  
 Lys Gly Ala Gly

<210> 1336  
 <211> 274  
 <212> PRT  
 <213> Unknown (H38g253 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(274)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1336

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp  
 1 5 10 15  
 Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu  
 20 25 30  
 Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile  
 35 40 45  
 Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu  
 50 55 60  
 Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser  
 65 70 75 80  
 Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe  
 85 90 95  
 Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala  
 100 105 110  
 Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr  
 115 120 125  
 Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg  
 130 135 140  
 Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe  
 145 150 155 160  
 Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln  
 165 170 175  
 Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser  
 180 185 190  
 Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys  
 195 200 205  
 Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn  
 210 215 220  
 Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe  
 225 230 235 240  
 Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr  
 245 250 255  
 Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln  
 260 265 270  
 Ile Leu

&lt;210&gt; 1337

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g254 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1337

Met Ser Ser Leu Asn Val Thr Glu Pro His Leu Ser Ser Phe Leu Leu  
 1 5 10 15  
 Leu Gly Ile Pro Gly Leu Glu Ala Ala Gln Arg Trp Leu Gly Phe Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Phe | Cys | Val | Val | Tyr | Leu | Ile | Ala | Leu | Val | Gly | Asn | Leu | Ile | Ile | Leu |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Val | Ile | Trp | Thr | Asp | Lys | Asn | Leu | His | Gln | Pro | Met | Phe | Tyr | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Met | Leu | Ser | Val | Ile | Asp | Leu | Ser | Leu | Ser | Thr | Ser | Thr | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Lys | Met | Leu | Gly | Ile | Phe | Trp | Phe | Ser | Leu | Gln | Glu | Leu | Cys | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Cys | Cys | Val | Ala | Gln | Val | Phe | Phe | Ile | His | Phe | Phe | Ser | Val | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ser | Ile | Val | Leu | Leu | Val | Met | Gly | Phe | Asp | Arg | Tyr | Val | Ala | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Asn | Pro | Phe | Arg | Xaa | Thr | Lys | Ile | Leu | Thr | Asn | Arg | Ile | Thr | Gly |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Ile | Ala | Met | Val | Val | Val | Leu | Arg | Ser | Leu | Cys | Met | Ile | Ala | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Ile | Phe | Leu | Leu | Met | Arg | Leu | Pro | Tyr | Cys | Gly | His | Arg | Ile | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Tyr | Thr | Tyr | Cys | Glu | His | Met | Gly | Val | Ala | Arg | Leu | Ala | Cys | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ile | Ser | Val | Asn | Val | Ser | His | Gly | Leu | Gly | Asn | Ile | Phe | Ile | Leu |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Phe | Leu | Asp | Met | Phe | Leu | Ile | Ile | Ser | Tyr | Ala | Arg | Ile | Leu | Cys |     |
| 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Thr | Val | Phe | His | Leu | Pro | Ser | Gln | Glu | Ala | His | Leu | Lys | Ala | Leu | Asn |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Thr | Cys | Ser | Ser | His | Ile | Cys | Val | Ile | Leu | Ala | Phe | Phe | Gly | Pro | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Phe | Ser | Phe | Leu | Thr | His | Arg | Phe | Gly | His | Gly | Ile | Pro | Gln | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | His | Ile | Leu | Leu | Ala | Asn | Leu | Tyr | Ile | Val | Val | Ile | Pro | Pro | Ala |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Leu | Asn | Pro | Val | Ile | Tyr | Gly | Val | Arg | Thr | Lys | Gln | Ile | Gln | Glu | Arg |
| 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Val | Glu | Ser | Leu | Phe | Thr | Lys | Asn | Xaa | Leu | Asn |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |

&lt;210&gt; 1338

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g255 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1338

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Asn | Ser | Pro | Met | Val | Thr | Asp | Phe | Ile | Phe | Leu | Gly | Met | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Asp | Asn | Ser | Gln | Leu | Glu | Val | Leu | Leu | Phe | Gly | Val | Phe | Leu | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Tyr | Ile | Ile | Thr | Val | Leu | Glu | Asn | Leu | Gly | Leu | Val | Val | Leu | Ile | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ser | Ser | Arg | Leu | His | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Ser | Asn | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Phe | Leu | Asp | Val | Cys | Phe | Ser | Ser | Ile | Thr | Ile | Pro | Gln | Asn | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |



Ala His Leu Phe Ser Lys Leu Gln Tyr Val Ser Phe Leu Phe Pro Tyr  
85 90 95  
Thr Xaa Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Phe  
100 105 110  
Leu Asn Leu Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys His Pro Leu  
115 120 125  
Phe Tyr His Ile Thr Met Ser Arg Gly His Tyr Leu Phe Leu Val Ala  
130 135 140  
Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val Thr Thr Ser  
145 150 155 160  
Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val Leu Pro Ala Phe Phe  
165 170 175  
Cys Asp Ile Pro Ser Leu Leu Val Leu Val Cys Ser Asp Pro Trp Ile  
180 185 190  
Thr Ser Ser Ile Leu Val Val Gly Cys Gly Gly Phe Thr Leu Val Thr  
195 200 205  
Ser Val Val Val Ile Leu Val Ser Tyr Met Ser Ser Leu Met Thr Ile  
210 215 220  
Leu Gly Ile Pro Leu Ala Ser Gly Lys Gln Arg Ala Phe Ser Thr Cys  
225 230 235 240  
Ala Ser His Leu Thr Ala Val Ser Leu Tyr Tyr Glu Thr Thr Met Tyr  
245 250 255  
Thr Tyr Leu Pro Ala Ser Arg His Gly Ser Gly Ala Gly Asn Gln Ile  
260 265 270  
Val Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile  
275 280 285  
Tyr Ser Leu Arg Asn Glu Glu Val Lys Val Ala Leu Xaa Lys Thr Leu  
290 295 300  
Arg His Ser Pro Xaa Ser Ser Leu Ser Val Ser Lys Met Gln Asn Ile  
305 310 315 320  
Leu Xaa Arg

&lt;210&gt; 1339

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g256 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1339

Trp Leu Asp Glu Lys Lys Gln Asp Ser Asn Val Thr Glu Leu Val Leu  
1 5 10 15  
Leu Gly Leu Ser Ser Trp Glu Leu Gln Leu Phe Leu Leu Leu  
20 25 30  
Phe Leu Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val  
35 40 45  
Val Thr Val Gln Ala His Ala His Leu Leu Gln Ser Pro Met Tyr Tyr  
50 55 60  
Phe Leu Gly His Leu Ser Phe Ile Asp Leu Cys Leu Ser Cys Val Thr  
65 70 75 80  
Leu Pro Lys Met Leu Gly Asp Phe Leu Gln Gln Gly Lys Ser Ile Ser  
85 90 95  
Phe Ser Gly Cys Leu Ala Gln Ile Tyr Phe Leu His Phe Leu Gly Ala  
100 105 110  
Ser Glu Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala  
115 120 125  
Ile Cys Asn Pro Leu Arg Tyr Leu Ile Ile Met Asn Pro Gln Leu Cys  
130 135 140  
Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His Ser Ile

```

145          150          155          160
Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro Asn Glu
165          170          175
Leu Asp Asn Phe Tyr Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys
180          185          190
Met Asp Thr Tyr Val Val Glu Val Leu Met Ile Ala Asn Ser Gly Leu
195          200          205
Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala Val Ile
210          215          220
Leu Ile Thr Leu Arg Thr His Phe Gly Gln Gly Gln Asn Lys Phe Leu
225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe Met Pro
245          250          255
Cys Ile Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val Asp Lys
260          265          270
Ile Phe Ser Met Phe Tyr Thr Val Met Thr Pro Met Leu Ser Pro Leu
275          280          285
Ile Tyr Thr Leu Arg Asn Ala Asp Met Lys Thr Ala Met Lys Lys Leu
290          295          300
Arg Ile Lys Pro Cys Asp Ile
305          310

```

&lt;210&gt; 1340

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g257 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1340

```

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1      5      10      15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
20     25     30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
35     40     45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
50     55     60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65     70     75     80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
85     90     95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
100    105    110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
115    120    125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
130    135    140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145    150    155    160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
165    170    175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
180    185    190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
195    200    205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
210    215    220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225    230    235    240

```

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro  
 245 250 255  
 Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser  
 260 265 270  
 Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val  
 275 280 285  
 Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg  
 290 295 300  
 Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
 305 310 315

&lt;210&gt; 1341

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g258 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1341

Met Ser Ser Arg Leu Met Asn Val Phe Ser Met Glu Thr Ile Asn Phe  
 1 5 10 15  
 Val Ser Cys Leu Ile Leu Met Gly Phe Pro Ser Ser Pro Glu Met Gln  
 20 25 30  
 Leu Leu Tyr Phe Gly Leu Phe Ser Val Ala Tyr Thr Leu Thr Pro Met  
 35 40 45  
 Gly Asn Ala Ala Ile Val Cys Ala Val Trp Xaa Asp Gln His Leu His  
 50 55 60  
 Thr Pro Met Tyr Thr Leu Leu Gly Asn Phe Ser Leu Leu Glu Ile Trp  
 65 70 75 80  
 Tyr Val Thr Ala Thr Lys Leu Leu Ala Asn Phe Leu Ser Thr Ser Lys  
 85 90 95  
 Ser Ile Ser Phe Met Ser Cys Phe Ala Gln Phe Tyr Phe Phe Ser Leu  
 100 105 110  
 Gly Tyr Asp Glu Gly Phe Phe Leu Cys Ile Thr Ala Phe Asp Arg Tyr  
 115 120 125  
 Leu Ala Ile Cys Arg Pro Leu Arg Tyr Pro Cys Ile Met Thr Lys Gln  
 130 135 140  
 Val Cys Thr Gly Leu Ile Ile Phe Ala Trp Ser Cys Val Phe Val Ile  
 145 150 155 160  
 Phe Leu Thr Leu Val Ile Leu Ile Ser Gln Leu Ser Tyr Cys Gly Pro  
 165 170 175  
 Asn Ile Ile Asn His Phe Ile Cys Asp Pro Val Pro Leu Lys Met Leu  
 180 185 190  
 Ser Cys Ser Glu Asp Ile Ile Ile Thr Gln Leu Ile Tyr Ser Thr Phe  
 195 200 205  
 Asn Ser Val Phe Ile Ile Gly Thr Phe Leu Phe Ile Leu Cys Ser Tyr  
 210 215 220  
 Ala Leu Val Ile Leu Ala Ile Ile Arg Met Pro Ser Glu Ala Gly Lys  
 225 230 235 240  
 Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Leu  
 245 250 255  
 Phe Tyr Gly Ser Ile Met Val Met Tyr Val Ser Pro Gly Ser Ala His  
 260 265 270  
 Pro Ala Lys Asn Glu Lys Ile Ile Thr Leu Phe Phe Ser Val Ile Thr  
 275 280 285  
 Pro Leu Cys Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys

290 295 300  
 Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile  
 305 310 315 320

<210> 1342  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g259 protein)

<220>  
 <223> Synthetic construct

<400> 1342  
 Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr  
 1 5 10 15  
 Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile  
 20 25 30  
 Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile  
 35 40 45  
 Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu  
 50 55 60  
 Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu  
 65 70 75 80  
 Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile  
 85 90 95  
 Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu  
 100 105 110  
 Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile  
 130 135 140  
 Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met  
 145 150 155 160  
 Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe  
 165 170 175  
 Cys Asp Val Lys Pro Leu Leu Lys Leu Ser Leu Ile Ser Gly Trp Leu  
 180 185 190  
 Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu  
 195 200 205  
 Leu Ser Tyr Phe Tyr Ile Ile Thr His Leu Phe Phe Lys Thr His Ser  
 210 215 220  
 Phe Ser Met Leu Arg Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met  
 225 230 235 240  
 Val Val Ile Leu Leu Tyr Ala Pro Val Leu Phe Thr Tyr Ile His His  
 245 250 255  
 Ala Ser Gly Thr Ser Met Asp Gln Asp Arg Ile Thr Ala Ile Met Tyr  
 260 265 270  
 Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn  
 275 280 285  
 Lys Glu Val Lys Gly Ala Phe Asn Arg Ala Met Lys Arg Trp Leu Trp  
 290 295 300  
 Pro Lys Glu Ile Leu  
 305

<210> 1343  
 <211> 331  
 <212> PRT  
 <213> Unknown (H38g260 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1343

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Val Phe Val Leu Val Leu
           20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
           35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
           50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
           85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
           100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
           115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
           130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145           150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
           165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
           180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
           195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
           210          215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
225           230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
           245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
           260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
           275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
           290          295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Arg Lys Ile Asp Cys
305           310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
           325          330

```

&lt;210&gt; 1344

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g261 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1344

```

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu
 1           5           10           15
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val

```

```
<210> 1345
<211> 312
<212> PRT
<213> Unknown (H38g262 protein)
```

<220>  
<223> Synthetic construct.

<400> 1345

|           |           |           |            |           |     |           |           |            |           |           |           |           |            |           |     |
|-----------|-----------|-----------|------------|-----------|-----|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----|
| Met<br>1  | Ser       | Ala       | Asn        | Thr<br>5  | Ser | Met       | Val       | Thr        | Glu<br>10 | Phe       | Leu       | Leu       | Leu        | Gly<br>15 | Phe |
| Ser       | His       | Leu       | Ala<br>20  | Asp       | Leu | Gln       | Gly       | Leu<br>25  | Leu       | Phe       | Ser       | Val       | Phe<br>30  | Leu       | Thr |
| Ile       | Tyr       | Leu<br>35 | Leu        | Thr       | Val | Ala       | Gly<br>40 | Asn        | Phe       | Leu       | Ile       | Val<br>45 | Val        | Leu       | Val |
| Ser       | Thr<br>50 | Asp       | Ala        | Ala       | Leu | Gln<br>55 | Ser       | Pro        | Met       | Tyr       | Phe<br>60 | Leu       | Arg        | Thr       |     |
| Leu<br>65 | Ser       | Ala       | Leu        | Glu<br>70 | Ile | Gly       | Tyr       | Thr        | Ser       | Val<br>75 | Thr       | Val       | Pro        | Leu<br>80 | Leu |
| Leu       | His       | His       | Leu        | Leu<br>85 | Thr | Gly       | Arg       | Arg        | His<br>90 | Ile       | Ser       | Arg       | Ser        | Gly<br>95 | Cys |
| Ala       | Leu       | Gln       | Met<br>100 | Phe       | Phe | Phe       | Leu       | Phe<br>105 | Phe       | Gly       | Ala       | Thr       | Glu<br>110 | Cys       | Cys |

Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro  
 115 120 125  
 Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala  
 130 135 140  
 Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro  
 145 150 155 160  
 Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe  
 165 170 175  
 Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser  
 180 185 190  
 Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys  
 195 200 205  
 Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile  
 210 215 220  
 Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe  
 245 250 255  
 Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu  
 260 265 270  
 Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile  
 290 295 300  
 Gln Lys Thr Val Pro Met Glu Ile  
 305 310

&lt;210&gt; 1346

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g263 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1346

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser  
 1 5 10 15  
 Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser  
 20 25 30  
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val  
 35 40 45  
 Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu  
 50 55 60  
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu  
 65 70 75 80  
 Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser  
 85 90 95  
 Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu  
 100 105 110  
 Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu  
 115 120 125  
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser  
 130 135 140  
 Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser  
 145 150 155 160  
 Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu  
 165 170 175  
 Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr  
 180 185 190  
 Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro

```

      195              200              205
Leu Ser Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln Ala Val Leu
  210              215              220
Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
  225              230              235              240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
      245              250              255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
      260              265              270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
      275              280              285
Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
      290              295              300
Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
  305              310              315

```

&lt;210&gt; 1347

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g264 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1347

```

Met Lys Ser Glu Leu Asn Arg Asn Tyr Ser Glu Val Thr Glu Phe Ile
  1          5          10          15
Leu Leu Gly Phe Arg Thr Ser Pro Glu Ala Gln Ile Leu Leu Phe Phe
      20          25          30
Leu Phe Leu Leu Ile Tyr Met Val Ile Val Leu Arg Asn Leu Ser Met
      35          40          45
Leu Val Val Ile Glu Ile Asp Ser Arg Leu His Thr Pro Val Tyr Phe
      50          55          60
Phe Leu Arg Asn Leu Ser Tyr Leu Asp Leu Arg Tyr Ser Thr Val Ile
      65          70          75          80
Ala Pro Lys Leu Thr Thr Leu Phe Ser Lys Glu Lys Lys Ile Ser Tyr
      85          90          95
Asn Gly Xaa Ala Thr Gln Leu Phe Phe Phe Ala Leu Phe Val Gly Thr
      100          105          110
Glu Gly Phe Phe Leu Asp Met Met Ala Tyr Asp Arg Phe Ser Ala Ile
      115          120          125
Cys Ser Pro Phe Phe Tyr Thr Val Cys Met Ser Gln Gln Ala Cys Val
      130          135          140
Cys Leu Val Val Gly Ser Ser Ile Cys Gly Cys Ile Asn Ser Met Ile
      145          150          155          160
Gln Thr Gly Phe Thr Phe Ser Leu His Phe Cys Gly Glu Asn Arg Leu
      165          170          175
Glu His Phe Phe Cys Asp Val Ser Val Met Ile Lys Ile Ser Cys Ile
      180          185          190
Asp Ile Leu Val Asn Glu Val Val Leu Phe Ile Leu Ser Ala Leu Ile
      195          200          205
Thr Thr Thr Thr Thr Val Ile Leu Ala Ser Tyr Val His Ile Leu Ser
      210          215          220
Thr Val Leu Lys Ile Leu Ser Thr His Gly Arg Arg Lys Thr Phe Ser
      225          230          235          240
Thr Cys Ser Ser His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Val
      245          250          255

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Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Ile  
                   260                  265                  270  
 Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr  
                   275                  280                  285  
 Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys  
                   290                  295                  300  
 Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile  
 305                  310                  315

&lt;210&gt; 1348

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g265 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1348

Met Ser Pro Arg Met Cys Leu Ser Phe Leu Ala Val Ala Trp Thr Leu  
   1                  5                  10                  15  
 Gly Val Ser His Ser Leu Phe Gln Leu Ala Phe Leu Val Asn Leu Pro  
                   20                  25                  30  
 Phe Cys Gly Pro Asn Val Leu Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
                   35                  40                  45  
 Leu Leu Arg Leu Ala Cys Thr Asp Thr Tyr Arg Leu Gln Phe Met Val  
   50                  55                  60  
 Thr Val Asn Ser Gly Phe Ile Cys Val Gly Thr Phe Phe Ile Leu Leu  
 65                  70                  75                  80  
 Ile Ser Tyr Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly  
                   85                  90                  95  
 Gly Ser Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ser Thr Ala Val  
                   100                  105                  110  
 Leu Leu Phe Phe Gly Pro Pro Met Phe Val Tyr Thr Trp Pro His Pro  
                   115                  120                  125  
 Asn Ser Gln Met Asp Lys Phe Leu Ala Ile Phe Asp Ala Val Leu Thr  
   130                  135                  140  
 Pro Phe Leu Asn Pro Val Val Tyr Thr Phe Arg Asn Lys Glu Met Lys  
 145                  150                  155                  160  
 Ala Ala Ile Lys Arg Val Cys Lys Gln Leu Val Ile Tyr Lys Lys Ile  
                   165                  170                  175  
 Ser

&lt;210&gt; 1349

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g266 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1349

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Lys Phe Leu Leu Leu Gly  
   1                  5                  10                  15  
 Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu  
                   20                  25                  30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala  
                   35                  40                  45  
 Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
   50                  55                  60  
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

```

65          70          75          80
Met Leu Val Ser Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
      85          90
Cys Leu Thr Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr
      100        105        110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
      115        120        125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu
      130        135        140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
145          150          155          160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
      165        170        175
Phe Phe Cys Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr
      180        185        190
Leu Leu Asn Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
      195        200        205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
      210        215        220
Leu Met Gly Met Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
      245        250        255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
      260        265        270
Thr Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
      275        280        285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu Arg Leu
      290        295        300
Leu Ser Arg Ala Asp Ser Cys Pro Leu Thr Asn Gln Gly Leu Arg Thr
305          310          315          320
Lys Arg

```

<210> 1350  
 <211> 322  
 <212> PRT  
 <213> Unknown (H38g267 protein)

<220>  
 <223> Synthetic construct  
  
 <221> VARIANT  
 <222> (1)...(322)  
 <223> Xaa = Any Amino Acid

```

<400> 1350
Tyr Thr Glu Pro Glu Asn Leu Thr Gly Val Leu Glu Phe Leu Leu Leu
  1          5          10          15
Gly Leu Pro Asp Asp Pro Glu Leu Gln Pro Val Leu Phe Gly Leu Phe
      20        25        30
Leu Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
      35        40        45
Ala Val Ser Ser Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu
      50        55        60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Ala Ser Thr Thr Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Gln Ala His Ser Arg Leu Ile Ser Tyr Val
      85        90        95
Gly Cys Leu Thr Gln Met Ser Phe Leu Ile Phe Phe Ala Cys Met Glu
      100       105       110

```

Ser Leu Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
 115 120 125  
 His Pro Leu His Tyr Gln Val Ile Met Ser Pro Arg Leu Cys Gly Phe  
 130 135 140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Asn Leu Ile Val Leu Gln Leu Thr Cys Phe Asn Asp Val Glu Ile Ser  
 165 170 175  
 Asn Phe Phe Cys Asp Pro Ser Xaa Leu Leu Lys Leu Ala Cys Ser Asp  
 180 185 190  
 Thr Ser Ile Asn Asn Met Val Val Tyr Phe Ile Gly Ala Ile Phe Gly  
 195 200 205  
 Phe Leu Pro Leu Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser  
 210 215 220  
 Ser Ile Leu Arg Val Leu Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Leu Tyr Gly Thr Ala  
 245 250 255  
 Leu Gly Gly Tyr Leu Ser Ser Ala Val Ser Leu Ser Ser Arg Lys Gly  
 260 265 270  
 Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Gln Arg  
 290 295 300  
 Leu His Gly Arg Ile Met Xaa Ser Pro Tyr Leu Leu His Leu Phe Cys  
 305 310 315 320  
 Ser Ile

&lt;210&gt; 1351

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g268 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1351

Met Arg Gln Ile Asn Gln Thr Gln Val Thr Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu  
 20 25 30  
 Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Leu Ile Ser Leu  
 35 40 45  
 Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys  
 50 55 60  
 Asn Leu Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln  
 65 70 75 80  
 Ala Leu Val His Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu  
 85 90 95  
 Cys Ala Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys  
 100 105 110  
 Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu  
 130 135 140  
 Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr  
 145 150 155 160  
 Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His  
 165 170 175  
 Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr

|            |           |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| Met<br>1   | Pro       | Ile        | Leu        | Met<br>5   | Ala        | Ile        | Gly        | Asn        | Trp<br>10  | Thr        | Glu        | Ile        | Ser        | Glu<br>15  | Phe |
| Ile        | Leu       | Met<br>20  | Ser        | Phe        | Ser        | Ser        | Leu        | Pro<br>25  | Thr        | Glu        | Ile        | Gln        | Ser<br>30  | Leu        | Leu |
| Phe        | Leu<br>35 | Thr        | Phe        | Leu        | Thr        | Ile        | Tyr<br>40  | Leu        | Val        | Thr        | Leu        | Lys<br>45  | Gly        | Asn        | Ser |
| Leu<br>50  | Ile       | Ile        | Leu        | Val        | Thr        | Leu<br>55  | Ala        | Asp        | Pro        | Met        | Leu<br>60  | His        | Ser        | Pro        | Met |
| Tyr<br>65  | Phe       | Phe        | Leu        | Arg        | Asn<br>70  | Leu        | Ser        | Phe        | Leu        | Glu<br>75  | Ile        | Gly        | Phe        | Asn        | Leu |
| Val        | Ile       | Val        | Pro        | Lys<br>85  | Met        | Leu        | Gly        | Thr        | Leu<br>90  | Leu        | Ala        | Gln        | Asp        | Thr<br>95  | Thr |
| Ile        | Ser       | Phe<br>100 | Leu        | Gly        | Cys        | Ala        | Thr        | Gln<br>105 | Met        | Tyr        | Phe        | Phe<br>110 | Phe        | Phe        | Phe |
| Gly        | Val       | Ala<br>115 | Glu        | Cys        | Phe        | Leu        | Leu        | Ala<br>120 | Thr        | Met        | Ala        | Tyr<br>125 | Asp        | Arg        | Tyr |
| Val<br>130 | Ala       | Ile        | Cys        | Ser        | Pro        | Leu<br>135 | His        | Tyr        | Pro        | Val        | Ile<br>140 | Met        | Asn        | Gln        | Arg |
| Thr<br>145 | Arg       | Ala        | Lys        | Leu        | Ala<br>150 | Ala        | Ala        | Ser        | Trp        | Phe<br>155 | Pro        | Gly        | Phe        | Pro        | Val |
| Ala        | Thr       | Val        | Gln        | Thr<br>165 | Thr        | Trp        | Leu        | Phe        | Ser<br>170 | Phe        | Pro        | Phe        | Cys        | Gly<br>175 | Thr |
| Asn        | Lys       | Val<br>180 | Asn        | His        | Phe        | Phe        | Cys        | Asp<br>185 | Ser        | Pro        | Pro        | Val        | Leu<br>190 | Lys        | Leu |
| Val        | Cys       | Ala<br>195 | Asp        | Thr        | Ala        | Leu        | Phe<br>200 | Glu        | Ile        | Tyr        | Ala        | Ile<br>205 | Val        | Gly        | Thr |
| Ile<br>210 | Leu       | Val        | Val        | Met        | Ile        | Pro<br>215 | Cys        | Leu        | Leu        | Ile        | Leu<br>220 | Cys        | Ser        | Tyr        | Thr |
| Arg<br>225 | Ile       | Ala        | Ala        | Ala        | Ile<br>230 | Leu        | Lys        | Ile        | Pro        | Ser<br>235 | Ala        | Lys        | Gly        | Lys        | His |
| Lys        | Ala       | Phe        | Ser        | Thr<br>245 | Cys        | Ser        | Ser        | His        | Leu<br>250 | Leu        | Val        | Val        | Ser        | Leu<br>255 | Phe |
| Tyr        | Ile       | Ser        | Ser<br>260 | Ser        | Leu        | Thr        | Tyr        | Phe<br>265 | Trp        | Pro        | Lys        | Ser        | Asn<br>270 | Asn        | Ser |

Pro Glu Ser Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro  
 275 280 285  
 Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ser Glu Val Lys Asn  
 290 295 300  
 Ala Leu Ser Arg Thr Phe His Lys Val Leu Ala Leu Arg Asn Cys Ile  
 305 310 315 320  
 Pro

&lt;210&gt; 1353

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g270 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(260)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1353

Ala His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro  
 1 5 10 15  
 Gln Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met  
 20 25 30  
 Gly Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu  
 35 40 45  
 Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys  
 50 55 60  
 Lys Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly  
 65 70 75 80  
 Leu Val Ser Val Thr Trp Ser Cys Trp Gly Gly Gln Leu Leu Gly His  
 85 90 95  
 Val Ser Trp Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp  
 100 105 110  
 His Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser  
 115 120 125  
 Thr Val Ala Ile Glu Gly Thr Val Phe Val Leu Ala Val Gly Val Val  
 130 135 140  
 Leu Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg  
 145 150 155 160  
 Ala Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly  
 165 170 175  
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile  
 180 185 190  
 Ile Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly  
 195 200 205  
 Met Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro  
 210 215 220  
 Leu Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg  
 225 230 235 240  
 Leu Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu Xaa Arg His Leu His  
 245 250 255  
 Leu Thr Ser Leu  
 260

&lt;210&gt; 1354

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g271 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1354

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Ile | Leu | Xaa | Ile | Ile | Ser | Gln | His | Val | His | Thr | Gly | Cys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Asn | Xaa | Glu | Leu | Gln | Pro | Ile | Leu | Phe | Gly | Leu | Phe | Leu | Ser | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Leu | Val | Met | Val | Leu | Gly | Asn | Leu | Leu | Ile | Ile | Leu | Ala | Val | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Ser | His | Leu | His | Thr | Pro | Thr | Tyr | Phe | Phe | Leu | Ser | Asn | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Ala | Asp | Ile | Gly | Phe | Pro | Ser | Thr | Thr | Val | Pro | Lys | Met | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Asp | Ile | Gln | Ser | His | Ser | Arg | Val | Ile | Ser | Tyr | Ala | Gly | Cys | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Gln | Ile | Ser | Leu | Phe | Ala | Val | Phe | Gly | Cys | Met | Glu | Asp | Met | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ser | Val | Met | Ala | Tyr | Asp | Arg | Phe | Val | Ala | Ile | Cys | His | Pro | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Tyr | Pro | Val | Ile | Met | Asn | Pro | Cys | Phe | Cys | Gly | Phe | Leu | Val | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Phe | Phe | Leu | Ser | Leu | Leu | Asp | Phe | Gln | Leu | His | Asn | Trp | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Leu | Gln | Ile | Thr | Cys | Phe | Lys | Asp | Val | Glu | Ile | Pro | Ser | Phe | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Asp | Pro | Ser | Gln | Leu | Pro | His | Leu | Ala | Cys | Cys | Asp | Thr | Phe | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Asn | Ile | Val | Met | Tyr | Phe | Leu | Ala | Ala | Ile | Leu | Gly | Phe | Leu | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Ser | Gly | Ile | Phe | Tyr | Ser | Tyr | Tyr | Lys | Ile | Val | Ser | Ser | Ile | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Val | Ser | Ser | Ser | Gly | Lys | Tyr | Lys | Ala | Phe | Ser | Thr | Cys | Gly |     |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Ser | His | Leu | Ser | Val | Val | Cys | Leu | Phe | Tyr | Gly | Thr | Ala | Leu | Gly | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | Leu | Ser | Ser | Asp | Met | Ser | Ser | Tyr | Pro | Arg | Lys | Gly | Ala | Val | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Val | Met | Tyr | Thr | Val | Val | Ala | Pro | Met | Leu | Asn | Pro | Phe | Ile | Tyr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Leu | Arg | Lys | Arg | Asp | Ile | Lys | Ser | Ala | Leu | Gln | Gln | Leu | His | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Ile | Val | Xaa | Ser | His | Asp | Leu | Ile | Ile | Gly | Ser | Ile | Leu | Xaa | Pro |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Trp | Val | Gly | Lys | Gly | Ser | Lys | Val | Lys |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 1355

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g272 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1355

```

Met Glu Ser Pro Asn His Thr Asp Val Asp Pro Ser Val Phe Phe Leu
 1      5      10      15
Leu Gly Ile Pro Gly Leu Glu Gln Phe His Leu Trp Leu Ser Leu Pro
 20      25      30
Val Cys Gly Leu Gly Thr Ala Thr Ile Val Gly Asn Ile Thr Ile Leu
 35      40      45
Val Val Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe
 50      55      60
Leu Cys Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val
 65      70      75      80
Pro Lys Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala
 85      90      95
Ser Ala Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met
100      105      110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115      120      125
Cys His Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala
130      135      140
His Ile Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro
145      150      155      160
Cys Pro Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile
165      170      175
Leu His Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly
180      185      190
Asp Thr Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val
195      200      205
Ile Gly Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala
210      215      220
Gln Ala Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu
225      230      235      240
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro
245      250      255
Ala Leu Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val
260      265      270
His Ile His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala
275      280      285
Leu Asn Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Lys Arg
290      295      300
Val Val Arg Val Phe Gln Ser Gly Gln Gly Met Gly Ile Lys Ala Ser
305      310      315      320
Glu

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&lt;210&gt; 1356

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g273 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1356

```

Met Thr Trp Ser Gly Gly Thr Ile Val Gly Glu Xaa Gly Glu Phe Val
 1      5      10      15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Leu Phe Ala
 20      25      30
Leu Leu Leu Leu Ala Tyr Val Leu Val Leu Thr Glu Asn Thr Leu Ile

```

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      35      40      45
Ile Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe
  50      55      60
Phe Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr
  65      70      75      80
Ile Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly
      85      90      95
Gln Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu
      100      105      110
Gly Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp
      115      120      125
Arg Tyr Met Ala Ile Cys Tyr Pro Leu His Tyr Pro Val Ile Val Ser
      130      135      140
Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe
      145      150      155      160
Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys
      165      170      175
Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu
      180      185      190
Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile
      195      200      205
Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser
      210      215      220
Tyr Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly
      225      230      235      240
Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile
      245      250      255
Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu
      260      265      270
Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile
      275      280      285
Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val
      290      295      300
Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro
      305      310      315      320
Asp Pro Lys Lys Ala Ser Arg
      325

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&lt;210&gt; 1357

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g274 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1357

```

Met Glu Ala Gly Asn Gln Thr Gly Phe Leu Glu Phe Ile Leu Leu Gly
  1      5      10      15
Leu Ser Glu Asp Pro Glu Leu Gln Pro Phe Ile Phe Gly Leu Phe Leu
      20      25      30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35      40      45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys
      65      70      75      80
Met Leu Val Asn Ile Gln Thr Glu Asn Lys Ala Ile Ser Tyr Met Asp
      85      90      95
Cys Leu Thr Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr
      100      105      110

```



Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His  
 115 120 125  
 Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu  
 130 135 140  
 Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile  
 145 150 155 160  
 Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val  
 195 200 205  
 Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser  
 210 215 220  
 Ile Arg Lys Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Val His Phe Thr Ser Ala Val Thr His Ser Ser Gln Lys Ile Ser  
 260 265 270  
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Ser Leu  
 290 295 300  
 Leu Ser Arg Ala Ala Ser Cys Leu  
 305 310

&lt;210&gt; 1358

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g275 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1358

Met Thr Ala Cys Asn Ala Ser Gln Gly His Pro Ser Phe Phe Ile Leu  
 1 5 10 15  
 Gln Gly Ile Pro Gly Met Glu Asp Lys His Arg Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Ser Ser Met Tyr Phe Ile Met Val Leu Gly Asn Cys Thr Ile Leu  
 35 40 45  
 Leu Thr Ile Ser Thr Glu Arg Ser Leu His Lys Pro Met Phe Leu Leu  
 50 55 60  
 Leu Cys Leu Leu Ala Leu Thr Asp Leu Gly Met Ser Thr Thr Thr Ile  
 65 70 75 80  
 Pro Lys Val Leu Cys Ile Phe Trp Phe Gly Gln Ser Glu Ile Ser Tyr  
 85 90 95  
 Glu Gly Cys Leu Val Gln Leu Phe Phe Ile His Ser Ile Ser Ala Met  
 100 105 110  
 Gln Ser Ala Val Leu Met Thr Met Ala Phe Asp His Tyr Val Ala Ile  
 115 120 125  
 Cys Lys Pro Leu Arg Tyr Ala Thr Ile Leu Ser Asn Ser Cys Thr Gly  
 130 135 140  
 Leu Ile Gly Leu Val Ser Leu Val Arg Ala Ile Leu Phe Ile Leu Pro  
 145 150 155 160  
 Met Pro Ile Leu Leu Gln Gln Met Pro Tyr His Ala Asn Arg Val Ile

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |  |  |
| Pro | Thr | Thr | Ser | Cys | Glu | His | Met | Ala | Val | Val | Lys | Met | Val | Cys | Val |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Asp | Thr | Thr | Val | Asn | Arg | Ile | Tyr | Gly | Leu | Val | Val | Ala | Leu | Leu | Val |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Ala | Gly | Tyr | Asp | Leu | Ser | Ala | Ile | Ala | Ser | Ser | Tyr | Val | Leu | Ile | Ile |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Gln | Ala | Ile | Met | His | Leu | Ser | Ser | Lys | Glu | Ala | His | His | Lys | Ala | Val |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Asn | Thr | Cys | Thr | Thr | His | Ile | Cys | Val | Met | Leu | Ile | Ser | Tyr | Thr | Pro |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Ser | Leu | Phe | Ser | Phe | Leu | Ala | His | Arg | Phe | Gly | Gln | Gly | Ile | Pro | Pro |  |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |  |
| His | Val | His | Ile | Ile | Leu | Gly | Asn | Leu | Tyr | Phe | Leu | Val | Pro | Pro | Met |  |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |  |
| Leu | Ser | Pro | Ile | Ile | Tyr | Gly | Val | Lys | Thr | Lys | Glu | Phe | Trp | Asp | Lys |  |  |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |  |
| Val | Thr | Lys | Xaa | Val | Ala | Gly | Lys | Lys | Asn | Pro | Gln | Pro | Leu | Thr | Met |  |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |  |  |

&lt;210&gt; 1359

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g276 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1359

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Glu | Leu | Trp | Asn | Phe | Thr | Leu | Gly | Ser | Gly | Phe | Ile | Leu | Val | Gly |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ile | Leu | Asn | Asp | Ser | Gly | Ser | Pro | Glu | Leu | Leu | Cys | Ala | Thr | Ile | Thr |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ile | Leu | Tyr | Leu | Leu | Ala | Leu | Ile | Ser | Asn | Gly | Leu | Leu | Leu | Leu | Ala |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Ile | Thr | Met | Glu | Ala | Arg | Leu | His | Met | Pro | Met | Tyr | Leu | Leu | Leu | Gly |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |  |
| Gln | Leu | Ser | Leu | Met | Asp | Leu | Leu | Phe | Thr | Ser | Val | Val | Thr | Pro | Lys |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Ala | Leu | Ala | Asp | Phe | Leu | Arg | Arg | Glu | Asn | Thr | Ile | Ser | Phe | Gly | Gly |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Cys | Ala | Leu | Gln | Met | Phe | Leu | Ala | Leu | Thr | Met | Gly | Gly | Ala | Glu | Asp |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |  |
| Leu | Leu | Leu | Ala | Phe | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | His |  |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |
| Pro | Leu | Thr | Tyr | Met | Thr | Leu | Met | Ser | Ser | Arg | Ala | Cys | Trp | Leu | Met |  |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |  |
| Val | Ala | Thr | Ser | Trp | Ile | Leu | Ala | Ser | Leu | Ser | Ala | Leu | Ile | Tyr | Thr |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |  |
| Val | Tyr | Thr | Met | His | Tyr | Pro | Phe | Cys | Arg | Ala | Gln | Glu | Ile | Arg | His |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |
| Leu | Leu | Cys | Glu | Ile | Pro | His | Leu | Leu | Lys | Val | Ala | Cys | Ala | Asp | Thr |  |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |  |
| Ser | Arg | Tyr | Glu | Leu | Met | Val | Tyr | Val | Met | Gly | Val | Thr | Phe | Leu | Ile |  |  |
|     | 195 |     |     |     | 200 |     |     |     |     |     |     | 205 |     |     |     |  |  |
| Pro | Ser | Leu | Ala | Ala | Ile | Leu | Ala | Ser | Tyr | Thr | Gln | Ile | Leu | Leu | Thr |  |  |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |  |
| Val | Leu | His | Met | Pro | Ser | Asn | Glu | Gly | Arg | Lys | Lys | Ala | Leu | Val | Thr |  |  |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |  |  |
| Cys | Ser | Ser | His | Leu | Thr | Val | Val | Gly | Met | Phe | Tyr | Gly | Ala | Ala | Thr |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |  |

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn  
 260 265 270  
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val  
 290 295 300  
 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu  
 305 310 315

&lt;210&gt; 1360

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g277 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1360

Met Lys Ala Gly Asn Phe Ser Asp Thr Pro Glu Phe Phe Leu Leu Gly  
 1 5 10 15  
 Leu Ser Gly Asp Pro Glu Leu Gln Pro Ile Leu Phe Met Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Ala Thr Met Leu Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Val Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Ile Leu Ser Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Met Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Ile Gln Ala Gln Ala Gln Ser Ile Asn Tyr Thr Gly  
 85 90 95  
 Cys Leu Thr Gln Ile Cys Phe Val Leu Val Phe Val Gly Leu Glu Asn  
 100 105 110  
 Gly Ile Leu Val Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Asn Val Ile Met Asn Pro Lys Leu Cys Gly Leu Leu  
 130 135 140  
 Leu Leu Leu Ser Phe Ile Val Ser Val Leu Asp Ala Leu Leu His Thr  
 145 150 155 160  
 Leu Met Val Leu Gln Leu Thr Phe Cys Ile Asp Leu Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Glu Leu Ala His Ile Leu Lys Leu Ala Cys Ser Asp Val  
 180 185 190  
 Leu Ile Asn Asn Ile Leu Val Tyr Leu Val Thr Ser Leu Leu Gly Val  
 195 200 205  
 Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr Arg Ile Val Ser Ser  
 210 215 220  
 Val Met Lys Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Ile  
 225 230 235 240  
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Gly Phe  
 245 250 255  
 Gly Val Tyr Leu Ser Ser Gly Ala Thr His Ser Ser Arg Lys Gly Ala  
 260 265 270  
 Ile Ala Ser Val Met Tyr Thr Val Thr Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Met Leu Lys Ala Leu Arg Lys Leu  
 290 295 300  
 Ile Ser Arg Ile Pro Ser Phe His  
 305 310

&lt;210&gt; 1361

&lt;211&gt; 328

<212> PRT  
 <213> Unknown (H38g278 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(328)  
 <223> Xaa = Any Amino Acid

<400> 1361  
 Lys Ile Ser Asn Ser Ser Lys Phe Gln Val Ser Glu Phe Ile Leu Leu  
 1 5 10 15  
 Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu  
 20 25 30  
 Ala Leu Leu Tyr Leu Ser Ala Leu Ala Ala Asn Thr Leu Ile Leu Ile  
 35 40 45  
 Ile Ile Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu  
 50 55 60  
 Gly Ile Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro  
 65 70 75 80  
 Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro  
 85 90 95  
 Glu Cys Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu  
 100 105 110  
 Ser Gly Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 His Pro Leu Arg Tyr Pro Ser Ile Val Thr Ser Ser Leu Ile Leu Lys  
 130 135 140  
 Ala Thr Leu Phe Met Val Leu Arg Asn Gly Leu Phe Val Thr Pro Val  
 145 150 155 160  
 Pro Val Leu Ala Ala Gln Arg Asp Tyr Cys Ser Lys Asn Glu Ile Glu  
 165 170 175  
 His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp  
 180 185 190  
 Arg Arg Pro Asn Ser Ile Cys Gln Leu Val Leu Ala Trp Leu Gly Met  
 195 200 205  
 Gly Ser Asp Leu Ser Leu Ile Ile Leu Ser Tyr Ile Leu Ile Leu Tyr  
 210 215 220  
 Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Ala Lys Ala Leu Ser  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Thr Leu Ile Leu Phe Phe Tyr Thr Ile Val  
 245 250 255  
 Val Val Ile Ser Val Thr His Leu Thr Glu Met Lys Ala Thr Leu Ile  
 260 265 270  
 Pro Val Leu Leu Asn Val Leu His Asn Ile Ile Pro Pro Ser Leu Asn  
 275 280 285  
 Pro Thr Val Tyr Ala Leu Gln Thr Lys Glu Leu Arg Ala Ala Phe Gln  
 290 295 300  
 Lys Val Leu Phe Ala Leu Thr Lys Glu Ile Arg Ser Xaa Arg Pro Ser  
 305 310 315 320  
 Pro Xaa Cys Thr Xaa Thr Ser Ala  
 325

<210> 1362  
 <211> 316  
 <212> PRT  
 <213> Unknown (H38g279 protein)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1362

```

Met Glu Leu Arg Asn Ser Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
 1           5           10           15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
      20           25           30
Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Leu Ala
      35           40           45
Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
      50           55           60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
      65           70           75           80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
      85           90           95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
      100          105          110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
      130          135          140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
      145          150          155          160
Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
      165          170          175
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
      180          185          190
Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
      195          200          205
Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
      210          215          220
Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
      225          230          235          240
Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr
      245          250          255
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
      260          265          270
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
      290          295          300
Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu
      305          310          315

```

&lt;210&gt; 1363

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g280 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1363

```

Met Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro
 1           5           10           15
Leu Ala Leu Leu Tyr Leu Leu Ala Leu Ser Ala Asn Ile Leu Ile Leu
      20           25           30
Ile Ile Ile Asn Lys Glu Ala Ala Leu His Gln Pro Met Tyr Tyr Phe
      35           40           45
Leu Gly Ile Leu Ala Met Ala Asp Ile Gly Leu Ala Thr Thr Ile Met
      50           55           60
Pro Lys Ile Leu Ala Ile Leu Trp Phe Asn Ala Lys Thr Ile Ser Leu

```

```

65          70          75          80
Leu Glu Cys Phe Ala Gln Met Tyr Ala Ile His Cys Phe Val Ala Met
      85          90          95
Glu Ser Ser Thr Phe Val Cys Met Ala Ile Asp Arg Tyr Val Ala Ile
      100         105         110
Cys Arg Pro Leu Arg Tyr Pro Ser Ile Ile Thr Glu Ser Phe Val Phe
      115         120         125
Lys Ala Asn Gly Phe Met Ala Leu Arg Asn Ser Leu Cys Leu Ile Ser
      130         135         140
Val Pro Leu Leu Ala Ala Gln Arg His Tyr Cys Ser Gln Asn Gln Ile
      145         150         155         160
Glu His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ser Cys Asp
      165         170         175
Asp Arg Arg Ile Asn Ser Ile Asn Gln Val Leu Leu Ala Trp Thr Leu
      180         185         190
Met Gly Ser Asp Leu Gly Leu Ile Ile Leu Ser Tyr Ala Leu Ile Leu
      195         200         205
Tyr Ser Val Leu Lys Leu Asn Ser Pro Glu Ala Ala Ser Lys Ala Leu
      210         215         220
Ser Thr Cys Thr Ser His Leu Ile Leu Ile Leu Phe Phe Tyr Thr Val
      225         230         235         240
Ile Ile Val Ile Ser Ile Thr Arg Ser Thr Gly Met Arg Val Pro Leu
      245         250         255
Ile Pro Val Leu Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu
      260         265         270
Asn Pro Met Val Tyr Ala Leu Lys Asn Lys Glu Leu Arg Gln Gly Leu
      275         280         285
Tyr Lys Val Leu Arg Leu Gly Val Lys Gly Thr
      290         295

```

&lt;210&gt; 1364

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g281 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1364

```

Met Thr Trp Ser Gly Gly Thr Leu Val Gly Glu Xaa Gly Glu Phe Val
1          5          10          15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Ser Phe Ala
      20          25          30
Arg Xaa Ser Ala Ala Tyr Ala Leu Val Leu Thr Glu Asn Thr Leu Ile
      35          40          45
Ile Met Ala Ser Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe
      50          55          60
Val Leu Ala Asn Met Ser Ser Leu Glu Ile Trp Tyr Val Thr Val Thr
      65          70          75          80
Ile Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly
      85          90          95
Gln Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu
      100         105         110
Gly Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp
      115         120         125
Arg Tyr Met Ala Ile Cys Tyr Pro Leu His Tyr Pro Val Ile Val Ser
      130         135         140

```

Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe  
 145 150 155 160  
 Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys  
 165 170 175  
 Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu  
 180 185 190  
 Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile  
 195 200 205  
 Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser  
 210 215 220  
 Tyr Val Ala Ile Thr Gly Ala Val Met His Thr Ser Ser Ala Ala Gly  
 225 230 235 240  
 Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile  
 245 250 255  
 Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu  
 260 265 270  
 Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile  
 275 280 285  
 Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val  
 290 295 300  
 Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro  
 305 310 315 320  
 Asp Pro Lys Lys Ala Ser Arg  
 325

&lt;210&gt; 1365

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g282 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1365

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly  
 1 5 10 15  
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser  
 20 25 30  
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser  
 35 40 45  
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val  
 50 55 60  
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys  
 115 120 125  
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe  
 130 135 140  
 Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu  
 145 150 155 160  
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser  
 165 170 175  
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr

|   |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|
|   | 180 |     | 185 |     | 190 |
| Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val |     |     |     |     |     |
| 195   |     | 200 |     | 205 |     |
| Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr |     |     |     |     |     |
| 210   |     | 215 |     | 220 |     |
| Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu |     |     |     |     |     |
| 225   |     | 230 |     | 235 | 240 |
| Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe |     |     |     |     |     |
|   | 245 |     | 250 |     | 255 |
| Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala |     |     |     |     |     |
|   | 260 |     | 265 |     | 270 |
| Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr |     |     |     |     |     |
|   | 275 |     | 280 |     | 285 |
| Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln |     |     |     |     |     |
|   | 290 |     | 295 |     | 300 |
| Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu |     |     |     |     |     |
| 305   |     | 310 |     | 315 | 320 |
| Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr             |     |     |     |     |     |
|   | 325 |     | 330 |     |     |

&lt;210&gt; 1366

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g283 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1366

|   |     |
|---|-----|
| Met Leu Leu Gly Asn Leu Ala Ile Ile Ser Phe Ile Cys Leu Asp Ser |     |
| 1   | 5   |
| Arg Leu His Ser Pro Met Tyr Phe Phe Leu Cys Asn Phe Ser Leu Met |     |
|   | 20  |
| Glu Met Val Val Thr Ser Thr Val Val His Arg Met Leu Ala Asp Leu |     |
|   | 35  |
| Leu Ser Thr His Lys Thr Met Ser Leu Ala Lys Cys Leu Thr Gln Ser |     |
|   | 50  |
| Phe Phe Tyr Phe Ser Leu Gly Ser Ala Asn Phe Leu Ile Leu Met Val |     |
| 65  | 70  |
| Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro |     |
|   | 85  |
| Thr Ile Thr Asn Gly Pro Val Cys Val Lys Leu Val Val Ala Cys Trp |     |
|   | 100 |
| Val Val Gly Phe Leu Ser Ile Val Ser Pro Thr Leu Gln Lys Thr Arg |     |
|   | 115 |
| Leu Trp Phe Cys Gly Pro Asn Ile Ile Gly His Tyr Phe Cys Asp Ser |     |
|   | 130 |
| Ala Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg His Ile Glu Arg |     |
| 145   | 150 |
| Met Asp Leu Phe Leu Ser Leu Leu Phe Val Leu Thr Thr Met Leu Leu |     |
|   | 165 |
| Ile Ile Leu Ser Tyr Ile Leu Ile Val Ala Ala Val Leu His Ile Pro |     |
|   | 180 |
| Ser Ser Ser Gly Cys Gln Lys Ala Phe Ser Thr Cys Ala Ser His Leu |     |
|   | 195 |
| Thr Val Val Val Leu Gly Tyr Gly Ser Ala Ile Phe Ile Tyr Val Arg |     |
|   | 210 |
| Pro Gly Lys Gly His Ser Thr Tyr Leu Asn Lys Ala Val Ala Met Val |     |
| 225   | 230 |
| Thr Ala Met Val Thr Pro Phe Leu Asn Pro Phe Ile Phe Thr Phe Arg |     |
|   | 245 |
|   | 250 |
|   | 255 |



Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe  
 260 265 270  
 Leu Gly Asp Pro Ala Ala Cys Arg  
 275 280

<210> 1367  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g284 protein)

<220>  
 <223> Synthetic construct

<400> 1367  
 Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly  
 1 5 10 15  
 Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu  
 20 25 30  
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr  
 35 40 45  
 Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu  
 65 70 75 80  
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly  
 85 90 95  
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met  
 100 105 110  
 Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu  
 130 135 140  
 Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val  
 145 150 155 160  
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser  
 165 170 175  
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr  
 180 185 190  
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val  
 195 200 205  
 Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu  
 210 215 220  
 Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser  
 225 230 235 240  
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser  
 245 250 255  
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val  
 260 265 270  
 Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val  
 290 295 300  
 Thr Lys Tyr Ile Leu Cys Lys Glu Lys  
 305 310

<210> 1368  
 <211> 214  
 <212> PRT  
 <213> Unknown (H38g285 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(214)

<223> Xaa = Any Amino Acid

<400> 1368

```

Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
 1           5           10           15
Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
          20           25           30
Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
          35           40           45
Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
          50           55           60
Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
65           70           75           80
Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
          85           90           95
Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
          100          105          110
Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
          115          120          125
Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
          130          135          140
Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
145           150           155           160
Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
          165          170          175
Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
          180          185          190
Gly Val Lys Ser Lys His Ile Gln Glu Asn Met Val Gln Arg Phe Cys
          195          200          205
Gly Lys Ile Ser Cys His
          210

```

<210> 1369

<211> 330

<212> PRT

<213> Unknown (H38g286 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1369

```

Met Cys Leu Leu Thr Leu Gln Val Thr Gly Pro Met Asn Val Ser Glu
 1           5           10           15
Pro Asn Ser Ser Phe Ala Leu Val Asn Glu Phe Ile Leu Gln Asp Leu
          20           25           30
Ser Phe Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe Thr Thr
          35           40           45
Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Cys Ala Leu
          50           55           60
Trp Cys Asp Arg Arg Arg His Thr Pro Met Tyr Met Phe Leu Gly Asn
65           70           75           80
Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro Lys Met
          85           90           95

```

```

Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly Cys
      100      105      110
Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu Cys Leu
      115      120      125
Ile Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Val Ile Cys His Pro
      130      135      140
Leu His Tyr Pro Asn Ile Ile Met Thr Gly His Leu Cys Ala Lys Leu
      145      150      155      160
Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro Thr
      165      170      175
Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Asn Asp His
      180      185      190
Val Val Cys Asp Pro Gly Pro Leu Phe Ala Leu Ala Cys Val Ser Ala
      195      200      205
Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile Phe
      210      215      220
Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys Ala
      225      230      235      240
Val Leu Gly Met Pro Ser Ser Thr Gly Lys His Lys Ala Phe Ser Thr
      245      250      255
Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
      260      265      270
Val Met Cys Val Ser Pro Gly Leu Gly His Ser Met Gly Met Gln Lys
      275      280      285
Ile Lys Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro Leu
      290      295      300
Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys Val
      305      310      315      320
Leu Gly Ser Ser Asn Ile Ile Xaa Ala Ile
      325      330

```

&lt;210&gt; 1370

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g287 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1370

```

Met Met Asp Asn His Ser Ser Ala Thr Glu Phe His Leu Leu Gly Phe
  1      5      10      15
Pro Gly Ser Gln Gly Leu His His Ile Leu Phe Ala Ile Phe Phe Phe
  20      25      30
Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Val Ile Val
  35      40      45
Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His
  50      55      60
Leu Ser Thr Leu Glu Ile Leu Val Thr Thr Ile Ile Val Pro Met Met
  65      70      75      80
Leu Trp Gly Leu Leu Phe Leu Gly Cys Arg Gln Tyr Leu Ser Leu His
  85      90      95
Val Ser Leu Asn Phe Ser Cys Gly Thr Met Glu Phe Ala Leu Leu Gly
  100     105     110
Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg Tyr
  115     120     125
Asn Ile Ile Met Asn Ser Ser Thr Cys Ile Trp Val Val Ile Val Ser
  130     135     140
Trp Val Phe Gly Phe Leu Ser Glu Ile Trp Pro Ile Tyr Ala Thr Phe
  145     150     155     160
Gln Phe Thr Phe Arg Lys Ser Asn Ser Leu Asp His Phe Tyr Cys Asp

```

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| Met<br>1   | Ser        | Asn        | Thr        | Asn<br>5   | Gly        | Ser        | Ala        | Ile        | Thr<br>10  | Glu        | Phe        | Ile        | Leu        | Leu<br>15  | Gly |
| Leu        | Thr        | Asp        | Cys<br>20  | Pro        | Glu        | Leu        | Gln        | Ser<br>25  | Leu        | Leu        | Phe        | Val        | Leu        | Phe        | Leu |
| Val        | Val        | Tyr<br>35  | Leu        | Val        | Thr        | Leu        | Leu<br>40  | Gly        | Asn        | Leu        | Gly        | Met<br>45  | Ile        | Met        | Leu |
| Met        | Arg<br>50  | Leu        | Asp        | Ser        | Arg        | Leu<br>55  | His        | Thr        | Pro        | Met        | Tyr<br>60  | Phe        | Phe        | Leu        | Thr |
| Asn<br>65  | Leu        | Ala        | Phe        | Val        | Asp<br>70  | Leu        | Cys        | Tyr        | Thr        | Ser<br>75  | Asn        | Ala        | Thr        | Pro        | Gln |
| Met        | Ser        | Thr        | Asn        | Ile<br>85  | Val        | Ser        | Glu        | Lys        | Thr<br>90  | Ile        | Ser        | Phe        | Ala        | Gly<br>95  | Cys |
| Phe        | Thr        | Gln        | Cys<br>100 | Tyr        | Ile        | Phe        | Ile<br>105 | Ala        | Leu        | Leu        | Leu        | Thr        | Glu<br>110 | Phe        | Tyr |
| Met        | Leu        | Ala<br>115 | Ala        | Met        | Ala        | Tyr        | Asp<br>120 | Arg        | Tyr        | Val        | Ala        | Ile<br>125 | Tyr        | Asp        | Pro |
| Leu        | Arg<br>130 | Tyr        | Ser        | Val        | Lys        | Thr<br>135 | Ser        | Arg        | Arg        | Val        | Cys<br>140 | Ile        | Cys        | Leu        | Ala |
| Thr<br>145 | Phe        | Pro        | Tyr        | Val        | Tyr<br>150 | Gly        | Phe        | Ser        | Asp        | Gly<br>155 | Leu        | Phe        | Gln        | Ala        | Ile |
| Leu        | Thr        | Phe        | Arg        | Leu<br>165 | Thr        | Phe        | Cys        | Arg        | Ser<br>170 | Ser        | Val        | Ile        | Asn        | His<br>175 | Phe |
| Tyr        | Cys        | Ala        | Asp<br>180 | Pro        | Pro        | Leu        | Ile        | Lys<br>185 | Leu        | Ser        | Cys        | Ser        | Asp<br>190 | Thr        | Tyr |
| Val        | Lys<br>195 | Glu        | His        | Ala        | Met        | Phe        | Ile<br>200 | Ser        | Ala        | Gly        | Phe        | Asn<br>205 | Leu        | Ser        | Ser |
| Ser        | Leu<br>210 | Thr        | Ile        | Val        | Leu        | Val<br>215 | Ser        | Tyr        | Ala        | Phe        | Ile<br>220 | Leu        | Ala        | Ala        | Ile |
| Leu<br>225 | Arg        | Ile        | Lys        | Ser        | Ala<br>230 | Glu        | Gly        | Arg        | His        | Lys<br>235 | Ala        | Phe        | Ser        | Thr        | Cys |
| Gly        | Ser        | His        | Met        | Met<br>245 | Ala        | Val        | Thr        | Leu        | Phe<br>250 | Tyr        | Gly        | Thr        | Leu        | Phe        | Cys |

Met Tyr Ile Arg Pro Pro Thr Asp Lys Thr Val Glu Glu Ser Lys Ile  
                   260                  265                  270  
 Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Val Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Leu Lys Asn Val Leu  
                   290                  295                  300

Arg  
 305

<210> 1372

<211> 313

<212> PRT

<213> Unknown (H38g289 protein)

<220>

<223> Synthetic construct

<400> 1372

Met Ala Asn Leu Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser  
   1                  5                  10                  15  
 Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu  
                   20                  25                  30  
 Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile  
                   35                  40                  45  
 Ala Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe  
   50                  55                  60  
 Ser Leu Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu  
   65                  70                  75                  80  
 Ser Asp Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met  
                   85                  90                  95  
 Val Gln Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile  
                   100                  105                  110  
 Leu Thr Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu  
                   115                  120                  125  
 Arg Tyr Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly  
   130                  135                  140  
 Ala Ala Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser  
   145                  150                  155                  160  
 Arg Ala His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe  
                   165                  170                  175  
 Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu  
                   180                  185                  190  
 Leu Glu Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser  
                   195                  200                  205  
 Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu  
                   210                  215                  220  
 Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly  
   225                  230                  235                  240  
 Ser His Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu  
                   245                  250                  255  
 Tyr Val Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val  
                   260                  265                  270  
 Ala Leu Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu  
                   275                  280                  285  
 Thr Phe Cys Asn Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln  
                   290                  295                  300  
 Arg Leu Lys Gly Leu Cys Lys Ala Gln  
   305                  310

<210> 1373

<211> 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g290 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1373

```

Met Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu
      20           25           30
Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100           105           110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
      115           120           125
Pro Leu His Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met
      130           135           140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145           150           155           160
Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165           170           175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180           185           190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195           200           205
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
      210           215           220
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
225           230           235           240
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
      245           250           255
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
      260           265           270
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
      275           280           285
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser Arg
      290           295           300
His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
305           310           315

```

&lt;210&gt; 1374

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g291 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(345)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1374

```

Met His Leu Pro Asn Ser Ser Glu Ile Ala Ile Thr Thr Phe Phe Leu
 1          5          10
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro
      20          25          30
Ile Cys Leu Met Tyr Leu Val Ala Ile Leu Gly Asn Cys Thr Ile Leu
      35          40          45
Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe
      50          55          60
Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu
      65          70          75          80
Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser
      85          90          95
Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
      100          105          110
Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile
      115          120          125
Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu
      130          135          140
Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg
      145          150          155          160
Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu
      165          170          175
Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys
      180          185          190
Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu
      195          200          205
Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala
      210          215          220
Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu
      225          230          235          240
Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys
      245          250          255
Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr
      260          265          270
Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn
      275          280          285
Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp
      290          295          300
Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val
      305          310          315          320
Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln
      325          330          335
Gln Arg Cys Gln Xaa Thr Trp Tyr Lys
      340          345

```

&lt;210&gt; 1375

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g292 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(238)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1375

```

Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe
 1          5          10          15
Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp

```

```

      20      25      30
Gln Ala Pro Xaa Ser Arg Ser Ile Ile Leu Asn Leu Cys Leu Ile Ser
      35      40      45
Phe Gly Ile Lys Gly Met Trp Ser Asn Val Asn Ser Cys Phe Leu Ser
      50      55      60
Ser Leu Pro Arg Glu Lys Glu Leu Gly Leu Lys Ser Glu Gly Asn Tyr
      65      70      75      80
Ser Ser Ala Thr Gln Phe Cys Leu Leu Gly Phe Pro Gly Phe Glu Glu
      85      90      95
Leu Pro His Phe Leu Leu Val Asn Phe Phe His Leu Met Arg Leu
      100      105      110
Met Gly Asn Ala Val Ile Tyr Met Val Arg Ile Asp Xaa Ser Leu Gln
      115      120      125
Ser Pro Gly Asp Phe Phe Leu Ser Gln Leu Phe Ile Phe Ser His Ser
      130      135      140
Leu Leu Met Asp Ile Ser Ile Val Ile Ala Ser Leu Ile Gln Ile Asp
      145      150      155      160
Ser Tyr Ser Ser Ile Pro Ser Ala Ser Gly Gln Lys Lys Ser Phe Ser
      165      170      175
Thr His Ala Ser His Phe Thr Cys Val Gly Ile Asp Tyr Asp Ser Cys
      180      185      190
Leu Phe Leu Tyr Val Lys Pro Lys Gln Ile Trp Ala Ala Glu Xaa Asn
      195      200      205
Lys Val Val Phe Leu Phe Ile Phe Leu Leu Thr Pro Phe Leu Asn Leu
      210      215      220
Leu Thr Gly Gln Ile Tyr Xaa Pro Lys Ser Val Leu Gly Gly
      225      230      235

```

&lt;210&gt; 1376

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g293 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1376

```

Pro Met Lys Val Ala Asn Asn Val Thr Glu Phe Ile Phe Leu Gly Leu
1      5      10      15
Ser Gln Asp Ser Gly Met Gln Leu Met Phe Phe Val Leu Phe Leu Leu
      20      25      30
Phe Tyr Val Val Ile Met Val Gly Asn Leu Leu Ile Leu Leu Met Val
      35      40      45
Phe Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
      50      55      60
Leu Ser Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met
      65      70      75      80
Ile Glu Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys
      85      90      95
Ile Thr Gln Met Phe Thr Phe His Phe Gly Cys Ala Glu Ile Phe
      100      105      110
Val Leu Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro
      115      120      125
Leu Arg Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala
      130      135      140
Ser Leu Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu
      145      150      155      160

```



Leu Thr Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr  
 165 170 175  
 Phe Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr  
 180 185 190  
 Leu Val Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly  
 195 200 205  
 Cys Phe Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu  
 210 215 220  
 Gln Lys Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile  
 245 250 255  
 Tyr Arg Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe  
 260 265 270  
 Tyr Thr Thr Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Glu Glu Val Lys Asn Ala Met Arg Arg Leu Trp Ser Ser Lys Ile  
 290 295 300  
 Ser Leu Lys Glu Lys Gln Arg  
 305 310

&lt;210&gt; 1377

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g294 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1377

Met Glu Ile Leu Ser Asn Ser Thr Ser Lys Phe Pro Thr Phe Leu Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Ala His Val Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Cys Cys Phe Tyr Ala Ile Ala Leu Ser Gly Asn Ser Val Ile Leu  
 35 40 45  
 Phe Val Ile Ile Thr Gln Gln Ser Leu His Glu Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Thr Val Ser Ser Leu  
 65 70 75 80  
 Ser Thr Thr Leu Gly Ile Leu Trp Phe Glu Ala Arg Glu Ile Ser Leu  
 85 90 95  
 Tyr Ser Cys Ile Val Gln Met Phe Phe Leu His Gly Phe Thr Phe Met  
 100 105 110  
 Glu Ser Gly Val Leu Val Ala Thr Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asp Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ser Arg Ile Ile  
 130 135 140  
 Gln Met Gly Leu Leu Met Ile Thr Arg Ala Ile Val Leu Ile Leu Pro  
 145 150 155 160  
 Leu Leu Leu Leu Leu Lys Pro Leu Tyr Phe Cys Arg Met Asn Ala Leu  
 165 170 175  
 Ser His Ser Tyr Cys Tyr His Pro Asp Val Ile Gln Leu Ala Cys Ser  
 180 185 190  
 Asp Ile Arg Ala Asn Ser Ile Cys Gly Leu Ile Asp Leu Ile Leu Thr  
 195 200 205  
 Thr Gly Ile Asp Thr Pro Cys Ile Val Leu Ser Tyr Ile Leu Ile Ile

|   |   |     |
|---|---|-----|
| 210   | 215                                     | 220 |
| Arg Phe Val Leu Arg Ile   | Ala Ser Pro Glu Glu Trp His Lys Val Phe |     |
| 225   | 230                                     | 235 |
| Ser Thr Cys Val Ser His Val Gly Ala Val Ala Phe Phe Tyr Ile His |   | 240 |
|   | 245                                     | 250 |
| Met Leu Ser Leu Ser Leu Val Tyr Arg Tyr Gly Arg Ser Ala Pro Arg |   | 255 |
|   | 260                                     | 265 |
| Val Val His Ser Val Met Ala Asn Val Tyr Leu Leu Leu Pro Pro Val |   | 270 |
|   | 275                                     | 280 |
| Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg Lys Ala |   | 285 |
|   | 290                                     | 295 |
| Met Leu Ser Leu Leu Leu Thr Lys Xaa Thr Asp Ile Val Leu Phe Asp |   | 300 |
| 305   | 310                                     | 315 |
| Thr Asn Leu   |   | 320 |

&lt;210&gt; 1378

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g295 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1378

|   |     |
|---|-----|
| His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu |     |
| 1   | 5   |
| Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser | 10  |
|   | 15  |
|   | 20  |
| Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser | 25  |
|   | 30  |
|   | 35  |
| Ile Leu Ala Val Cys Ser Asp Ser Pro Leu His Thr Pro Arg Tyr Phe | 40  |
|   | 45  |
|   | 50  |
| Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr | 55  |
|   | 60  |
| 65  | 70  |
| Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Thr Ser | 75  |
|   | 80  |
|   | 85  |
| His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys | 90  |
|   | 95  |
|   | 100 |
| Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala | 105 |
|   | 110 |
|   | 115 |
| Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys | 120 |
|   | 125 |
|   | 130 |
| Val Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu | 135 |
|   | 140 |
| 145   | 150 |
| His Ser Trp Ile Val Leu Gln Phe Thr Ile Val Xaa Asn Leu Glu Ile | 155 |
|   | 160 |
|   | 165 |
| Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser | 170 |
|   | 175 |
|   | 180 |
| Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe | 185 |
|   | 190 |
|   | 195 |
| Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Ile | 200 |
|   | 205 |
|   | 210 |
| Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe | 215 |
|   | 220 |
| 225   | 230 |
| Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr | 235 |
|   | 240 |
|   | 245 |
|   | 250 |
|   | 255 |

Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Gln Pro Pro Arg Asn  
 260 265 270  
 Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn  
 275 280 285  
 Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asn Ile Gln Ser Ala Leu Trp  
 290 295 300  
 Arg Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe  
 305 310 315 320  
 Ser

&lt;210&gt; 1379

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g296 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1379

Met Ala Ile Phe Asn Asn Thr Thr Ser Ser Ser Ser Asn Phe Leu Leu  
 1 5 10 15  
 Thr Ala Phe Pro Gly Leu Glu Cys Ala His Val Trp Ile Ser Ile Pro  
 20 25 30  
 Val Cys Cys Leu Tyr Thr Ile Ala Leu Leu Gly Asn Ser Met Ile Phe  
 35 40 45  
 Leu Val Ile Ile Thr Lys Arg Arg Leu His Lys Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ala Ala Val Asp Leu Cys Leu Thr Ile Thr Thr Leu  
 65 70 75 80  
 Pro Thr Val Leu Gly Val Leu Trp Phe His Ala Arg Glu Ile Ser Phe  
 85 90 95  
 Lys Ala Cys Phe Ile Gln Met Phe Phe Val His Ala Phe Ser Leu Leu  
 100 105 110  
 Glu Ser Ser Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Asn Tyr Ala Thr Ile Leu Thr Asp Arg Met Val Leu  
 130 135 140  
 Val Ile Gly Leu Val Ile Cys Ile Arg Pro Ala Val Phe Leu Leu Pro  
 145 150 155 160  
 Leu Leu Val Ala Ile Asn Thr Val Ser Phe His Gly Gly His Glu Leu  
 165 170 175  
 Ser His Pro Phe Cys Tyr His Pro Glu Val Ile Lys Tyr Thr Tyr Ser  
 180 185 190  
 Lys Pro Trp Ile Ser Ser Phe Trp Gly Leu Phe Leu Gln Leu Tyr Leu  
 195 200 205  
 Asn Gly Thr Asp Val Leu Phe Ile Leu Phe Ser Tyr Val Leu Ile Leu  
 210 215 220  
 Arg Thr Val Leu Gly Ile Val Ala Arg Lys Lys Gln Gln Lys Ala Leu  
 225 230 235 240  
 Ser Thr Cys Val Cys His Ile Cys Ala Val Thr Ile Phe Tyr Val Pro  
 245 250 255  
 Leu Ile Ser Leu Ser Leu Ala His Arg Leu Phe His Ser Thr Pro Arg  
 260 265 270  
 Val Leu Cys Ser Thr Leu Ala Asn Ile Tyr Leu Leu Leu Pro Pro Val  
 275 280 285  
 Leu Asn Pro Ile Ile Tyr Ser Leu Lys Thr Lys Thr Ile Arg Gln Ala  
 290 295 300  
 Met Phe Gln Leu Leu Gln Ser Lys Gly Ser Trp Gly Phe Asn Val Arg  
 305 310 315 320  
 Gly Leu Arg Gly Arg

325

<210> 1380  
 <211> 315  
 <212> PRT  
 <213> Unknown (H38g297 protein)

<220>  
 <223> Synthetic construct

<400> 1380  
 Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu  
 1 5 10 15  
 Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val  
 20 25 30  
 Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe  
 35 40 45  
 Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro  
 65 70 75 80  
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val  
 85 90 95  
 Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu  
 100 105 110  
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser  
 115 120 125  
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln  
 130 135 140  
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln  
 145 150 155 160  
 Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn  
 165 170 175  
 His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp  
 180 185 190  
 Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu  
 195 200 205  
 Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala Arg Ile Leu Gly  
 210 215 220  
 Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala  
 245 250 255  
 Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp  
 260 265 270  
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys  
 290 295 300  
 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His  
 305 310 315

<210> 1381  
 <211> 323  
 <212> PRT  
 <213> Unknown (H38g298 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1381

```

Met Ser Pro Leu Asn Gln Thr Thr Glu Asn His Gln Ser Phe Phe Thr
 1          5          10          15
Leu Thr Gly Ile Pro Gly Met Pro Glu Lys Asp Leu Trp Met Ala Leu
 20          25          30
Pro Leu Cys Leu Leu Tyr Ser Thr Thr Ile Leu Gly Asn Val Thr Ile
 35          40          45
Leu Val Val Ile Lys Val Glu Gln Ser Leu His Glu Pro Met Tyr Tyr
 50          55          60
Phe Leu Ala Met Leu Ala Ala Thr Asp Leu Ser Leu Ser Leu Ser Ser
 65          70          75          80
Met Pro Thr Met Val Ser Val His Trp Phe Asn Trp Arg Ser Ile Thr
 85          90          95
Phe Asn Gly Cys Leu Ile Gln Met Phe Phe Ile His Thr Phe Gly Gly
 100         105         110
Val Glu Ser Gly Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala
 115         120         125
Ile Arg Phe Pro Leu His Tyr Ala Thr Ile Leu Thr His Ser Val Ile
 130         135         140
Ser Lys Ile Ala Ala Ile Leu Leu Arg Ser Val Gly Ala Val Leu
 145         150         155         160
Pro Val Pro Phe Leu Ile Lys Arg Leu Pro Phe Cys His Ser Asn Val
 165         170         175
Leu Ser His Ala Tyr Cys Leu His Gln Asp Ala Met Arg Leu Ala Cys
 180         185         190
Ala Asp Thr Gly Val Asn Ser Ile Tyr Gly Leu Leu Ala Val Ile Phe
 195         200         205
Ile Ile Val Leu Asp Ala Leu Ile Leu Leu Ala Ser Tyr Ile Leu Ile
 210         215         220
Leu Gln Ala Val Leu Ser Ile Ala Ser Gln Glu Asp Arg Leu Lys Ala
 225         230         235         240
Leu Asn Thr Cys Leu Ser His Met Ser Ala Val Leu Leu Phe Tyr Val
 245         250         255
Pro Leu Ile Gly Met Thr Leu Ile His Arg Tyr Gly Lys His Leu Ser
 260         265         270
Pro Leu Ile His Thr Phe Met Ala Asn Ile Tyr Leu Leu Leu Pro Pro
 275         280         285
Val Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Xaa Xaa
 290         295         300
Gln Ile Val Gln Ala Phe Cys Gly Ala Arg Val Ser Pro Xaa Trp His
 305         310         315         320
Leu Leu Phe

```

&lt;210&gt; 1382

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g299 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1382

```

Met Ser Val Leu Asn Asn Ser Glu Val Lys Leu Phe Leu Leu Ile Gly
 1          5          10          15
Ile Pro Gly Leu Glu His Ala His Ile Trp Phe Ser Ile Pro Ile Cys
 20          25          30
Leu Met Tyr Leu Leu Ala Ile Met Gly Asn Cys Thr Ile Leu Phe Ile

```

```

      35      40      45
Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala
 50      55      60
Met Leu Ala Val Ser Asp Met Gly Leu Ser Leu Ser Ser Leu Pro Thr
 65      70      75      80
Met Leu Arg Val Phe Leu Phe Asn Ala Met Gly Ile Ser Pro Asn Ala
      85      90      95
Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Val Met Glu Ser
      100      105      110
Ser Val Leu Leu Ile Met Ser Leu Asp Arg Phe Leu Ala Ile His Asn
      115      120      125
Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Asn Arg Val Ala Lys Met
      130      135      140
Gly Leu Ile Leu Ala Ile Arg Ser Ile Leu Leu Val Ile Pro Phe Pro
      145      150      155      160
Phe Thr Leu Arg Arg Leu Lys Tyr Cys Gln Lys Asn Leu Leu Ser His
      165      170      175
Ser Tyr Cys Leu His Gln Asp Thr Met Lys Leu Ala Cys Ser Asp Asn
      180      185      190
Lys Thr Asn Val Ile Tyr Gly Phe Phe Ile Ala Leu Cys Thr Met Leu
      195      200      205
Asp Leu Ala Leu Ile Val Leu Ser Tyr Val Leu Ile Leu Lys Thr Ile
      210      215      220
Leu Ser Ile Ala Ser Leu Ala Glu Arg Leu Lys Ala Leu Asn Thr Cys
      225      230      235      240
Val Ser His Ile Cys Ala Val Leu Thr Phe Tyr Val Pro Ile Ile Thr
      245      250      255
Leu Ala Ala Met His His Phe Ala Lys His Lys Ser Pro Leu Val Val
      260      265      270
Ile Leu Ile Ala Asp Met Phe Leu Leu Val Pro Pro Leu Met Asn Pro
      275      280      285
Ile Val Tyr Cys Val Lys Thr Arg Gln Ile Trp Glu Lys Ile Leu Gly
      290      295      300
Lys Leu Leu Asn Val Cys Gly Arg
      305      310

```

&lt;210&gt; 1383

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g300 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(308)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1383

```

Met Lys Ile Asn Asp Ser Ser Gly Glu Asp Phe Ile Leu Val Gly Phe
 1      5      10      15
Ser Glu Tyr Pro Gln Ala Glu Phe Ile Leu Ser Leu Phe Val Ser Gly
      20      25      30
Phe Tyr Thr Met Thr Phe Thr Gly Asn Thr Ala Ile Ile Leu Val Ser
      35      40      45
Leu Leu Asp Tyr Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg Lys
      50      55      60
Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Cys Ile Val Leu Gln Met
      65      70      75      80
Leu Val Asn Ile Trp Gly Glu Ser Lys Lys Val Ser Tyr Val Gly Cys
      85      90      95

```

```

Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val
      100                      105                      110
Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro
      115                      120                      125
Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala
      130                      135                      140
Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser
      145                      150                      155                      160
Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe
      165                      170                      175
Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly
      180                      185                      190
Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu
      195                      200                      205
Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val
      210                      215                      220
Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys
      225                      230                      235                      240
Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe
      245                      250                      255
Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu
      260                      265                      270
Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile
      275                      280                      285
Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile
      290                      295                      300
Trp Lys Asp Ser
      305

```

&lt;210&gt; 1384

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g301 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1384

```

Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu Gly
  1          5          10          15
Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe Leu
      20          25          30
Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
      35          40          45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50          55          60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
      65          70          75          80
Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
      85          90          95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
      100          105          110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser Asp
      115          120          125
Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
      130          135          140
Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln Thr
      145          150          155          160
Ala Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp His
      165          170          175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Asn | Glu | Ala | Ala | Ile | Met | Val | Ser | Ser | Ile | Val | Leu | Leu | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Pro | Phe | Cys | Leu | Val | Leu | Leu | Ser | Tyr | Ile | Arg | Ile | Ile | Ser | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Leu | Lys | Ile | Gln | Ser | Arg | Glu | Gly | Arg | Lys | Lys | Ala | Phe | His | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Ala | Ser | His | Leu | Thr | Val | Val | Ala | Leu | Cys | Tyr | Gly | Thr | Thr | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Thr | Tyr | Ile | Gln | Pro | His | Ser | Gly | Pro | Ser | Val | Leu | Gln | Glu | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Ile | Ser | Val | Phe | Tyr | Ala | Ile | Val | Met | Pro | Leu | Leu | Asn | Pro | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Tyr | Ser | Leu | Arg | Asn | Lys | Glu | Val | Lys | Gly | Ala | Trp | His | Lys | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Glu | Lys | Phe | Ser | Gly | Leu | Thr | Ser | Lys | Leu | Gly | Thr |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |

<210> 1385

<211> 306

<212> PRT

<213> Unknown (H38g302 protein)

**<220>**

<223> Synthetic construct

**<400> 1385**

|            |            |            |            |           |            |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Glu        | Gly        | Lys        | Asn<br>5  | Gln        | Thr        | Asn        | Ile        | Ser<br>10  | Glu        | Phe        | Leu        | Leu        | Leu<br>15 | Gly        |
| Phe        | Ser        | Ser        | Trp<br>20  | Gln       | Gln        | Gln        | Gln        | Val<br>25  | Leu        | Leu        | Phe        | Ala        | Leu        | Phe       | Leu        |
| Cys        | Leu        | Tyr<br>35  | Leu        | Thr       | Gly        | Leu        | Phe<br>40  | Gly        | Asn        | Leu        | Leu        | Ile<br>45  | Leu        | Leu       | Ala        |
| Ile        | Gly<br>50  | Ser        | Asp        | His       | Cys        | Leu<br>55  | His        | Thr        | Pro        | Met        | Tyr<br>60  | Phe        | Phe        | Leu       | Ala        |
| Asn<br>65  | Leu        | Ser        | Leu        | Val       | Asp<br>70  | Leu        | Cys        | Leu        | Pro        | Ser<br>75  | Ala        | Thr        | Val        | Pro       | Lys<br>80  |
| Met        | Leu        | Leu        | Asn        | Ile<br>85 | Gln        | Thr        | Gln        | Thr        | Gln<br>90  | Thr        | Ile        | Ser        | Tyr        | Pro<br>95 | Gly        |
| Cys        | Leu        | Ala        | Gln<br>100 | Met       | Tyr        | Phe        | Cys        | Met<br>105 | Met        | Phe        | Ala        | Asn        | Met        | Asp       | Asn        |
| Phe        | Leu        | Leu        | Thr<br>115 | Val       | Met        | Ala        | Tyr<br>120 | Asp        | Arg        | Tyr        | Val        | Ala<br>125 | Ile        | Cys       | His        |
| Pro        | Leu<br>130 | His        | Tyr        | Ser       | Thr        | Ile<br>135 | Met        | Ala        | Leu        | Arg        | Leu<br>140 | Cys        | Ala        | Ser       | Leu        |
| Val<br>145 | Ala        | Ala        | Pro        | Trp       | Val<br>150 | Ile        | Ala        | Ile        | Leu        | Asn<br>155 | Pro        | Leu        | Leu        | His       | Thr<br>160 |
| Leu        | Met        | Met        | Ala<br>165 | His       | Leu        | His        | Phe        | Cys        | Ser<br>170 | Asp        | Asn        | Val        | Ile        | His       | His        |
| Phe        | Phe        | Cys        | Asp<br>180 | Ile       | Asn        | Ser        | Leu        | Leu<br>185 | Pro        | Leu        | Ser        | Cys        | Ser        | Asp       | Thr        |
| Ser        | Leu        | Asn<br>195 | Gln        | Leu       | Ser        | Val        | Leu<br>200 | Ala        | Thr        | Val        | Gly        | Leu<br>205 | Ile        | Phe       | Val        |
| Val        | Pro<br>210 | Ser        | Val        | Cys       | Ile        | Leu<br>215 | Val        | Ser        | Tyr        | Ile        | Leu<br>220 | Ile        | Val        | Ser       | Ala        |
| Val<br>225 | Met        | Lys        | Val        | Pro       | Ser<br>230 | Ala        | Gln        | Gly        | Lys        | Leu<br>235 | Lys        | Ala        | Phe        | Ser       | Thr<br>240 |
| Cys        | Gly        | Ser        | His<br>245 | Leu       | Ala        | Leu        | Val        | Ile        | Leu<br>250 | Phe        | Tyr        | Gly        | Ala        | Asn       | Thr        |
| Gly        | Val        | Tyr        | Met<br>260 | Ser       | Pro        | Leu        | Ser        | Asn<br>265 | His        | Ser        | Thr        | Glu        | Lys<br>270 | Asp       | Ser        |



Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr  
 290 295 300  
 Leu Ser  
 305

&lt;210&gt; 1386

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g303 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1386

Met Gly Pro Arg Asn Gln Thr Ala Val Ser Glu Phe Leu Leu Met Lys  
 1 5 10 15  
 Val Thr Glu Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala  
 35 40 45  
 Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe  
 50 55 60  
 Asn Leu Ser Phe Thr Asp Ile Cys Leu Thr Thr Thr Thr Val Pro Lys  
 65 70 75 80  
 Ile Leu Val Asn Ile Gln Ala Gln Asn Gln Ser Ile Thr Tyr Thr Gly  
 85 90 95  
 Cys Leu Thr Gln Ile Cys Leu Val Leu Val Phe Ala Gly Leu Glu Ser  
 100 105 110  
 Cys Phe Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Thr Val Leu Met Asn Val His Phe Trp Gly Leu Leu  
 130 135 140  
 Ile Leu Leu Ser Met Phe Met Ser Thr Met Asp Ala Leu Val Gln Ser  
 145 150 155 160  
 Leu Met Val Leu Gln Leu Ser Phe Cys Lys Asn Val Glu Ile Pro Leu  
 165 170 175  
 Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser Ser Val Phe Gly Ala  
 195 200 205  
 Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser Gln Ile Val Thr Ser  
 210 215 220  
 Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe Tyr Gly Thr Ala Phe  
 245 250 255  
 Gly Val Tyr Ile Ser Ser Ala Val Ala Glu Ser Ser Arg Ile Thr Ala  
 260 265 270  
 Val Ala Ser Val Met Tyr Thr Val Val Pro Gln Met Met Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Lys Ala Leu Arg Lys Leu  
 290 295 300  
 Ile Gly Arg Leu Phe Pro Phe  
 305 310

&lt;210&gt; 1387

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g304 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1387

```

Met Glu Ala Arg Asn Gln Thr Ala Ile Ser Lys Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ile Glu Asp Pro Glu Leu Gln Pro Val Leu Phe Ser Leu Phe Leu
          20           25           30
Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Ala
          35           40           45
Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Leu Ser Thr Thr Thr Ile Pro Lys
          65           70           75           80
Met Leu Val Asn Ile Gln Ala Gln Asn Arg Ser Ile Thr Tyr Ser Gly
          85           90           95
Cys Leu Thr Gln Ile Cys Phe Val Leu Phe Phe Ala Gly Leu Glu Asn
          100          105          110
Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
          130          135          140
Ile Leu Leu Ser Leu Leu Thr Ser Val Val Asn Ala Leu Leu Leu Ser
          145          150          155          160
Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Leu
          165          170          175
Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu Thr Cys Ser Asp Thr
          180          185          190
Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala Cys Ile Phe Gly Gly
          195          200          205
Val Pro Leu Ser Gly Ile Ile Leu Ser Tyr Thr Gln Ile Thr Ser Cys
          210          215          220
Val Leu Arg Met Pro Ser Ala Ser Gly Lys His Lys Ala Val Ser Thr
          225          230          235          240
Cys Gly Ser His Leu Ser Ile Val Leu Leu Phe Tyr Gly Ala Gly Leu
          245          250          255
Gly Val Tyr Ile Ser Ser Val Val Thr Asp Ser Pro Arg Lys Ala Ala
          260          265          270
Val Ala Ser Val Met Tyr Ser Val Phe Pro Gln Met Val Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Thr Leu Arg Lys Phe
          290          295          300
Ile Gly Arg Ile Pro Ser Leu Leu Trp
          305          310

```

&lt;210&gt; 1388

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g305 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1388

```

Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe
          20           25           30
Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala
          35           40           45

```

```

Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys
 65          70          75          80
Met Leu Val Ser Leu Gln Thr Gly Ser Lys Ala Ile Ser Tyr Pro Cys
          85          90          95
Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser
          100          105          110
Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu
          130          135          140
Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile
 145          150          155          160
Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His
          165          170          175
Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr
          180          185          190
Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala
          195          200          205
Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala
          210          215          220
Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr
 225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile
          245          250          255
Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys
          260          265          270
Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu
          290          295          300
Val Asn Arg Lys Ile Thr Ser Ser Ser
305          310

```

&lt;210&gt; 1389

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g306 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1389

```

Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1          5          10          15
Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
          20          25          30
Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
          35          40          45
Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe Leu
          50          55          60
Ala Met Leu Ala Ala Ile Asp Gln Leu Ser Ile Ser Ser Ala Leu Pro
 65          70          75          80
Pro Gly Gln Thr Val Phe Trp Phe Thr Asp Gln Lys Asn Lys Pro Phe
          85          90          95
Ala Gly

```

&lt;210&gt; 1390

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g307 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1390

```

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn
 1           5           10           15
Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His
      20           25           30
Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val
      35           40           45
Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His
      50           55           60
Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile
      65           70           75           80
Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly
      85           90           95
Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu
      100          105          110
His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe
      115          120          125
Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu
      130          135          140
Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser
      145          150          155          160
Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe
      165          170          175
Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val
      180          185          190
Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe
      195          200          205
Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val
      210          215          220
Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Glu
      225          230          235          240
Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile
      245          250          255
Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe
      260          265          270
Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr
      275          280          285
Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr
      290          295          300
Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly
      305          310          315          320

```

&lt;210&gt; 1391

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g308 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1391

```

Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
      20           25           30

```

```

Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser
   35           40           45
Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
   50           55           60
Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys
   65           70           75           80
Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly
           85           90           95
Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn
           100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His
           115          120          125
Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu
           130          135          140
Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr
   145           150           155           160
Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His
           165           170           175
Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
           180           185           190
His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile
           195           200           205
Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr
           210           215           220
Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr
   225           230           235           240
Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile
           245           250           255
Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr
           260           265           270
Met Ala Thr Val Leu Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
           275           280           285
Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val
           290           295           300
Val Gly Arg Val Val Phe Ser Val
   305           310

```

&lt;210&gt; 1392

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g309 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1392

```

Met Tyr Phe Phe Leu Arg Gln Leu Ser Val Val Glu Leu Phe Tyr Thr
   1           5           10           15
Thr Asp Ile Val Pro Arg Thr Leu Ala Asn Leu Gly Ser Pro His Pro
           20           25           30
Gln Ala Ile Ser Phe Gln Gly Cys Ala Ala His Met Tyr Val Phe Ile
           35           40           45
Val Leu Gly Ile Ser Glu Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp
           50           55           60
Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser
           65           70           75           80
Pro Arg Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile
           85           90           95
Ile Thr Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg
           100          105          110
Ser His Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu

```

```

      115              120              125
Arg  Leu  Ala  Ser  Ala  Gly  Lys  His  Arg  Ser  Glu  Ile  Ser  Val  Met  Thr
 130              135              140
Ala  Thr  Ile  Val  Phe  Ile  Met  Ile  Pro  Phe  Ser  Leu  Ile  Val  Thr  Ser
145              150              155              160
Tyr  Ile  Arg  Ile  Leu  Gly  Ala  Ile  Leu  Ala  Met  Ala  Ser  Thr  Gln  Ser
      165              170              175
Arg  Arg  Lys  Val  Phe  Ser  Thr  Cys  Ser  Ser  His  Leu  Leu  Val  Val  Ser
      180              185              190
Leu  Phe  Phe  Gly  Thr  Ala  Ser  Ile  Thr  Tyr  Ile  Arg  Pro  Gln  Ala  Gly
      195              200              205
Ser  Ser  Val  Thr  Thr  Asp  Arg  Val  Leu  Ser  Leu  Phe  Tyr  Thr  Val  Ile
      210              215              220
Thr  Pro  Met  Leu  Asn  Pro  Ile  Ile  Tyr  Thr  Leu  Arg  Asn  Lys  Asp  Val
225              230              235              240
Arg  Arg  Ala  Leu  Arg  His  Leu  Val  Lys  Arg  Gln  Arg  Pro  Ser
      245              250

```

&lt;210&gt; 1393

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g310 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1393

```

Met  Asp  Gly  Glu  Asn  His  Ser  Val  Val  Ser  Glu  Phe  Leu  Phe  Leu  Gly
 1              5              10              15
Leu  Thr  His  Ser  Trp  Glu  Ile  Gln  Leu  Leu  Leu  Leu  Val  Phe  Ser  Ser
      20              25              30
Val  Leu  Tyr  Val  Ala  Ser  Ile  Thr  Gly  Asn  Ile  Leu  Ile  Val  Phe  Ser
      35              40              45
Val  Thr  Thr  Asp  Pro  His  Leu  His  Ser  Pro  Met  Tyr  Phe  Leu  Leu  Val
      50              55              60
Ser  Leu  Ser  Phe  Ile  Asp  Leu  Gly  Ala  Cys  Ser  Val  Thr  Ser  Pro  Lys
65              70              75              80
Met  Ile  Tyr  Asp  Leu  Phe  Arg  Lys  Arg  Lys  Val  Ile  Ser  Phe  Gly  Gly
      85              90              95
Cys  Ile  Ala  Gln  Ile  Phe  Phe  Ile  His  Val  Ile  Gly  Gly  Val  Glu  Met
      100              105              110
Val  Leu  Leu  Ile  Ala  Met  Ala  Phe  Asp  Ser  Tyr  Val  Ala  Leu  Cys  Lys
      115              120              125
Pro  Leu  His  Tyr  Leu  Thr  Ile  Met  Ser  Pro  Arg  Met  Cys  Leu  Ser  Phe
      130              135              140
Leu  Ala  Val  Ala  Trp  Thr  Leu  Val  Val  Ser  His  Ser  Leu  Phe  Gln  Leu
145              150              155              160
Ala  Phe  Leu  Val  Asn  Leu  Pro  Phe  Cys  Gly  Pro  Asn  Val  Leu  Asp  Ser
      165              170              175
Phe  Tyr  Cys  Asp  Leu  Pro  Gln  Leu  Leu  Arg  Leu  Ala  Cys  Thr  Asp  Thr
      180              185              190
Tyr  Arg  Leu  Gln  Phe  Met  Val  Thr  Val  Asn  Ser  Gly  Phe  Ile  Cys  Val
      195              200              205
Gly  Thr  Phe  Phe  Ile  Leu  Leu  Ile  Ser  Tyr  Val  Phe  Ile  Leu  Phe  Thr
      210              215              220
Val  Trp  Lys  His  Ser  Ser  Gly  Gly  Ser  Ser  Lys  Ala  Leu  Ser  Thr  Leu
225              230              235              240

```

Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe  
 245 250 255  
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln  
 290 295 300  
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu  
 305 310 315 320  
 Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr  
 325 330

&lt;210&gt; 1394

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g311 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1394

Met Glu Glu Tyr Asn Thr Ser Ser Thr Asp Phe Thr Phe Met Gly Leu  
 1 5 10 15  
 Phe Asn Arg Lys Glu Thr Ser Gly Leu Ile Phe Ala Ile Ile Ser Ile  
 20 25 30  
 Ile Phe Phe Thr Ala Leu Met Ala Asn Gly Val Met Ile Phe Leu Ile  
 35 40 45  
 Gln Thr Asp Leu Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser His  
 50 55 60  
 Leu Ser Leu Ile Asp Met Tyr Ile Ser Thr Ile Val Pro Lys Met  
 65 70 75 80  
 Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys  
 85 90 95  
 Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe  
 100 105 110  
 Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
 115 120 125  
 Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile  
 130 135 140  
 Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro  
 145 150 155 160  
 Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe  
 165 170 175  
 Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala  
 180 185 190  
 Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile  
 195 200 205  
 Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val  
 210 215 220  
 Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys  
 225 230 235 240  
 Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr  
 245 250 255  
 Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val  
 260 265 270  
 Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala Leu  
 290 295 300  
 Gly Arg Phe Lys Gly Pro Gln

305

310

&lt;210&gt; 1395

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g312 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(295)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1395

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Cys | Lys | Gly | Xaa | Xaa | Lys | Xaa | Ile | Lys | Thr | Phe | Ser | Val | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ile | Leu | Asn | Gly | Asn | Arg | Glu | Ile | Ala | Arg | Phe | Leu | Ser | Asn | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Leu | Ala | Gly | Ile | Gly | Phe | Pro | Ser | Thr | Ile | Val | Ser | Lys | Met | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asp | Ile | Gln | Ser | His | Ser | Arg | Val | Ile | Ser | Tyr | Ala | Gly | Cys | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Gln | Val | Ser | Leu | Phe | Ala | Val | Phe | Gly | Cys | Met | Glu | Asp | Met | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ser | Val | Met | Ala | Tyr | Asp | Arg | Phe | Val | Asp | Ile | Cys | His | Pro | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Tyr | Pro | Val | Ile | Met | Asn | Pro | Cys | Phe | Cys | Gly | Phe | Leu | Val | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ser | Phe | Phe | Leu | Ser | Leu | Leu | Asp | Ser | Gln | Leu | His | Asn | Trp | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Leu | Gln | Ile | Thr | Cys | Phe | Lys | Asp | Val | Glu | Ile | Pro | Asn | Phe | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Asp | Pro | Ser | Gln | Leu | Pro | His | Leu | Ala | Cys | Cys | Asp | Thr | Phe | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Asp | Ile | Val | Met | Tyr | Phe | Leu | Ala | Ala | Ile | Phe | Gly | Phe | Leu | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ser | Gly | Thr | Phe | Phe | Ser | Tyr | Tyr | Lys | Ile | Val | Ser | Ser | Ile | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Val | Ser | Ser | Ser | Gly | Gly | Lys | Tyr | Lys | Ala | Phe | Ser | Thr | Cys | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | His | Leu | Ser | Val | Val | Cys | Leu | Phe | Tyr | Gly | Thr | Gly | Phe | Gly | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Leu | Ser | Ser | Asp | Met | Ser | Ser | Tyr | Pro | Arg | Lys | Gly | Ala | Val | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Val | Met | Tyr | Thr | Val | Val | Thr | Pro | Met | Leu | Asn | Pro | Phe | Ile | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Arg | Asn | Arg | Glu | Ile | Lys | Ser | Ala | Leu | Arg | Gln | Leu | His | Cys | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Val | Xaa | Ser | His | Phe | Leu | Ile | Ile | Cys | Ser | Ile | Pro | Ser | Val | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Xaa | Val | Arg | Lys | Gly | Ser | Lys |     |     |     |     |     |     |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 1396

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g313 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;400&gt; 1396

```

Met Thr Leu Gly Ser Leu Gly Asn Ser Ser Ser Ser Val Ser Ala Thr
 1           5           10           15
Phe Leu Leu Ser Gly Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile
      20           25           30
Ser Ile Pro Leu Cys Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys
      35           40           45
Thr Ile Leu Phe Ile Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met
      50           55           60
Tyr Leu Phe Leu Ser Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu
      65           70           75           80
Cys Thr Leu Pro Thr Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu
      85           90           95
Ile Ser His Asp Ala Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe
      100          105          110
Ser Phe Leu Glu Ser Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe
      115          120          125
Val Ala Ile Cys His Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr
      130          135          140
Val Ile Gly Arg Ile Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu
      145          150          155          160
Ile Phe Pro Leu Pro Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser
      165          170          175
Pro Val Leu Ser His Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu
      180          185          190
Ala Cys Ala Asp Met Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile
      195          200          205
Val Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala
      210          215          220
Leu Ile Leu Arg Thr Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe
      225          230          235          240
Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe
      245          250          255
Tyr Thr Pro Met Ile Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln
      260          265          270
Ala Pro His Leu Val Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe
      275          280          285
Pro Pro Val Met Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
      290          295          300
Arg Asp Arg Val Thr His Ala Phe Cys Tyr
305          310

```

&lt;210&gt; 1397

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g314 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1397

```

Met Gly Leu Phe Arg Gln Ser Lys His Pro Met Ala Asn Ile Thr Trp
 1           5           10           15
Met Ala Asn His Thr Gly Trp Ser Asp Phe Ile Leu Leu Gly Leu Phe
      20           25           30
Arg Gln Ser Lys His Pro Ala Leu Cys Val Val Ile Phe Val Val
      35           40           45
Phe Leu Met Ala Leu Ser Gly Asn Ala Val Leu Ile Leu Leu Ile His
      50           55           60
Cys Asp Ala His Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln Leu

```

```

65          70          75          80
Ser Leu Met Asp Met Ala Tyr Ile Ser Val Thr Val Pro Lys Met Leu
      85
Leu Asp Gln Val Met Gly Val Asn Lys Ile Ser Ala Pro Glu Cys Gly
      100      105      110
Met Gln Met Phe Phe Tyr Val Thr Leu Ala Gly Ser Glu Phe Phe Leu
      115      120      125
Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
      130      135      140
Arg Tyr Pro Val Leu Met Asn His Arg Val Cys Leu Phe Leu Ser Ser
145      150      155      160
Gly Cys Trp Phe Leu Gly Ser Val Asp Gly Phe Thr Phe Thr Pro Ile
      165      170      175
Thr Met Thr Phe Pro Phe Arg Gly Ser Arg Glu Ile His His Phe Phe
      180      185      190
Cys Glu Val Pro Ala Val Leu Asn Leu Ser Cys Ser Asp Thr Ser Leu
      195      200      205
Tyr Glu Ile Phe Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile Pro
      210      215      220
Val Val Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Ile His
225      230      235      240
Gly Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys Ser
      245      250      255
Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Ile Tyr Thr
      260      265      270
Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met Val
      275      280      285
Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Val Asn Pro Leu Ile Tyr
      290      295      300
Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu Thr
305      310      315      320
Val Glu Pro Ala Phe Gln Lys Ala Met Glu
      325      330

```

&lt;210&gt; 1398

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g315 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(197)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1398

```

Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn Pro Leu Leu
1          5          10          15
Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu Ala Ile Gly
      20      25      30
Ala Phe Leu Gly Gly Thr Met Ser Ile Ile His Thr Thr Asn Thr
      35      40      45
Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe Phe Cys Asp
      50      55      60
Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr Met His Asp
65      70      75      80
Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile Cys Leu Leu
      85      90      95
Ser Val Leu Leu Ser Tyr Val Phe Ile Met Ala Ala Ile Leu Arg Thr
100      105      110

```

Gly Ser Val Glu Gly Arg Arg Arg Gly Phe Ser Thr Cys Ala Ser His  
 115 120 125  
 Leu Thr Val Val Thr Met Tyr His Gly Thr Leu Ile Phe Ile Tyr Leu  
 130 135 140  
 Arg Pro Ser Thr Gly His Ser Leu Asp Ile Asp Lys Val Thr Ser Val  
 145 150 155 160  
 Phe Tyr Thr Leu Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu  
 165 170 175  
 Arg Asn Lys Asp Val Lys Asn Ala Phe Arg Lys Val Ile Gly Arg Lys  
 180 185 190  
 Leu Leu Pro Xaa Gly  
 195

&lt;210&gt; 1399

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g316 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1399

Met Met Thr Leu Lys Asn Cys Thr Val Phe Thr Asp Phe Ile Phe Leu  
 1 5 10 15  
 Gly Leu Ser Gly Thr Gln Asp Ile Gln Gln Gly Leu Phe Val Leu Phe  
 20 25 30  
 Phe Leu Ile Tyr Gly Ile Thr Val Ile Val Asn Leu Gly Met Ile Leu  
 35 40 45  
 Leu Ile Lys Met Asp Leu Arg Leu His Thr Pro Val Tyr Tyr Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Cys Asp Val Cys Tyr Ser Ser Val Ser Pro  
 65 70 75 80  
 Arg Met Leu Ala Asp Phe Leu Ser Asp Gln Lys Trp Ile Pro Tyr Asn  
 85 90 95  
 Leu Cys Ala Ile Gln Met Tyr Leu Phe Gly Val Phe Ala Asp Val Glu  
 100 105 110  
 Cys Leu Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Leu Tyr Thr Ile Thr Met Pro Arg Arg Ile Cys Thr Gln  
 130 135 140  
 Leu Val Ala Leu Ala Tyr Val Val Gly Leu Val Asp Ser Ala Ile His  
 145 150 155 160  
 Thr Cys Cys Thr Phe Arg Leu Ser Phe Cys Asn Ser Asn Val Ile Asn  
 165 170 175  
 His Phe Phe Cys Asp Ile Pro Pro Leu Ala Leu Asn Pro Thr Ile  
 180 185 190  
 Asn Ser Ile Asn Glu Ile Val Met Phe Thr Phe Val Gly Cys Val Ala  
 195 200 205  
 Gly Cys Ser Ile Val Thr Val Phe Leu Ser Tyr Ser Tyr Ile Ile Ile  
 210 215 220  
 Thr Ile Leu Lys Met Ser Ser Ala Glu Gly Arg Arg Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Thr Ser His Leu Met Ala Val Ala Val Phe His Gly Thr Leu  
 245 250 255  
 Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Met Glu Thr Asp  
 260 265 270  
 Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Lys Gly Ala Leu Lys Lys  
 290 295 300  
 Ala Ile Ser Thr Lys Leu Tyr Ser Val

305

310

&lt;210&gt; 1400

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g317 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1400

```

Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met
 1           5           10           15
Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro
      20           25           30
Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu
      35           40           45
Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His
      50           55           60
Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly
      65           70           75           80
Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly
      85           90           95
Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile
      100          105          110
His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile
      115          120          125
Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu
      130          135          140
Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys
      145          150          155          160
Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr
      165          170          175
Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val
      180          185          190
Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe
      195          200          205
Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser
      210          215          220
Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu Ser Arg Glu Asp
      225          230          235          240
Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu
      245          250          255
Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu
      260          265          270
Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe
      275          280          285
Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys
      290          295          300
Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly
      305          310          315          320
Gly Ala Gln

```

&lt;210&gt; 1401

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g318 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(128)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1401

```

Ser Arg Ser Asp Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe
 1           5           10           15
Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys
          20           25           30
Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe
          35           40           45
Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe
          50           55           60
Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser
65           70           75           80
Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro
          85           90           95
Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu
          100          105          110
Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys
          115          120          125

```

&lt;210&gt; 1402

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g319 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1402

```

Met Phe Leu Leu Asn Thr Ser Glu Val Glu Val Ser Thr Phe Leu Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Ile Pro
          20           25           30
Ile Cys Leu Met Tyr Leu Met Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35           40           45
Phe Val Ile Arg Thr Glu His Ser Leu Gln Glu Pro Met Tyr Tyr Phe
          50           55           60
Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser Phe Ser Ser Leu
65           70           75           80
Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Asn Met Gly Ile Ser Ala
          85           90           95
Asp Thr Cys Ile Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp His Leu Val Ala Ile
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Phe Arg Val Leu
          130          135          140
Gln Ile Gly Leu Ala Phe Ala Ile Lys Ser Ile Leu Leu Val Leu Pro
145          150          155          160
Pro Phe Thr Leu Lys Arg Leu Arg Tyr Cys Asn Lys His Leu Leu Ser
          165          170          175
His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser Asp
          180          185          190
Asn Arg Val Asn Phe Tyr Tyr Gly Leu Phe Val Ala Leu Cys Met Met

```

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| Met<br>1   | Met        | Ala        | Ser        | Glu<br>5   | Arg        | Asn        | Gln        | Ser        | Ser<br>10  | Thr        | Pro        | Thr        | Phe        | Ile<br>15  | Leu |
| Leu        | Gly        | Phe        | Ser<br>20  | Glu        | Tyr        | Pro        | Glu        | Ile<br>25  | Gln        | Val        | Pro        | Leu        | Phe<br>30  | Leu        | Val |
| Phe        | Leu        | Phe<br>35  | Val        | Tyr        | Thr        | Val        | Thr<br>40  | Val        | Val        | Gly        | Asn<br>45  | Leu        | Gly        | Met        | Ile |
| Ile<br>50  | Ile        | Ile        | Arg        | Leu        | Asn<br>55  | Ser        | Lys        | Leu        | His        | Thr<br>60  | Ile        | Met        | Cys        | Phe        | Phe |
| Leu<br>65  | Ser        | His        | Leu        | Ser<br>70  | Leu        | Thr        | Asp        | Phe        | Cys        | Phe<br>75  | Ser        | Thr        | Val        | Val        | Thr |
| Pro        | Lys        | Leu        | Leu<br>85  | Glu        | Asn        | Leu        | Val        | Val        | Glu<br>90  | Tyr        | Arg        | Thr        | Ile        | Ser<br>95  | Phe |
| Ser        | Gly        | Cys<br>100 | Ile        | Met        | Gln        | Phe        | Cys        | Phe<br>105 | Ala        | Cys        | Ile        | Phe        | Gly<br>110 | Val        | Thr |
| Glu        | Thr        | Phe<br>115 | Met        | Leu        | Ala        | Ala        | Met<br>120 | Ala        | Tyr        | Asp        | Arg        | Phe<br>125 | Val        | Ala        | Val |
| Cys<br>130 | Lys        | Pro        | Leu        | Leu<br>135 | Tyr        | Thr        | Thr        | Ile        | Met        | Ser<br>140 | Gln        | Lys        | Leu        | Cys        | Ala |
| Leu<br>145 | Leu        | Val        | Ala        | Gly<br>150 | Ser        | Tyr        | Thr        | Trp        | Gly        | Ile<br>155 | Val        | Cys        | Ser        | Leu        | Ile |
| Leu        | Thr        | Tyr        | Phe<br>165 | Leu        | Leu        | Asp        | Leu        | Ser        | Phe<br>170 | Cys        | Glu        | Ser        | Thr        | Phe<br>175 | Ile |
| Asn        | Asn        | Phe<br>180 | Ile        | Cys        | Asp        | His        | Ser<br>185 | Val        | Ile        | Val        | Ser        | Ala<br>190 | Ser        | Tyr        | Ser |
| Asp        | Pro        | Tyr<br>195 | Ile        | Ser        | Gln        | Arg        | Leu<br>200 | Cys        | Phe        | Ile        | Ile        | Ala<br>205 | Ile        | Phe        | Asn |
| Glu        | Val<br>210 | Ser        | Ser        | Leu        | Ile<br>215 | Ile        | Ile        | Leu        | Thr        | Ser<br>220 | Tyr        | Met        | Leu        | Ile        | Phe |
| Thr<br>225 | Thr        | Ile        | Met        | Lys<br>230 | Met        | Arg        | Ser        | Ala        | Ser<br>235 | Gly        | Arg        | Gln        | Lys        | Thr        | Phe |
| Ser        | Thr        | Cys        | Ala<br>245 | Ser        | His        | Leu        | Thr        | Ala<br>250 | Ile        | Thr        | Ile        | Phe<br>255 | His        | Gly        | Thr |
| Ile        | Leu        | Phe<br>260 | Leu        | Tyr        | Cys        | Val        | Pro<br>265 | Asn        | Pro        | Lys        | Thr        | Ser<br>270 | Ser        | Leu        | Ile |
| Val        | Thr<br>275 | Val        | Ala        | Ser        | Val        | Phe<br>280 | Tyr        | Thr        | Val        | Ala        | Ile<br>285 | Pro        | Met        | Leu        | Asn |

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Asn Met Phe Glu  
 290 295 300  
 Lys Leu Val Val Thr Lys Leu Ile Tyr His  
 305 310

<210> 1404  
 <211> 322  
 <212> PRT  
 <213> Unknown (H38g321 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(322)  
 <223> Xaa = Any Amino Acid

<400> 1404  
 His Thr Glu Pro Arg Asn His Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser  
 35 40 45  
 Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Asn Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr  
 65 70 75 80  
 Val Ala Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys  
 100 105 110  
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala  
 115 120 125  
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln  
 145 150 155 160  
 Leu His Ser Ser Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu  
 165 170 175  
 Ile Ser His Phe Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys  
 180 185 190  
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile  
 210 215 220  
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg  
 260 265 270  
 Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu  
 290 295 300  
 Arg Arg Leu Leu Ser Arg Thr Val Glu Phe His Asp Leu Phe His Ser  
 305 310 315 320  
 Phe Ser

<210> 1405  
 <211> 330  
 <212> PRT  
 <213> Unknown (H38g322 protein)

<220>  
 <223> Synthetic construct

<400> 1405  
 Met Ser Val Leu Asn Asn Thr Ile Ala Glu Pro Leu Ile Phe Leu Leu  
 1 5 10 15  
 Met Gly Ile Pro Gly Leu Lys Ala Thr Gln Tyr Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Cys Leu Leu Tyr Val Val Ala Val Ser Gly Asn Ser Met Ile Leu  
 35 40 45  
 Phe Val Val Leu Cys Glu Arg Ser Leu His Lys Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ser Ala Thr Asp Leu Ser Leu Ser Leu Cys Thr Leu  
 65 70 75 80  
 Ser Thr Thr Leu Gly Val Phe Trp Phe Glu Ala Arg Glu Ile Asn Leu  
 85 90 95  
 Asn Ala Cys Ile Ala Gln Met Phe Phe Leu His Gly Phe Thr Phe Met  
 100 105 110  
 Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Arg Ile Ala  
 130 135 140  
 Lys Ile Gly Met Ser Met Leu Ile Arg Asn Val Ala Val Met Leu Pro  
 145 150 155 160  
 Val Met Leu Phe Val Lys Arg Leu Ser Phe Cys Ser Ser Met Val Leu  
 165 170 175  
 Ser His Ser Tyr Cys Tyr His Val Asp Leu Ile Gln Leu Ser Cys Thr  
 180 185 190  
 Asp Asn Arg Ile Asn Ser Ile Leu Gly Leu Phe Ala Leu Leu Ser Thr  
 195 200 205  
 Thr Gly Phe Asp Cys Pro Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ile  
 210 215 220  
 Arg Ser Val Leu Ser Ile Ala Ser Ser Glu Glu Arg Arg Lys Ala Phe  
 225 230 235 240  
 Asn Thr Cys Thr Ser His Ile Ser Ala Val Ser Ile Phe Tyr Leu Pro  
 245 250 255  
 Leu Ile Ser Leu Ser Leu Val His Arg Tyr Gly His Ser Ala Pro Pro  
 260 265 270  
 Phe Val His Ile Ile Met Ala Asn Val Phe Leu Leu Ile Pro Pro Val  
 275 280 285  
 Leu Asn Pro Ile Ile Tyr Ser Val Lys Ile Lys Gln Ile Gln Lys Ala  
 290 295 300  
 Ile Ile Lys Val Leu Ile Gln Lys His Ser Lys Ser Asn His Gln Leu  
 305 310 315 320  
 Phe Leu Ile Arg Asp Lys Ala Ile Tyr Glu  
 325 330

<210> 1406  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g323 protein)

<220>  
 <223> Synthetic construct

<400> 1406



```

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu
 1          5          10          15
Leu Gly Phe Thr Asp Tyr Pro Lys Leu Gln Ile Pro Leu Phe Leu Val
          20          25          30
Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly Met Ile
          35          40          45
Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe
          50          55          60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr
65          70          75          80
Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr
          85          90          95
Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr
          100          105          110
Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile
          115          120          125
Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala
          130          135          140
Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val
145          150          155          160
Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile
          165          170          175
Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser
          180          185          190
Asp Ile Leu Ile Pro His Leu Leu Leu Phe Ser Phe Ala Thr Phe Asn
          195          200          205
Glu Met Cys Thr Leu Leu Ile Ile Leu Thr Ser Tyr Val Phe Ile Phe
          210          215          220
Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe
225          230          235          240
Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
          245          250          255
Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr
          260          265          270
Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn
          275          280          285
Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp
290          295          300
Lys Leu Ile His Thr Gln Val Pro Phe His
305          310

```

&lt;210&gt; 1407

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g324 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1407

```

Met Val Leu Ala Ser Gly Asn Ser Ser Ser His Pro Val Ser Phe Ile
 1          5          10          15
Leu Leu Gly Ile Pro Gly Leu Glu Ser Phe Gln Leu Trp Ile Ala Phe
          20          25          30
Pro Phe Cys Ala Thr Tyr Ala Val Ala Val Val Gly Asn Ile Thr Leu
          35          40          45
Leu His Val Ile Arg Ile Asp His Thr Leu His Glu Pro Met Tyr Leu
          50          55          60
Phe Leu Ala Met Leu Ala Ile Thr Asp Leu Val Leu Ser Ser Ser Thr
65          70          75          80
Gln Pro Lys Met Leu Ala Ile Phe Trp Phe His Ala His Glu Ile Gln

```

```

      85      90      95
Tyr His Ala Cys Leu Ile Gln Val Phe Phe Ile His Ala Phe Ser Ser
      100      105      110
Val Glu Ser Gly Val Leu Met Ala Met Ala Leu Asp Cys Tyr Val Ala
      115      120      125
Thr Cys Phe Pro Leu Arg His Ser Ser Ile Leu Thr Pro Ser Val Val
      130      135      140
Ile Lys Leu Gly Thr Ile Val Met Leu Arg Gly Leu Leu Trp Val Ser
      145      150      155      160
Pro Phe Cys Phe Met Val Ser Arg Met Pro Phe Cys Gln His Gln Ala
      165      170      175
Ile Pro Gln Ser Tyr Cys Glu His Met Ala Val Leu Lys Leu Val Cys
      180      185      190
Ala Asp Thr Ser Ile Ser Arg Gly Tyr Gly Leu Phe Val Ala Phe Ser
      195      200      205
Val Ala Gly Phe Asp Met Ile Val Ile Gly Met Ser Tyr Val Met Ile
      210      215      220
Leu Arg Ala Val Leu Gln Leu Pro Ser Gly Glu Ala Arg Leu Lys Ala
      225      230      235      240
Phe Ser Thr Arg Ala Ser His Ile Cys Val Ile Leu Ala Leu Tyr Ile
      245      250      255
Pro Ala Leu Phe Ser Phe Leu Thr Tyr Arg Phe Gly His Asp Val Pro
      260      265      270
Arg Val Val His Ile Leu Phe Ala Asn Leu Tyr Leu Leu Ile Pro Pro
      275      280      285
Met Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gly Asp
      290      295      300
Arg Val Ile Gln Gly Cys Cys Gly Asn Ile
      305      310

```

&lt;210&gt; 1408

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g325 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(287)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1408

```

Tyr Ile Leu Leu Asp Ile Tyr Ile Cys Leu Asn Asn Thr His Val Xaa
  1           5           10           15
Leu Cys Val Glu Ser Gln Arg Gln Phe Lys Ile Ser Phe Tyr Phe Ser
      20           25           30
Phe Phe Leu Leu Ala Ile Thr Xaa Phe Xaa Xaa Xaa Ile Leu Ile Ile
      35           40           45
Met Lys Thr Xaa Gln Tyr Phe Leu Lys His Lys His Leu Lys Lys Lys
      50           55           60
Phe Ser Xaa Cys Leu Val Tyr Ile Leu Thr Tyr Ile Leu Ser Leu Xaa
      65           70           75           80
Ser Lys Phe Phe Ala Leu Cys Xaa Ile Phe Ala Asp Lys Ala Phe Gln
      85           90           95
Glu Gln Val Ser Gly Asn Xaa Xaa Ser Arg Ser Xaa Glu Ser Pro Val
      100          105          110
His Tyr Thr Leu Thr Met Ser Gln Lys Phe Cys Ser Ile His Pro Ala
      115          120          125
Gly Cys Tyr Asp Gln Gly Ile Xaa Ser Ile Pro Gly His Ser Phe Ser
      130          135          140

```

His Cys Ile Ala Tyr Cys Gly His Asn Val Val Asn Ile Phe Xaa Asn  
 145 150 155 160  
 Lys Tyr Ser Val Ala Ile Ser Asp Ser Cys Ser Ser Ser Trp Ile Ala  
 165 170 175  
 Asp Phe Cys Leu Phe Val Cys Phe Ala Leu Val Asn Phe Asp Xaa Leu  
 180 185 190  
 Arg Asn Leu Arg Val Leu Leu Leu Ser Phe His Phe Gln Leu Val Xaa  
 195 200 205  
 Lys Ala Leu Ser Ala Ser Ala His Gln Pro Ser Pro Pro Ile Ser His  
 210 215 220  
 Ile Ser Thr Ile Phe Leu Thr Leu Val Pro Asn Ser Lys Asn Ser Gln  
 225 230 235 240  
 Ala Thr Val Lys Ala His Ser Val Cys Tyr Ala Met Leu Ile Pro Met  
 245 250 255  
 Leu Asn Ser Gln Thr Cys Ser Met Arg Tyr Lys Asn Val Asn Glu Ser  
 260 265 270  
 Leu Gln Lys Leu Met Asp Phe Lys Ile Phe Xaa His Xaa Lys Gln  
 275 280 285

&lt;210&gt; 1409

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g326 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1409

Ser His Thr Glu Pro Xaa Asn Leu Thr Ser Val Ser Glu Phe Leu Leu  
 1 5 10 15  
 Gln Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu  
 20 25 30  
 Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Ile Ile  
 35 40 45  
 Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val  
 65 70 75 80  
 Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Xaa  
 85 90 95  
 Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile  
 100 105 110  
 Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile  
 115 120 125  
 Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val  
 130 135 140  
 Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu  
 145 150 155 160  
 His Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile  
 165 170 175  
 Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser  
 180 185 190  
 Asp Gly Ile Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Leu Phe  
 195 200 205  
 Ser Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val  
 210 215 220  
 Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe

225                      230                      235                      240  
 Ser Ile Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr  
                                  245                      250                      255  
 Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Gly Asn  
                                  260                      265                      270  
 Gly Val Val Ala Ser Val Met Tyr Ala Val Gly Thr Pro Met Leu Asn  
                                  275                      280                      285  
 Ser Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp  
                                  290                      295                      300  
 Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Leu  
 305                      310                      315                      320  
 Phe Leu Cys

&lt;210&gt; 1410

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g327 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1410

Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met  
 1                      5                      10                      15  
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu  
                                  20                      25                      30  
 Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile  
                                  35                      40                      45  
 Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe  
                                  50                      55                      60  
 Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val  
 65                      70                      75                      80  
 Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile  
                                  85                      90                      95  
 Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly  
                                  100                      105                      110  
 Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val  
                                  115                      120                      125  
 Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr  
                                  130                      135                      140  
 Cys Ile Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro  
 145                      150                      155                      160  
 Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn  
                                  165                      170                      175  
 Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser  
                                  180                      185                      190  
 Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu  
                                  195                      200                      205  
 Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn  
                                  210                      215                      220  
 Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys  
 225                      230                      235                      240  
 Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr  
                                  245                      250                      255  
 Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile  
                                  260                      265                      270  
 Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met  
                                  275                      280                      285  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala  
 290                      295                      300

Leu Gly Arg Val Phe Ser Leu Asn Phe Trp Lys Gly Gln  
 305 310 315

<210> 1411  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g328 protein)

<220> .  
 <223> Synthetic construct

<400> 1411  
 Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly  
 1 5 10 15  
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser  
 20 25 30  
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser  
 35 40 45  
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys  
 115 120 125  
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe  
 130 135 140  
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu  
 145 150 155 160  
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser  
 165 170 175  
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val  
 195 200 205  
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr  
 210 215 220  
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu  
 225 230 235 240  
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe  
 245 250 255  
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln  
 290 295 300  
 Leu Val Ile Tyr Lys Lys Ile Ser  
 305 310

<210> 1412  
 <211> 223  
 <212> PRT  
 <213> Unknown (H38g329 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(223)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1412

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pro
 1          5          10          15
Pro Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
 20          25          30
Leu Val Leu Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
 35          40          45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
 50          55          60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
 65          70          75          80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
 85          90          95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
100          105          110
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Arg Gly Lys Tyr Lys Ala
115          120          125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
130          135          140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
145          150          155          160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
165          170          175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
180          185          190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
195          200          205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
210          215          220

```

&lt;210&gt; 1413

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g330 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1413

```

Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu Ala Val
 1          5          10          15
Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu Ser Asn
 20          25          30
Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met
 35          40          45
Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys
 50          55          60
Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp Met
 65          70          75          80
Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro
 85          90          95
Leu His Tyr Pro Val Ile Met Asn Pro His Leu Gly Val Phe Leu Val
100          105          110
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
115          120          125
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
130          135          140

```

Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val  
 145 150 155 160  
 Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Met Phe Gly Phe Leu  
 165 170 175  
 Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ala Asn Asn Val Pro Ser Ile  
 180 185 190  
 Leu Arg Ile Ser Ser Ser Asp Arg Lys Ser Lys Ala Phe Ser Thr Cys  
 195 200 205  
 Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly  
 210 215 220  
 Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val  
 225 230 235 240  
 Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile  
 245 250 255  
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu Arg  
 260 265 270  
 Ser Arg Thr Val Glu Ser His Asp  
 275 280

&lt;210&gt; 1414

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g331 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1414

Met Glu Thr Gln Asn Leu Thr Val Val Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr Gln Ser Gln Asp Ala Gln Leu Val Phe Val Leu Val Leu  
 20 25 30  
 Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr  
 35 40 45  
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ala Leu Leu Asp Ala Ser Tyr Ser Phe Ile Val Val Pro Arg  
 65 70 75 80  
 Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Ser  
 85 90 95  
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Ala Gly Glu Met  
 100 105 110  
 Phe Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ser Thr Ile Met Asn Pro Arg Ala Cys Tyr Ala Leu  
 130 135 140  
 Ser Leu Val Leu Trp Leu Gly Gly Phe Ile His Ser Ile Val Gln Val  
 145 150 155 160  
 Ala Leu Ile Leu His Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn  
 165 170 175  
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asn Thr  
 180 185 190  
 Phe Val Val Glu Leu Leu Met Val Ser Asn Ser Gly Leu Leu Ser Leu  
 195 200 205  
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg  
 210 215 220  
 Ile Arg Glu His Ser Ser Glu Gly Lys Ser Lys Ala Ile Ser Thr Cys  
 225 230 235 240  
 Thr Thr His Ile Ile Ile Phe Leu Met Phe Gly Pro Ala Ile Phe  
 245 250 255  
 Ile Tyr Thr Cys Pro Phe Gln Ala Phe Pro Ala Asp Lys Val Val Ser

260 265 270  
 Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Val Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Arg Lys Leu Leu Ser Gln  
 290 295 300  
 His Met Phe Cys  
 305

&lt;210&gt; 1415

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g332 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(154)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1415

Gly Met Arg Lys Glu Gln Ala Val Cys Gly Ser His Arg Met Ile Glu  
 1 5 10 15  
 Met Met Cys Gly Pro Xaa Val Arg Leu Pro Gly Ser Asn Ala Gly Ser  
 20 25 30  
 Leu Leu Phe Thr His Leu Ile Leu Ala Cys Gly Ser Leu Leu Ile  
 35 40 45  
 Pro Phe His Leu Gly Leu Val Ala Ser His Thr Ser Ile Phe Leu Thr  
 50 55 60  
 Val Leu His Met Lys Ser Pro Xaa Ser Arg Asn Lys Ala Leu Ala Asn  
 65 70 75 80  
 Cys Ser Ser His Leu Ser Val Gly Leu Tyr Leu Gly Thr Val Cys Leu  
 85 90 95  
 Ile Tyr Val Thr Gln Gly Phe Ser His Ile Pro Glu Gln Lys Gln Ala  
 100 105 110  
 Val Ser Val Phe Cys Thr Val Leu Thr Pro Met Leu Asn Pro Leu Ile  
 115 120 125  
 Tyr Ile Leu Arg Asn Lys Asp Val Val Arg Ala Leu Gln Lys Val Leu  
 130 135 140  
 Gly Thr His Gln Val Ser Lys Gln Asn Thr  
 145 150

&lt;210&gt; 1416

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g333 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1416

Met Ser Phe Phe Val Asp Leu Arg Pro Met Asn Arg Ser Ala Thr  
 1 5 10 15  
 His Ile Val Thr Glu Phe Ile Leu Leu Gly Phe Pro Gly Cys Trp Lys  
 20 25 30  
 Ile Gln Ile Phe Leu Phe Ser Leu Phe Leu Val Ile Tyr Val Leu Thr  
 35 40 45  
 Leu Leu Gly Asn Gly Ala Ile Ile Tyr Ala Val Arg Cys Asn Pro Leu  
 50 55 60  
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu  
 65 70 75 80



```

Ile Trp Tyr Val Ser Ser Thr Ile Pro Asn Met Leu Val Asn Ile Leu
      85          90          95
Ser Lys Thr Lys Ala Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr
      100        105        110
Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Leu Phe Leu Ala Val Met
      115        120        125
Ala Tyr Asp Arg Tyr Leu Ala Ile Cys His Pro Leu Gln Tyr Pro Ala
      130        135        140
Ile Met Thr Val Arg Phe Cys Gly Lys Leu Val Ser Phe Cys Trp Leu
      145        150        155        160
Ile Gly Phe Leu Gly Tyr Pro Ile Pro Ile Phe Tyr Ile Ser Gln Leu
      165        170        175
Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Leu Cys Asp Met Asp
      180        185        190
Pro Leu Met Ala Leu Ser Cys Ala Pro Ala Pro Ile Thr Glu Cys Ile
      195        200        205
Phe Tyr Thr Gln Ser Ser Leu Val Leu Phe Phe Thr Ser Met Tyr Ile
      210        215        220
Leu Arg Ser Tyr Ile Leu Leu Leu Thr Ala Val Phe Gln Val Pro Ser
      225        230        235        240
Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val
      245        250        255
Val Val Ser Leu Phe Tyr Gly Thr Val Met Val Met Tyr Val Ser Pro
      260        265        270
Thr Tyr Gly Ile Pro Thr Leu Leu Gln Lys Ile Leu Thr Leu Val Tyr
      275        280        285
Ser Val Thr Thr Pro Leu Phe Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      290        295        300
Lys Asp Met Lys Leu Ala Leu Arg Asn Val Leu Phe Gly Met Arg Ile
      305        310        315        320
Arg Gln Asn Ser

```

&lt;210&gt; 1417

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g334 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1417

```

Met Ala Asn Ile Thr Arg Met Ala Asn His Thr Gly Lys Leu Asp Phe
1      5      10      15
Ile Leu Met Gly Leu Phe Arg Arg Ser Lys His Pro Ala Leu Leu Ser
      20      25      30
Val Val Ile Phe Val Val Phe Leu Lys Ala Leu Ser Gly Asn Ala Val
      35      40      45
Leu Ile Leu Leu Ile His Cys Asp Ala His Leu His Ser Pro Met Tyr
      50      55      60
Phe Phe Ile Ser Gln Leu Ser Leu Met Asp Met Ala Tyr Ile Ser Val
      65      70      75      80
Thr Val Pro Lys Met Leu Leu Asp Gln Val Met Gly Val Asn Lys Val
      85      90      95
Ser Ala Pro Glu Cys Gly Met Gln Met Phe Leu Tyr Leu Thr Leu Ala
      100     105     110
Gly Ser Glu Phe Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val
      115     120     125
Ala Ile Cys His Pro Leu Arg Tyr Pro Val Leu Met Asn His Arg Val
      130     135     140
Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp Gly

```

```

145          150          155          160
Phe Met Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Arg Ser Trp
          165          170          175
Glu Ile His His Phe Phe Cys Glu Val Pro Ala Val Thr Ile Leu Ser
          180          185          190
Cys Ser Asp Thr Ser Leu Tyr Glu Thr Leu Met Tyr Leu Cys Cys Val
          195          200          205
Leu Met Leu Leu Ile Pro Val Thr Ile Ile Ser Ser Ser Tyr Leu Leu
          210          215          220
Ile Leu Leu Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Lys Lys
225          230          235          240
Ala Phe Ala Thr Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr
          245          250          255
Gly Ala Ala Val Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr Pro
          260          265          270
Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Val
          275          280          285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Met Gly Ala
          290          295          300
Leu Lys Lys Met Leu Thr Val Arg Phe Val Leu
305          310          315

```

&lt;210&gt; 1418

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g335 protein)

&lt;220&gt; .

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(253)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1418

```

Ser His Leu Ser Val Ile Asp Thr Leu Tyr Ile Ser Thr Ile Val Pro
1          5          10          15
Lys Met Leu Val Asp Tyr Leu Met Gly Glu Gly Thr Ile Ser Phe Ile
          20          25          30
Ala Cys Thr Ala Gln Cys Phe Leu Tyr Met Gly Phe Met Gly Ala Glu
          35          40          45
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          50          55          60
Asn Pro Leu Arg Tyr Pro Val Leu Ile Ser Trp Arg Val Cys Trp Met
65          70          75          80
Ile Leu Ala Ser Ser Trp Phe Gly Gly Ala Leu Asp Ser Phe Leu Leu
          85          90          95
Thr Pro Ile Thr Met Ser Leu Pro Phe Cys Ala Ser His Gln Ile Asn
          100          105          110
His Phe Phe Cys Glu Ala Pro Thr Met Leu Arg Leu Ala Cys Gly Asp
          115          120          125
Lys Thr Thr Tyr Glu Thr Val Met Tyr Val Cys Cys Val Ala Met Leu
          130          135          140
Leu Ile Pro Phe Ser Val Val Thr Ala Ser Tyr Thr Arg Ile Leu Ile
145          150          155          160
Thr Val His Gln Met Thr Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala
          165          170          175
Thr Cys Ser Ser His Met Met Val Val Thr Leu Phe Tyr Gly Ala Ala
          180          185          190
Leu Tyr Thr Tyr Thr Leu Pro Gln Ser Tyr His Thr Pro Ile Lys Asp
          195          200          205

```

Lys Val Phe Ser Ala Phe Tyr Thr Ile Leu Thr Pro Leu Leu Asn Pro  
 210 215 220  
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Met Gly Ala Leu Lys Arg  
 225 230 235 240  
 Val Val Ala Arg Cys Xaa Gly Thr Cys Gly Val Met Arg  
 245 250

&lt;210&gt; 1419

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g336 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(285)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1419

Val Phe Ser Arg Thr Arg Val Arg Leu Asn Cys Lys Arg Ile Phe Trp  
 1 5 10 15  
 Leu Thr Pro Val Phe Phe Leu Ser Pro Ser Cys Pro Ser Pro Ile Ala  
 20 25 30  
 Val Ser Lys Ser Ala Val Ser Phe Val Ser Gln Ser Arg Arg Ile Arg  
 35 40 45  
 Phe Leu Gly Cys Asp Ile Gln Thr Tyr Val Phe Leu Ala Pro Gly Gly  
 50 55 60  
 Thr Glu Ala Leu Leu Phe Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala  
 65 70 75 80  
 Ile Cys His Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys  
 85 90 95  
 Cys Leu Met Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe  
 100 105 110  
 Ile His Thr Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu  
 115 120 125  
 Ile Asn His Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys  
 130 135 140  
 Gln Asp Thr Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile  
 145 150 155 160  
 Ile Leu Leu Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val  
 165 170 175  
 Leu Ile Val Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala  
 180 185 190  
 Val Ser Thr Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala  
 195 200 205  
 Thr Thr Leu Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser  
 210 215 220  
 Arg Asp Lys Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu  
 225 230 235 240  
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val  
 245 250 255  
 Arg Arg Leu Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr Asp Phe Arg  
 260 265 270  
 Ser Leu Tyr Xaa Leu Ser Ile Asn Asn Ile Lys Ser Cys  
 275 280 285

&lt;210&gt; 1420

&lt;211&gt; 271

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g337 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(271)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1420

```

Arg Arg Asp Ile Phe Tyr Phe Ala Phe Ile Cys Ser Tyr Ser Xaa Leu
 1           5           10           15
Thr Leu Arg Ser Phe Val Tyr Leu Phe Ile Arg Pro Ser Ile His Pro
          20           25           30
Ser Ile His Ser Ala Ile Leu Leu Phe Asn Ser Asp Leu Leu Asn Ser
          35           40           45
Leu Leu Cys Ser Ser Ile Phe Asp Met Pro His Asp Val Gln Gln Xaa
          50           55           60
Leu Leu Leu Lys Ser Xaa Phe Leu Val Ser His Cys Phe Ser Leu Val
          65           70           75           80
Leu Tyr Leu Leu Leu Leu Xaa Leu Arg Thr Glu Lys Ser Ile Glu Lys
          85           90           95
Ile Leu Leu Pro Gly Tyr Gly Thr Leu Leu Ser Met Ala Ile Ser Tyr
          100          105          110
Cys Leu Cys Val Phe Gly Leu Ser Asn Pro Ala Ala Cys Val Tyr Ala
          115          120          125
Gln Xaa Cys Ser Trp Asn Lys Met Val Trp Phe Leu Phe Gln Glu Val
          130          135          140
Leu Pro Ser Leu Phe Xaa Leu Arg Ile Gly Leu Pro Arg Cys Ile Thr
          145          150          155          160
Ser Leu Thr Leu Tyr Ser Cys Asp Phe Phe Leu Met Ile Gly Gln Ile
          165          170          175
Cys Thr Lys Lys Ser Lys Ile Ile Tyr Tyr Ile Met Pro Phe Leu Leu
          180          185          190
Leu Phe Met Pro Asp Xaa Ile Phe Leu Val Leu Gln Cys Pro Leu Leu
          195          200          205
Ile Ser Ile Asn Lys Xaa Pro Phe Pro Asn Leu Leu Lys Ser Pro Cys
          210          215          220
Gly Ile Gly His Leu Ser Val Asp Ser Ile Ser Ser Pro Ser Phe Phe
          225          230          235          240
Cys Leu Pro Val Cys Pro Ser Ile Tyr Pro Ser Thr Xaa Leu Phe Val
          245          250          255
Arg Ser Thr Met Ile Xaa Xaa Ile Pro Thr Tyr Cys Asp Pro Ile
          260          265          270

```

&lt;210&gt; 1421

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g338 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1421

```

Met Ser Leu Ala Glu Gly Asn Gln Ser Ser Gly Ala Val Phe Thr Leu
 1           5           10           15
Leu Gly Phe Ser Glu Tyr Ala Asp Leu Gln Val Pro Leu Phe Leu Val
          20           25           30

```

```

Phe Leu Thr Ile Tyr Thr Ile Thr Val Leu Gly Asn Leu Gly Met Ile
   35                               40                               45
Met Ile Ile Arg Ile Asn Pro Lys Leu His Thr Arg Met Tyr Phe Phe
   50                               55                               60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Val Thr
   65                               70                               75                               80
Pro Lys Leu Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe
   85                               90                               95
Thr Gly Cys Ile Met Gln Phe Phe Leu Ala Cys Ile Cys Ala Val Ala
  100                               105                               110
Glu Thr Phe Met Leu Ala Val Met Ala Tyr Asp Xaa Tyr Val Ala Val
  115                               120                               125
Cys Asn Pro Leu Leu Tyr Thr Val Val Arg Ser Gln Lys Leu Cys Ala
  130                               135                               140
Ser Leu Val Ala Gly Pro Tyr Thr Trp Gly Ile Ile Ser Ser Leu Thr
  145                               150                               155                               160
Leu Thr Tyr Phe Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Ile Ile
  165                               170                               175
Asn Asn Phe Val Cys Glu His Ser Val Ile Ile Ser Val Ser Cys Ser
  180                               185                               190
Asp Pro Tyr Ile Ser Gln Met Leu Cys Phe Val Ile Ala Ile Phe Asn
  195                               200                               205
Glu Val Ser Ser Leu Gly Val Ile Leu Thr Thr Tyr Ile Phe Ile Phe
  210                               215                               220
Ile Ala Val Ile Lys Met Pro Ser Ala Val Gly His Gln Lys Ala Phe
  225                               230                               235                               240
Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
  245                               250                               255
Val Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Trp Leu Ile
  260                               265                               270
Val Lys Val Gly Ser Val Phe Tyr Thr Val Ile Ile Pro Thr Leu Asn
  275                               280                               285
Pro Leu Thr Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Met Phe Glu
  290                               295                               300
Ser Xaa Xaa Ile Thr Gln
  305                               310

```

&lt;210&gt; 1422

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g339 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(217)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1422

```

Phe Leu Val Leu Phe Ala Cys Ile Glu Asp Met Phe Leu Thr Val Met
  1                               5                               10                               15
Ala Tyr Asp Cys Phe Ile Ala Ile Cys His Pro Leu His Tyr Pro Val
  20                               25                               30
Ile Val Asn Pro His Leu Cys Val Phe Phe Ile Leu Val Ser Phe Phe
  35                               40                               45
Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Phe
  50                               55                               60
Thr Ile Ile Lys Asn Val Glu Val Ser Asn Phe Val Cys Asp Pro Ser
  65                               70                               75                               80
Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Tyr | Phe | Asp | Asn | Thr | Met | Phe | Gly | Phe | Leu | Pro | Ile | Ser | Gly | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Trp | Ser | Tyr | Tyr | Lys | Ile | Val | Pro | Tyr | Ile | Leu | Arg | Ile | Ser | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Asp | Gly | Lys | Tyr | Lys | Ala | Phe | Ala | Thr | Cys | Gly | Ser | His | Leu | Ala |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Ala | Cys | Xaa | Phe | Tyr | Gly | Thr | Gly | Ile | Gly | Met | Tyr | Leu | Thr | Ser |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Val | Ser | Pro | Pro | Pro | Arg | Asn | Gly | Val | Val | Ala | Ser | Val | Met | Tyr |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Val | Val | Thr | Pro | Met | Leu | Asn | Leu | Phe | Ile | Tyr | Ser | Leu | Arg | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Arg | Asp | Ile | Gln | Ser | Ala | Leu | Arg | Arg | Leu | Arg | Pro | Arg | Thr | Val | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | His | Asp | Leu | Phe | His | Pro | Phe | Ser |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

**<210> 1423**

**<211> 311**

<212> PRT

<213> Unknown (H38g340 protein)

**<220>**

<223> Synthetic construct

**<400> 1423**

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| Met<br>1   | Gly        | Lys        | Glu        | Asn<br>5   | Cys        | Thr        | Thr        | Val        | Ala<br>10  | Glu        | Phe        | Ile        | Leu        | Leu<br>15  | Gly |
| Leu        | Ser        | Asp        | Val<br>20  | Pro        | Glu        | Leu        | Arg        | Val<br>25  | Cys        | Leu        | Phe        | Leu        | Leu<br>30  | Phe        | Leu |
| Leu        | Ile        | Tyr<br>35  | Gly        | Val        | Thr        | Leu        | Leu<br>40  | Ala        | Asn        | Leu        | Gly        | Met<br>45  | Thr        | Ala        | Leu |
| Ile        | Gln<br>50  | Val        | Ser        | Ser        | Arg        | Leu<br>55  | His        | Thr        | Pro        | Val        | Tyr<br>60  | Phe        | Phe        | Leu        | Ser |
| His<br>65  | Leu        | Ser        | Phe        | Val        | Asp<br>70  | Phe        | Cys        | Tyr        | Ser        | Ser<br>75  | Ile        | Ile        | Val        | Pro<br>80  | Lys |
| Met        | Leu        | Ala        | Asn        | Ile<br>85  | Phe        | Asn        | Lys        | Asp<br>90  | Lys        | Ala        | Ile        | Ser        | Phe        | Leu<br>95  | Gly |
| Cys        | Met        | Val        | Gln<br>100 | Phe        | Tyr        | Leu        | Phe        | Cys<br>105 | Thr        | Cys        | Gly        | Val        | Thr<br>110 | Glu        | Val |
| Phe        | Leu        | Leu        | Ala<br>115 | Val        | Met        | Ala        | Tyr<br>120 | Asp        | Arg        | Phe        | Val        | Ala<br>125 | Ile        | Cys        | Asn |
| Pro        | Leu<br>130 | Leu        | Tyr        | Met        | Val        | Thr<br>135 | Met        | Ser        | Gln        | Lys        | Leu<br>140 | Arg        | Val        | Glu        | Leu |
| Thr<br>145 | Ser        | Cys        | Cys        | Tyr        | Phe<br>150 | Cys        | Gly        | Thr        | Val        | Cys<br>155 | Ser        | Leu        | Ile        | His<br>160 | Ser |
| Ser        | Leu        | Ala        | Leu        | Arg<br>165 | Ile        | Leu        | Phe        | Tyr<br>170 | Arg        | Ser        | Asn        | Val        | Ile<br>175 | Asn        | His |
| Phe        | Phe        | Cys        | Asp<br>180 | Leu        | Pro        | Pro        | Leu        | Leu<br>185 | Ser        | Leu        | Ala        | Cys        | Ser<br>190 | Asp        | Val |
| Thr        | Val        | Asn<br>195 | Glu        | Thr        | Leu        | Leu        | Phe<br>200 | Leu        | Val        | Ala        | Thr        | Leu<br>205 | Asn        | Glu        | Ser |
| Val        | Thr<br>210 | Ile        | Met        | Ile        | Ile        | Leu<br>215 | Thr        | Ser        | Tyr        | Leu        | Leu<br>220 | Ile        | Leu        | Thr        | Thr |
| Ile<br>225 | Leu        | Lys        | Ile        | His        | Ser<br>230 | Ala        | Glu        | Ser        | Arg        | His<br>235 | Lys        | Ala        | Phe        | Ser<br>240 | Thr |
| Cys        | Ala        | Ser        | His        | Leu<br>245 | Thr        | Ala        | Ile        | Thr        | Val<br>250 | Ser        | His        | Gly        | Thr        | Ile<br>255 | Leu |
| Tyr        | Ile        | Tyr        | Cys<br>260 | Arg        | Pro        | Ser        | Ser        | Gly<br>265 | Asn        | Ser        | Gly        | Asp        | Val<br>270 | Asp        | Lys |

Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Asn Lys Ala Leu Arg Lys Val  
 290 295 300  
 Met Gly Ser Lys Ile His Ser  
 305 310

&lt;210&gt; 1424

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g341 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1424

Met Phe Leu Thr Glu Arg Asn Thr Thr Ser Glu Ala Thr Phe Thr Leu  
 1 5 10 15  
 Leu Gly Phe Ser Asp Tyr Leu Glu Leu Gln Ile Pro Leu Phe Phe Val  
 20 25 30  
 Phe Leu Ala Val Tyr Gly Phe Ser Val Val Gly Asn Leu Gly Met Ile  
 35 40 45  
 Val Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Asn His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala  
 65 70 75 80  
 Pro Met Met Leu Val Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe  
 85 90 95  
 Ser Gly Cys Leu Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr  
 100 105 110  
 Glu Leu Ile Leu Phe Ala Val Met Ala Tyr Asp His Phe Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Ile Ser Gln Lys Leu Cys Ala  
 130 135 140  
 Met Leu Val Val Val Leu Tyr Ala Trp Gly Val Ala Cys Ser Leu Thr  
 145 150 155 160  
 Leu Ala Cys Ser Ala Leu Lys Leu Ser Phe His Gly Phe Asn Thr Ile  
 165 170 175  
 Asn His Phe Phe Cys Glu Leu Ser Ser Leu Ile Ser Leu Ser Tyr Pro  
 180 185 190  
 Asp Ser Tyr Leu Ser Gln Leu Leu Leu Phe Thr Val Ala Thr Phe Asn  
 195 200 205  
 Glu Ile Ser Thr Leu Leu Ile Ile Leu Thr Ser Tyr Ala Phe Ile Ile  
 210 215 220  
 Val Thr Thr Leu Lys Met Pro Ser Ala Ser Gly His Arg Lys Val Phe  
 225 230 235 240  
 Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr  
 245 250 255  
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr  
 260 265 270  
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Leu Leu Asn  
 275 280 285  
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ile Arg  
 290 295 300  
 Lys Ile Ile Asn Thr Lys Tyr Phe His Ile Lys His Arg His Trp Tyr  
 305 310 315 320  
 Pro

&lt;210&gt; 1425

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g342 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(101)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1425

|     |     |     |     |     |     |     |     |     |                  |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------------|-----|-----|-----|-----|-----|-----|
| Cys | Cys | Pro | Leu | His | His | His | Tyr | Leu | Pro              | Arg | Gln | Ser | Leu | Asp | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |                  |     |     |     |     | 15  |     |
| Leu | Thr | Tyr | Leu | Ile | Ala | Leu | Ile | Phe | Asn <sup>1</sup> | Phe | Leu | Phe | Val | Phe | Gly |
|     |     |     | 20  |     |     |     |     | 25  |                  |     |     |     | 30  |     |     |
| Leu | Gln | Ser | Ser | Phe | Ile | Phe | Leu | Lys | Ala              | Xaa | Gln | Cys | Phe | Pro | Lys |
|     |     | 35  |     |     |     |     | 40  |     |                  |     |     | 45  |     |     |     |
| Asp | Ile | His | Tyr | Ile | Phe | Val | Lys | Ala | Arg              | Arg | Ala | Ser | Gly | Tyr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |                  |     | 60  |     |     |     |     |
| Thr | Tyr | His | Ile | Ala | Gly | Asn | Arg | Ser | Xaa              | Thr | Val | Phe | Phe | Leu | Val |
| 65  |     |     |     |     | 70  |     |     |     |                  | 75  |     |     |     |     | 80  |
| Cys | Asn | Cys | His | Tyr | Tyr | Gly | Asp | Asp | Ile              | Gly | Xaa | Val | Xaa | Ile | Phe |
|     |     |     |     | 85  |     |     |     | 90  |                  |     |     |     |     | 95  |     |
| Tyr | Val | Asn | Ile | Leu |     |     |     |     |                  |     |     |     |     |     |     |
|     |     |     |     | 100 |     |     |     |     |                  |     |     |     |     |     |     |

&lt;210&gt; 1426

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g343 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1426

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Gly | Lys | Leu | Val | Phe | Asn | Gln | Ser | Glu | Pro | Thr | Glu | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Phe | Arg | Ala | Phe | Thr | Thr | Ala | Thr | Glu | Phe | Gln | Val | Leu | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Phe | Leu | Leu | Leu | Tyr | Leu | Met | Ile | Leu | Cys | Gly | Asn | Thr | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ile | Trp | Val | Val | Cys | Thr | His | Ser | Thr | Leu | Arg | Thr | Pro | Met | Tyr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Phe | Phe | Leu | Ser | Asn | Leu | Ser | Phe | Leu | Glu | Leu | Cys | Tyr | Thr | Thr | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Val | Pro | Leu | Met | Leu | Ser | Asn | Ile | Leu | Gly | Ala | Gln | Lys | Pro | Ile |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Leu | Ala | Gly | Cys | Gly | Ala | Gln | Met | Phe | Phe | Phe | Val | Thr | Leu | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Thr | Asp | Cys | Phe | Leu | Leu | Ala | Ile | Met | Ala | Tyr | Asp | Arg | Tyr | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ile | Cys | His | Pro | Leu | His | Tyr | Thr | Leu | Ile | Met | Thr | Arg | Glu | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Thr | Gln | Met | Leu | Gly | Ala | Leu | Gly | Leu | Ala | Leu | Phe | Pro | Ser |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Gln | Leu | Thr | Ala | Leu | Ile | Phe | Thr | Leu | Pro | Phe | Cys | Gly | His | His |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gln | Glu | Ile | Asn | His | Phe | Leu | Cys | Asp | Val | Pro | Pro | Val | Leu | Arg | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Cys | Ala | Asp | Ile | Arg | Val | His | Gln | Ala | Val | Leu | Tyr | Val | Val | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |



```

Ile Leu Val Leu Thr Ile Pro Phe Leu Leu Ile Cys Val Ser Tyr Val
  210                215                220
Phe Ile Thr Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg Arg
 225                230                235                240
Arg Ala Phe Ser Thr Cys Ser Phe His Leu Thr Val Val Leu Leu Gln
                245                250                255
Tyr Gly Cys Cys Ser Leu Val Tyr Leu Arg Pro Arg Ser Ser Thr Ser
                260                265                270
Glu Asp Glu Asp Ser Gln Ile Ala Leu Val Tyr Thr Phe Val Thr Pro
                275                280                285
Leu Leu Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly
                290                295                300
Ala Leu Arg Ser Ala Ile Ile Arg Lys Ala Ala Ser Asp Ala Asn
 305                310                315

```

<210> 1427  
 <211> 208  
 <212> PRT  
 <213> Unknown (H38g344 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(208)  
 <223> Xaa = Any Amino Acid

```

<400> 1427
Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly
 1                5                10                15
Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe
                20                25                30
Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu
                35                40                45
Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys
                50                55                60
Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys
 65                70                75                80
Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly
                85                90                95
Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser
                100                105                110
Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn
                115                120                125
Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu
                130                135                140
Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr
 145                150                155                160
Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe
                165                170                175
Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr
                180                185                190
Met His Asp Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile
                195                200                205

```

<210> 1428  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g345 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1428

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Glu | Pro | Arg | Asn | Leu | Thr | Gly | Val | Ser | Glu | Phe | Leu | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Ser | Glu | Asp | Pro | Glu | Leu | Gln | Pro | Val | Leu | Pro | Gly | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Met | Tyr | Leu | Leu | Thr | Val | Leu | Arg | Asn | Leu | Leu | Ile | Ile | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Val | Ser | Ser | Asp | Ser | His | Leu | His | Thr | Pro | Met | Tyr | Phe | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asn | Pro | Ser | Trp | Ala | Asp | Ile | Ala | Phe | Thr | Ser | Ala | Thr | Val | Pro |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Met | Ile | Val | Asp | Met | Gln | Ser | His | Arg | Val | Ile | Ser | Tyr | Ala | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Leu | Thr | Gln | Met | Ser | Phe | Phe | Ala | Leu | Phe | Ala | Cys | Ile | Glu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Leu | Leu | Ile | Val | Met | Ala | Tyr | Asp | Arg | Phe | Val | Ala | Val | Cys | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Pro | His | Tyr | Pro | Val | Ile | Met | Asn | Pro | Arg | Leu | Gly | Val | Phe | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Leu | Val | Ser | Phe | Phe | Leu | Ser | Leu | Leu | Asp | Ser | Gln | Leu | His | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Trp | Thr | Val | Leu | Gln | Phe | Thr | Phe | Phe | Lys | Asn | Val | Glu | Ile | Ser | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Val | Cys | Asp | Pro | Ser | Gln | Leu | Leu | Asn | Leu | Ala | Cys | Ser | Asp | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Ile | Asp | Ser | Ile | Phe | Ile | Tyr | Leu | Asp | Ser | Thr | Met | Phe | Arg | Phe |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Pro | Ile | Ser | Gly | Ile | Leu | Leu | Ser | Tyr | Ser | Asn | Ile | Val | Pro | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Leu | Arg | Ile | Ser | Ser | Ser | Asp | Gly | Lys | Ser | Lys | Ala | Phe | Ser | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Arg | Ser | His | Leu | Ala | Val | Val | Cys | Leu | Phe | Tyr | Gly | Thr | Gly | Ile |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Val | Tyr | Leu | Thr | Ser | Ala | Val | Ala | Pro | Pro | Pro | Gly | Asp | Gly | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Val | Ser | Val | Met | Tyr | Thr | Val | Val | Thr | Pro | Met | Leu | Asn | Pro | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Tyr | Cys | Leu | Arg | Asn | Arg | Asp | Ile | Gln | Ser | Ala | Leu | Trp | Arg | Leu |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Arg | Ser | Arg | Thr | Val | Glu | Ser | Pro | Xaa | Ser | Val | Pro | Ser | Phe | Phe | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 1429

<211> 310

<212> PRT

<213> Unknown (H38g346 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

&lt;400&gt; 1429

```

Glu Lys Asn Leu Ile Ser Met Asn Gly Phe Met Asn Phe Thr Asp Tyr
 1           5           10           15
Pro Glu Leu Glu Met Pro Leu Phe Leu Val Phe Leu Ser Cys Phe Leu
      20           25           30
Ala Ile Ile Leu Arg Asn Met Glu Trp Val Ile Leu Thr Gln Val Asn
      35           40           45
Val His Leu Phe Thr Pro Ile Tyr Phe Phe Leu Thr Asn Val Thr Leu
      50           55           60
Trp Asp Thr Ser Val Ile Met Pro Gln Ile Leu Ala Ile Leu Ala Thr
      65           70           75           80
Gly Lys Thr Thr Ile Ser Tyr Val Pro Leu Ile Lys Ala Met Arg Ser
      85           90           95
Phe Phe Phe Ile Cys Val Gly Thr Xaa Cys Phe Leu Pro Thr Ala Met
      100          105          110
Thr Ile Ser Ser His Cys Pro Thr Leu Gln Ala Met Asn Phe Lys Thr
      115          120          125
Cys Trp Gly Phe Phe Leu Val Gly Ile Cys Cys Cys Thr Cys Trp Val
      130          135          140
Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly Leu Ser Gly Ala
      145          150          155          160
Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe Cys Asp Asp Asn
      165          170          175
Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys Leu Ile Xaa Asn
      180          185          190
Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Leu Thr Ala Phe Met
      195          200          205
Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile
      210          215          220
Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Arg Ser Gln Xaa Phe Tyr
      225          230          235          240
Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr Phe Phe Gly Ile
      245          250          255
Pro Ile Phe Arg His Val Lys Tyr Leu Arg Xaa Ile Thr Asp Arg Arg
      260          265          270
Gln Val Gly Ile Met Thr Cys Thr Ile Phe Ile Pro Met Leu Glu Leu
      275          280          285
Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val Ala Phe Lys Lys Ala
      290          295          300
Ile Gly Asn Phe Trp Val
      305          310

```

&lt;210&gt; 1430

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g347 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(336)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1430

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Arg
 1           5           10           15
Gly Thr Ser Glu Asp Pro Glu Trp Gln Leu Val Leu Ala Gly Leu Phe
      20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu

```

```

      35      40      45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
  50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala
  65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Pro Phe Ala Ile Phe Gly Val Met Glu
      100      105      110
Glu Asn Thr Leu Leu Ser Val Met Ala Ser Asp Arg Phe Val Ala Ile
      115      120      125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
      130      135      140
Phe Leu Val Leu Leu Ser Phe Phe Phe Phe Cys Cys Leu Leu Asp Ala
      145      150      155      160
Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
      165      170      175
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
      180      185      190
Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala
      195      200      205
Ile Phe Gly Phe Leu Pro Ile Ser Gly Ser Leu Phe Ser Tyr Tyr Lys
      210      215      220
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Xaa
      225      230      235      240
Ala Phe Ser Ser Cys Trp Ser His Leu Ser Val Val Cys Xaa Phe Tyr
      245      250      255
Gly Thr Gly Val Gly Gly Tyr Leu Ser Xaa Asp Val Ser Ser Ser Pro
      260      265      270
Arg Lys Val Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met
      275      280      285
Leu Asn Pro Phe Val Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val
      290      295      300
Leu Arg Trp Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu Ile
      305      310      315      320
Cys Ser Ile Pro Phe Val Val Xaa Val Lys Lys Gly Ser Lys Val Lys
      325      330      335

```

&lt;210&gt; 1431

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g348 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1431

```

Met Lys Thr Phe Ser Ser Phe Leu Gln Ile Gly Arg Asn Met His Gln
  1      5      10      15
Gly Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Phe Phe Lys
      20      25      30
Gln Asp Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Gly Met Tyr
      35      40      45
Leu Val Thr Val Ile Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu
      50      55      60
Asp Thr Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser
      65      70      75      80
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val
      85      90      95
Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr
      100      105      110

```

Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu  
 115 120 125  
 Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro Leu Asn  
 130 135 140  
 Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile  
 145 150 155 160  
 Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu  
 165 170 175  
 Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys  
 180 185 190  
 Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn  
 195 200 205  
 Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe  
 210 215 220  
 Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg  
 225 230 235 240  
 Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser  
 245 250 255  
 His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr  
 260 265 270  
 Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala  
 275 280 285  
 Val Leu Phe Thr Val Val Thr Pro Met Ile Asn Pro Phe Ile Tyr Ser  
 290 295 300  
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Lys Leu Ile Asn Arg  
 305 310 315 320  
 Lys Ile Ser Ser Leu  
 325

&lt;210&gt; 1432

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g349 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1432

Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Asp Thr Cys Tyr Ser  
 1 5 10 15  
 Asn Val Phe Thr Pro Lys Leu Leu Glu Ile Leu Val Val Glu Asp Arg  
 20 25 30  
 Thr Ile Ser Phe Lys Gly Cys Met Val Gln Phe Phe Phe Gly Cys Ala  
 35 40 45  
 Phe Val Ile Thr Glu Met Phe Met Leu Ala Val Met Ala Tyr Asp Leu  
 50 55 60  
 Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro  
 65 70 75 80  
 Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly Leu  
 85 90 95  
 Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly  
 100 105 110  
 Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser  
 115 120 125  
 Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile  
 130 135 140  
 Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr  
 145 150 155 160  
 Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro  
 165 170 175  
 Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile

```
<210> 1433
<211> 318
<212> PRT
<213> Unknown (H38q350 protein)
```

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(318)
<223> Xaa = Any Amino Acid
```

726

Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu  
 305 310 315

<210> 1434

<211> 313

<212> PRT

<213> Unknown (H38g351 protein)

<220>

<223> Synthetic construct

<400> 1434

Met Leu Leu Thr Asp Arg Asn Thr Ser Gly Thr Thr Phe Thr Leu Leu  
 1 5 10 15  
 Gly Phe Ser Asp Tyr Pro Glu Leu Gln Val Pro Leu Phe Leu Val Phe  
 20 25 30  
 Leu Ala Ile Tyr Asn Val Thr Val Leu Gly Asn Ile Gly Leu Ile Val  
 35 40 45  
 Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Gln Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala Pro  
 65 70 75 80  
 Lys Met Leu Val Asn Leu Val Val Lys Asp Arg Thr Ile Ser Phe Leu  
 85 90 95  
 Gly Cys Val Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr Glu  
 100 105 110  
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Leu Tyr Thr Val Asp Met Ser Gln Lys Leu Cys Val Leu  
 130 135 140  
 Leu Val Val Gly Ser Tyr Ala Trp Gly Val Ser Cys Ser Leu Glu Leu  
 145 150 155 160  
 Thr Cys Ser Ala Leu Lys Leu Cys Phe His Gly Phe Asn Thr Ile Asn  
 165 170 175  
 His Phe Phe Cys Glu Phe Ser Ser Leu Leu Ser Leu Ser Cys Ser Asp  
 180 185 190  
 Thr Tyr Ile Asn Gln Trp Leu Leu Phe Phe Leu Ala Thr Phe Asn Glu  
 195 200 205  
 Ile Ser Thr Leu Leu Ile Val Leu Thr Ser Tyr Ala Phe Ile Val Val  
 210 215 220  
 Thr Ile Leu Lys Met Arg Ser Val Ser Gly Arg Arg Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile  
 245 250 255  
 Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr Val  
 260 265 270  
 Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Thr Val Thr Glu  
 290 295 300  
 Ile Leu Asp Thr Lys Val Phe Ser Tyr  
 305 310

<210> 1435

<211> 312

<212> PRT

<213> Unknown (H38g352 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1435

```

Met Ala Glu Arg Asn Tyr Thr Val Val Thr Glu Phe Phe Leu Thr Ala
1      5      10      15
Phe Thr Glu His Leu Gln Trp Arg Val Pro Leu Phe Leu Ile Phe Leu
20     25     30
Ser Phe Tyr Leu Ala Thr Met Leu Gly Asn Thr Gly Met Ile Leu Leu
35     40     45
Ile Arg Gly Asp Arg Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50     55     60
His Leu Ser Leu Val Asp Ile Cys Tyr Ser Ser Ala Ile Ile Pro Gln
65     70     75     80
Met Leu Ala Val Leu Trp Glu His Gly Thr Thr Ile Ser Gln Ala Arg
85     90     95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Ala Ser Ile Asp Cys
100    105    110
Tyr Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Thr Ala Val Cys Gln
115    120    125
Pro Leu Leu Tyr Val Thr Ile Ile Thr Glu Lys Asp Arg Leu Gly Leu
130    135    140
Val Thr Gly Ala Tyr Val Ala Gly Phe Phe Ser Ala Phe Val Arg Thr
145    150    155    160
Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn Asn Glu Ile Asn Phe
165    170    175
Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Gly Asp Ser
180    185    190
Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala Leu Phe Val Met Pro
195    200    205
Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
210    215    220
Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala Lys Thr Phe Ser Thr
225    230    235    240
Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe Phe Gly Thr Leu Ile
245    250    255
Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser Ser Glu Gly Asp Arg
260    265    270
Val Val Ser Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu
275    280    285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Thr Arg Lys Ala
290    295    300
Leu Ser Lys Ser Lys Pro Ala Arg
305    310

```

&lt;210&gt; 1436

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g353 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1436

```

Met Tyr Tyr Phe Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Ser
1      5      10      15
Ile Ser Thr Leu Val Thr Met Leu Ser Ile Phe Trp Phe Asn Val Arg
20     25     30
Glu Ile Ser Phe Asn Ala Cys Leu Ser His Met Phe Phe Ile Lys Phe
35     40     45
Phe Thr Val Met Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg
50     55     60
Phe Val Ala Val Ser Asn Pro Leu Arg Tyr Ala Met Ile Leu Thr Asp
65     70     75     80

```



```

Ser Arg Ile Ala Gln Ile Gly Val Ala Ser Val Ile Arg Gly Leu Leu
      85                      90                      95
Met Leu Thr Pro Met Val Ala Leu Leu Ile Arg Leu Ser Tyr Cys His
      100                    105                    110
Ser Gln Val Leu His His Ser Tyr Cys Tyr His Pro Asp Val Met Lys
      115                    120                    125
Leu Ser Cys Thr Asp Thr Arg Ile Asn Ser Ala Val Gly Leu Thr Ala
      130                    135                    140
Met Phe Ser Thr Val Gly Val Asp Leu Leu Leu Ile Leu Leu Ser Tyr
      145                    150                    155                    160
Val Leu Ile Ile Arg Thr Val Leu Ser Val Ala Ser Pro Glu Glu Arg
      165                    170                    175
Lys Glu Thr Phe Ser Thr Cys Val Ser His Ile Val Ala Phe Ala Ile
      180                    185                    190
Tyr Tyr Ile Pro Leu Ile Ser Leu Ser Ile Val His Arg Phe Gly Lys
      195                    200                    205
Gln Ala Pro Ala Tyr Val His Thr Met Ile Ala Asn Thr Tyr Leu Leu
      210                    215                    220
Ile Ser Pro Leu Met Asn Pro Val Ile Tyr Ser Val Lys Thr Lys Gln
      225                    230                    235                    240
Ile Arg Arg Ala Val Ile Lys Ile Leu His Ser Lys Glu Thr
      245                    250

```

<210> 1437  
 <211> 188  
 <212> PRT  
 <213> Unknown (H38g354 protein)

<220>  
 <223> Synthetic construct

```

<400> 1437
Met Asp Trp Glu Asn Cys Ser Ser Leu Thr Asp Phe Phe Leu Leu Gly
  1                      5                      10                      15
Ile Thr Asn Asn Pro Glu Met Lys Val Thr Leu Phe Ala Val Phe Leu
      20                    25                    30
Ala Val Tyr Ile Ile Asn Phe Ser Ala Asn Leu Gly Met Ile Val Leu
      35                    40                    45
Ile Arg Met Asp Tyr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50                    55                    60
His Leu Ser Phe Cys Asp Leu Cys Tyr Ser Thr Ala Thr Gly Pro Lys
      65                    70                    75                    80
Met Leu Val Asp Leu Leu Ala Lys Asn Lys Ser Ile Pro Phe Tyr Gly
      85                    90                    95
Cys Ala Leu Gln Phe Leu Val Phe Cys Ile Phe Ala Asp Ser Glu Cys
      100                    105                    110
Leu Leu Leu Ser Val Met Ala Phe Asp Arg Tyr Lys Ala Ile Ile Asn
      115                    120                    125
Pro Leu Leu Tyr Thr Val Asn Met Ser Ser Arg Val Cys Tyr Leu Leu
      130                    135                    140
Leu Thr Gly Val Tyr Leu Val Gly Ile Ala Asp Ala Leu Ile His Met
      145                    150                    155                    160
Thr Leu Ala Phe Arg Leu Cys Phe Cys Gly Ser Asn Glu Ile Asn His
      165                    170                    175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Leu Ser
      180                    185

```

<210> 1438  
 <211> 326  
 <212> PRT  
 <213> Unknown (H38g355 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1438

```

Leu Asn Phe Ile Ile Phe Phe Arg Xaa Thr Ser Tyr Ile Glu Pro Met
 1           5           10           15
Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val Phe
 20           25           30
Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu Ser
 35           40           45
Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu Ile
 50           55           60
Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser His
 65           70           75           80
Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln Ile
 85           90           95
Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys Arg
 100          105          110
Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys Tyr
 115          120          125
Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn Pro
 130          135          140
Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe Leu
 145          150          155          160
Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr Thr
 165          170          175
Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe Phe
 180          185          190
Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met Thr
 195          200          205
Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu Ala
 210          215          220
Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala Ile
 225          230          235          240
Leu Arg Val Lys Ser Ala Gly Gly Xaa Ala Lys Thr Phe Ser Thr Cys
 245          250          255
Thr Ser His Leu Thr Thr Val Val Leu Phe Phe Gly Thr Leu Ala Phe
 260          265          270
Met Tyr Gln Arg Ser Asn Ser Ala Lys Ser Ser Glu Glu Asp Lys Ile
 275          280          285
Val Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu Ile
 290          295          300
Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Gly Lys Leu Val
 305          310          315          320
Gly Lys Phe Gln Phe Pro
 325

```

&lt;210&gt; 1439

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g356 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1439

```

Met Leu Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro
 1          5          10          15
Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp
          20          25          30
Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn
          35          40          45
Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro
          50          55          60
Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr
65          70          75          80
Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg
          85          90          95
Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser
          100          105          110
Ser Val Val Glu Ser Ser Val Leu Leu Ala Ile Ser Phe Asp His Phe
          115          120          125
Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser
          130          135          140
Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val
145          150          155          160
Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly
          165          170          175
Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg
          180          185          190
Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val
          195          200          205
Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr
          210          215          220
Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg
225          230          235          240
Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val
          245          250          255
Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg
          260          265          270
His Leu Pro His Ile Val His Ala Leu Val Thr Tyr Val Tyr Leu Val
          275          280          285
Met Pro Ser Val Leu His Pro Ile Ile Tyr Ser Met Lys Ser Lys Pro
          290          295          300
Ile Arg Glu Ala Ile Leu Arg Met Leu Met Gly Arg Ser Gln Gly Xaa
305          310          315          320
Xaa Asn Tyr Lys Ile Leu Xaa Gly
          325

```

&lt;210&gt; 1440

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g357 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1440

```

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
          20          25          30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu

```

```

      35      40      45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
  50      55      60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
  65      70      75      80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
      85      90      95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
      100      105      110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
      115      120      125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
      130      135      140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
  145      150      155      160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
      165      170      175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
      180      185      190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
      195      200      205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
  210      215      220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
  225      230      235      240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
      245      250      255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
      260      265      270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val
  290      295      300
Met Gly Ser Lys Ile His Ser
  305      310

```

&lt;210&gt; 1441

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g358 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(209)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1441

```

Cys His Pro Pro Leu Arg Trp Gly Ser Xaa Glu Pro Ala Glu Glu Glu
  1      5      10      15
Gly Leu Ala Leu Ser Ser Arg Phe Phe Phe Phe Leu Ser Val Leu Asp
      20      25      30
Ala Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp
      35      40      45
Ala Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu
  50      55      60
Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala
  65      70      75      80
Val Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr
      85      90      95

```

Lys Ile Val Ser Ser Ile Leu Ser Val Ser Ser Ser Arg Gly Gln Tyr  
 100 105 110  
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe  
 115 120 125  
 Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser Ser  
 130 135 140  
 Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Pro  
 145 150 155 160  
 Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys Ser  
 165 170 175  
 Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu Leu  
 180 185 190  
 Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys Val  
 195 200 205  
 Lys

&lt;210&gt; 1442

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g359 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1442

Ile Xaa Leu Lys Leu Ile Phe Gly Asn Pro Arg Xaa Xaa Xaa Ile Phe  
 1 5 10 15  
 Arg Cys Val Tyr Asp Tyr Leu Trp Asp Cys Gln Pro Leu Leu Tyr Asp  
 20 25 30  
 Thr Ile Thr Thr Leu Lys Met Ser Gly Arg Ser Trp Xaa Leu His Ile  
 35 40 45  
 Val Glu Gly Leu Thr Asn Val Ile Gln Cys Ile His Phe Thr Cys Ser  
 50 55 60  
 Leu Ser Phe Cys Gly Thr Ser Ser Ile Gly Phe Thr Leu Cys Asp Leu  
 65 70 75 80  
 Pro Leu Leu Leu Thr Leu Asn Cys Gly Asp Ser Phe Leu Gln Gln Leu  
 85 90 95  
 Leu Ile Phe His Phe Ala Leu Tyr Met Ile Leu Thr Arg Leu Val Leu  
 100 105 110  
 Ile Leu Phe Ser Asp Leu Phe Ile Ser Lys Ala Ile Xaa Thr Pro Ala  
 115 120 125  
 Asn Gln Val Ser Arg Gln Arg Phe Leu Asn Leu Phe Leu Pro Leu Pro  
 130 135 140  
 His Ala Glu Leu Gln Phe Gly Xaa Leu Leu Arg Leu Gln Leu Xaa Ser  
 145 150 155 160  
 Met Cys Ala Ala Val Gly Lys Ser Leu Thr Gly Glu Arg Ala Val Thr  
 165 170 175  
 Met Phe Xaa Thr Glu Xaa Thr Pro Gly Xaa Pro Phe Gln Phe Tyr Ser  
 180 185 190  
 Leu Arg Asn Lys Lys Ala Lys Glu Ala Leu Arg Lys Gly Leu Asn Lys  
 195 200 205  
 Ala Lys Leu Phe  
 210

&lt;210&gt; 1443

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g360 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1443

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
 1          5          10          15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
      20          25          30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
      35          40          45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
      50          55          60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
      65          70          75          80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
      85          90          95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
      100          105          110
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
      115          120          125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
      130          135          140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
      145          150          155          160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
      165          170          175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
      180          185          190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
      195          200          205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
      210          215          220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
      225          230          235          240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
      245          250          255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
      260          265          270
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
      275          280          285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
      290          295          300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln
      305          310          315

```

&lt;210&gt; 1444

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g361 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1444

```

Met Tyr Ala Leu Ala Thr Leu Gly Asn Leu Thr Ile Val Leu Ile Ile
 1          5          10          15
Arg Val Glu Arg Arg Leu His Glu Pro Met Tyr Leu Phe Leu Ala Met
      20          25          30

```

```

Leu Ser Thr Ile Asp Leu Val Leu Ser Ser Ile Thr Met Pro Lys Met
   35                               40                               45
Ala Ser Leu Phe Leu Met Gly Ile Gln Glu Ile Glu Phe Asn Ile Cys
   50                               55                               60
Leu Ala Gln Met Phe Leu Ile His Ala Leu Ser Ala Val Glu Ser Ala
   65                               70                               75                               80
Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro
   85                               90                               95
Leu Arg His Ala Ser Val Leu Thr Gly Cys Thr Val Ala Lys Ile Gly
  100                               105                               110
Leu Ser Ala Leu Thr Arg Gly Phe Val Phe Phe Phe Pro Leu Pro Phe
  115                               120                               125
Ile Leu Lys Trp Leu Ser Tyr Cys Gln Thr His Thr Val Thr His Ser
  130                               135                               140
Phe Cys Leu His Gln Asp Ile Met Lys Leu Ser Cys Thr Asp Thr Arg
  145                               150                               155                               160
Val Asn Val Val Tyr Gly Leu Phe Ile Ile Leu Ser Val Met Gly Val
  165                               170                               175
Asp Ser Leu Phe Ile Gly Phe Ser Tyr Ile Leu Ile Leu Trp Ala Val
  180                               185                               190
Leu Glu Leu Ser Ser Arg Arg Ala Ala Leu Lys Ala Phe Asn Thr Cys
  195                               200                               205
Ile Ser His Leu Cys Ala Val Leu Val Phe Tyr Val Pro Leu Ile Gly
  210                               215                               220
Leu Ser Val Val His Arg Leu Gly Gly Pro Thr Ser Leu Leu His Val
  225                               230                               235                               240
Val Met Ala Asn Thr Tyr Leu Leu Leu Pro Pro Val Val Asn Pro Leu
  245                               250                               255
Val Tyr Gly Ala Lys Thr Lys Glu Ile Cys Ser Arg Val Leu Cys Met
  260                               265                               270
Phe Ser Gln Gly Gly Lys
  275

```

&lt;210&gt; 1445

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g362 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1445

```

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
  1                               5                               10                               15
Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
  20                               25                               30
Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu
  35                               40                               45
Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
  50                               55                               60
Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
  65                               70                               75                               80
Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
  85                               90                               95
Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
  100                               105                               110
Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
  115                               120                               125
Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
  130                               135                               140
Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met

```

```

145          150          155          160
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
          165          170          175
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
          180          185          190
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
          195          200          205
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
          210          215          220
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
225          230          235          240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
          245          250          255
Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile
          260          265          270
Val Pro Leu His Thr Gln Val Leu Ala Asp Leu Tyr Val Ile Ile
          275          280          285
Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu
          290          295          300
Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His
305          310          315

```

&lt;210&gt; 1446

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g363 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1446

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
1      5      10      15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
20     25     30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
35     40     45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
50     55     60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
65     70     75     80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
85     90     95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
100    105    110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
115    120    125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
130    135    140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
145    150    155    160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
165    170    175
Phe Phe Cys Asp Leu Pro Leu Ala Thr Lys Leu Ala Cys Ile Asp Thr
180    185    190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
195    200    205
Ser Ser Phe Leu Leu Leu Val Ser Tyr Thr Val Ile Leu Val Thr
210    215    220
Val Arg Asn Arg Ser Ser Val Ser Met Val Lys Ala His Ser Thr Leu
225    230    235    240

```



Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Ser Cys Ile Phe  
 245 250 255  
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala  
 260 265 270  
 Val Phe Tyr Thr Ile Phe Thr Ser Ile Leu Asn Pro Val Ile Tyr Met  
 275 280 285  
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg  
 290 295 300  
 Tyr Gln Lys Leu Gly Gln Val Ser Val Val Ile Arg Asn Val Leu Phe  
 305 310 315 320  
 Leu Glu

&lt;210&gt; 1447

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g364 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1447

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
 1 5 10 15  
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
 20 25 30  
 Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Ile  
 35 40 45  
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
 50 55 60  
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
 65 70 75 80  
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
 85 90 95  
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
 100 105 110  
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
 130 135 140  
 Met Leu Gly Met Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile  
 145 150 155 160  
 Thr Pro Leu Ser Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn  
 165 170 175  
 Val Val Val His Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala  
 180 185 190  
 Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
 195 200 205  
 Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
 210 215 220  
 Ile Leu Lys Ala Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys  
 225 230 235 240  
 Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
 245 250 255  
 Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val  
 260 265 270  
 Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
 275 280 285  
 Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
 290 295 300  
 Arg Glu Arg Ile Trp Ser Tyr Leu Met His Val Leu Phe Asp His Ser

305  
Asn Leu

310

315

320

<210> 1448  
<211> 314  
<212> PRT  
<213> Unknown (H38g365 protein)

<220>

<223> Synthetic construct

<400> 1448

```

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1           5           10           15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
          20           25           30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
          35           40           45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
          50           55           60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
65           70           75           80
Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys
          85           90           95
Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
          100          105          110
Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
          115          120          125
Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
          130          135          140
Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145          150          155          160
Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
          180          185          190
Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
          195          200          205
Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
          210          215          220
Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
225          230          235          240
Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
          245          250          255
Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
          260          265          270
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
          275          280          285
Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile
          290          295          300
Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305          310

```

<210> 1449  
<211> 317  
<212> PRT  
<213> Unknown (H38g366 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1449

```

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
 1           5           10           15
Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
          20           25           30
Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
          35           40           45
Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
          50           55           60
Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
65           70           75           80
Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu
          85           90           95
Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
          100          105          110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
130          135          140
Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
145          150          155          160
Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
          165          170          175
Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
          180          185          190
Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu
          195          200          205
Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile
210          215          220
Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr
225          230          235          240
Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val
          245          250          255
Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro
          260          265          270
Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro
          275          280          285
Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu
290          295          300
Ser Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg
305          310          315

```

&lt;210&gt; 1450

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g367 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(101)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1450

```

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val
 1           5           10           15
Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
          20           25           30
Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr

```

```

      35      40      45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
  50      55      60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
  65      70      75      80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
      85      90      95
Cys Cys Leu Ala Glu
      100

```

<210> 1451  
 <211> 169  
 <212> PRT  
 <213> Unknown (H38g368 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(169)  
 <223> Xaa = Any Amino Acid

```

<400> 1451
Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe
  1      5      10
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
      20      25      30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
      35      40      45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
      50      55      60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
  65      70      75      80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
      85      90      95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
      100      105      110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
      115      120      125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
      130      135      140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
  145      150      155      160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
      165

```

<210> 1452  
 <211> 279  
 <212> PRT  
 <213> Unknown (H38g369 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(279)  
 <223> Xaa = Any Amino Acid

```

<400> 1452
Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu
  1      5      10      15

```

```

Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys
      20              25              30
Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser
      35              40              45
Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met
      50              55              60
Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu
      65              70              75              80
Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp
      85              90              95
Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile
      100             105             110
Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe
      115             120             125
Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val
      130             135             140
Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala
      145             150             155             160
His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa
      165             170             175
Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys
      180             185             190
Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu
      195             200             205
Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu
      210             215             220
Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr
      225             230             235             240
Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe
      245             250             255
Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu
      260             265             270
Ser Ile Ile Leu Thr Leu Val
      275

```

&lt;210&gt; 1453

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g370 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(154)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1453

```

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile
  1              5              10              15
His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe
      20              25              30
Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg
      35              40              45
Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys
      50              55              60
Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile
      65              70              75              80
Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu
      85              90              95
Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |     |     |
| Ser | Glu | Ile | Leu | Ser | Met | Ile | Tyr | Phe | Met | Gly | Thr | Lys | Lys | Asn | Glu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Lys | Pro | Arg | Lys | Lys | Asp | Cys | Glu | Ser | His | Xaa | Lys | Gly | Leu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Xaa | Met | Gly | Gln | Ile | Ile | Ile | Leu | Phe | Tyr |     |     |     |     |     |     |
| 145 |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 1454

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g371 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(186)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1454

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | His | Pro | Arg | Ser | Pro | His | His | Pro | Leu | Phe | Pro | Pro | Tyr | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Leu | Lys | Asn | Phe | Phe | Pro | Thr | Ile | Phe | Pro | Gln | Asn | Leu | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Leu | Phe | Thr | Thr | Val | Phe | Pro | Pro | Pro | Pro | Thr | Pro | Asn | Ile | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Pro | Pro | Ser | Phe | Pro | His | Cys | Leu | Phe | Cys | Asn | Thr | Phe | Ser | Cys |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Leu | Ile | Leu | Tyr | Phe | Pro | Leu | Ala | Leu | Thr | Thr | Leu | Phe | Thr | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Ser | Thr | Pro | Lys | Leu | Phe | Ser | Pro | Ser | Tyr | Arg | Ser | Ser | His | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Val | Ser | Val | Ala | Ala | Thr | Asn | Arg | Ser | Glu | Ala | Ser | Cys | Ala | Cys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Ser | His | Ser | Leu | Gln | His | Ala | Ala | Val | Ala | Ser | Pro | Cys | Pro | Gly |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Pro | Leu | Ser | Arg | Glu | Arg | Ser | Ser | Pro | Ala | Arg | Arg | His | Ala | Xaa | Ala |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Xaa | Asn | Gly | Leu | Thr | Pro | Leu | Leu | Ala | Pro | Phe | Ile | Tyr | Xaa | Gly | Tyr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Tyr | Glu | Val | Pro | Gly | Leu | Leu | Phe | Gln | Asp | Trp | Val | Arg | Glu | Asn |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Glu | Ala | Tyr | Ser | Asp | Trp | Thr | Leu | Leu |     |     |     |     |     |     |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |     |

&lt;210&gt; 1455

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g372 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(142)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1455

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Glu | Met | Asp | Asn | Tyr | Phe | Leu | Thr | Xaa | Leu | Xaa | Arg | Tyr | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |

Leu Phe Phe His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Ile Lys Lys  
                   20                  25                  30  
 Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile  
                   35                  40                  45  
 Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys  
                   50                  55                  60  
 Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe  
 65                  70                  75                  80  
 Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu  
                   85                  90                  95  
 Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met  
                   100                  105                  110  
 Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr  
                   115                  120                  125  
 Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe  
                   130                  135                  140

<210> 1456  
 <211> 82  
 <212> PRT  
 <213> Unknown (H38g373 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(82)  
 <223> Xaa = Any Amino Acid

<400> 1456  
 Asn Val Phe Arg Xaa Phe Leu Asp Phe Cys Arg Asp Ser Asp Ile His  
   1                  5                  10                  15  
 Arg Ala Tyr Leu Cys Ile Leu Ser Ser Xaa Leu Arg Phe Ser Val Leu  
                   20                  25                  30  
 Gly Ile Phe Xaa Gly Arg Ala Met Asn Ile Leu Ile Gly Leu Thr Lys  
                   35                  40                  45  
 Val Leu Lys Cys Pro Ile Leu Cys Val Val Phe Asn His Thr Cys Ile  
                   50                  55                  60  
 Leu Ile Thr Thr Leu Ala Val Ile Ala Tyr Arg Phe Arg Gln Ser Gly  
 65                  70                  75                  80  
 Tyr Ser

<210> 1457  
 <211> 207  
 <212> PRT  
 <213> Unknown (H38g374 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(207)  
 <223> Xaa = Any Amino Acid

<400> 1457  
 Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe  
   1                  5                  10                  15  
 Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys  
                   20                  25                  30  
 Asn Met Arg Leu Pro Ser Asp Phe Phe Leu Ser Gln Ala Ile Tyr Tyr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| Xaa | Trp | Ala | Leu | Met | Cys | Val | Leu | Glu | Asn | Lys | Thr | Tyr | Ala | Ser | Val |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Val | Xaa | Arg | Phe | Gly | Trp | Xaa | Lys | Leu | Ala | Asn | Xaa | Met | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Leu | Tyr | Leu | Glu | Ala | Asn | Leu | Gly | Asn | Met | Asp | Asn | Ala | Leu | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Xaa | Leu | Lys | Arg | Asn | Tyr | Phe | Val | Phe | Val | Phe | Thr | Ser | Phe | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gly | Cys | Ile | Ala | Phe | Lys | Xaa | Lys | Glu | Ile | Phe | Tyr | Pro | Tyr | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ile | Cys | Ile | Tyr | His | Leu | Leu | Met | Met | Glu | Arg | Lys | Val | Ser | Cys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Thr | Leu | Ile | Cys | Leu | Ala | Xaa | Asp | Leu | Xaa | His | Phe | Xaa | Cys | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Val | Thr | Val | Leu | Ser | Leu | Glu | Cys | Xaa | Gln | Leu | Asp | Ile | Cys | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Val | Thr | Tyr | Phe | Asn | Thr | Met | Val | Xaa | Ser | Thr | Thr | Gly | Ser | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Xaa | Thr | Pro | Asn | His | Ser | Val | Leu | Ile | Cys | Asn | Met | Leu | Lys |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

&lt;210&gt; 1458

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g375 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1458

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Asn | Leu | Ser | Gly | Gly | His | Val | Glu | Glu | Phe | Val | Leu | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Phe | Pro | Thr | Thr | Pro | Pro | Leu | Gln | Leu | Leu | Leu | Phe | Val | Leu | Phe | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Tyr | Leu | Leu | Thr | Leu | Leu | Glu | Asn | Ala | Leu | Ile | Val | Phe | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Trp | Leu | Ala | Pro | Ser | Leu | His | Arg | Pro | Met | Tyr | Phe | Phe | Leu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Leu | Ser | Phe | Leu | Glu | Leu | Trp | Tyr | Ile | Asn | Val | Thr | Ile | Pro | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Leu | Ala | Ala | Phe | Leu | Thr | Gln | Asp | Gly | Arg | Val | Ser | Tyr | Val | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Met | Thr | Gln | Leu | Tyr | Phe | Phe | Ile | Ala | Leu | Ala | Cys | Thr | Glu | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Leu | Leu | Ala | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Leu | Ala | Ile | Cys | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Leu | Tyr | Pro | Ser | Leu | Met | Pro | Ser | Ser | Leu | Ala | Thr | Arg | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ala | Ala | Ala | Ser | Trp | Gly | Ser | Gly | Phe | Phe | Ser | Ser | Met | Met | Lys | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Phe | Ile | Ser | Gln | Leu | Ser | Tyr | Cys | Gly | Pro | Asn | Ile | Ile | Asn | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Phe | Cys | Asp | Ile | Ser | Pro | Leu | Leu | Asn | Leu | Thr | Cys | Ser | Asp | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Gln | Ala | Glu | Leu | Val | Asp | Phe | Leu | Leu | Ala | Leu | Val | Met | Ile | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Pro | Leu | Leu | Ala | Val | Val | Ser | Ser | Tyr | Thr | Ala | Ile | Ile | Ala | Ala |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Ile | Leu | Arg | Ile | Pro | Thr | Ser | Arg | Gly | Arg | His | Lys | Ala | Phe | Ser | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |



Cys Ala Ala His Leu Ala Val Val Val Ile Tyr Tyr Ser Ser Thr Leu  
 245 250 255  
 Phe Thr Tyr Ala Arg Pro Arg Ala Met Tyr Thr Phe Asn His Asn Lys  
 260 265 270  
 Ile Ile Ser Val Leu Tyr Thr Ile Ile Val Pro Phe Phe Asn Pro Ala  
 275 280 285  
 Ile Tyr Cys Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Arg Lys Thr  
 290 295 300  
 Val Met Gly Arg Cys His Tyr Pro Arg  
 305 310

&lt;210&gt; 1459

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g376 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1459

His Thr Glu Pro Leu Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser  
 35 40 45  
 Ile Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Tyr Thr Ser Ala Thr  
 65 70 75 80  
 Val Pro Lys Met Ile Val Asp Thr Gln Ser His Gly Arg Val Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys  
 100 105 110  
 Ile Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala  
 115 120 125  
 Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln  
 145 150 155 160  
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu  
 165 170 175  
 Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys  
 180 185 190  
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile  
 210 215 220  
 Val Pro Ser Val Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg  
 260 265 270  
 Asn Gly Val Val Glu Ser Gly Met Tyr Ala Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg His Thr Gln Ser Ala Leu

290 295 300  
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Leu His Pro  
 305 310 315 320  
 Phe Ser

<210> 1460  
 <211> 186  
 <212> PRT  
 <213> Unknown (H38g377 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(186)  
 <223> Xaa = Any Amino Acid

<400> 1460  
 Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu  
 1 5 10 15  
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser  
 20 25 30  
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn  
 35 40 45  
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val  
 50 55 60  
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr  
 65 70 75 80  
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp  
 85 90 95  
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly  
 100 105 110  
 Xaa Lys Leu Pro Met His Val Glu Asp Gly Met Gln Thr Ala Leu His  
 115 120 125  
 Ala Cys Pro Leu Leu Met Gln Leu Leu Leu Ser Ile Pro His Ser Tyr  
 130 135 140  
 Pro Leu Leu Leu Asp Asn Ser Phe Leu Phe Leu Arg Leu His Pro Arg  
 145 150 155 160  
 Ser Lys Leu Ser Tyr Phe Leu His Ile Leu Leu Ser Xaa Pro Phe Thr  
 165 170 175  
 Tyr Val Asn His Leu Leu Pro Phe Leu Leu  
 180 185

<210> 1461  
 <211> 336  
 <212> PRT  
 <213> Unknown (H38g378 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(336)  
 <223> Xaa = Any Amino Acid

<400> 1461  
 Ser Arg Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Gly Ser Ser Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe  
 20 25 30

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Leu Ser Thr Cys Leu Val Met Ala Leu Gly Asn Leu Leu Ile Ile Leu
  35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
  50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro
  65          70          75          80
Lys Met Thr Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Asp Asn Ile Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys
          115          120          125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
          130          135          140
Phe Leu Leu Leu Leu Ser Phe Phe Ser Ser Leu Ser Leu Leu Asp Ala
          145          150          155          160
Gln Leu Tyr Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
          165          170          175
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
          180          185          190
Cys Cys Asp Thr Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala
          195          200          205
Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys
          210          215          220
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
          225          230          235          240
Ala Phe Ser Thr Tyr Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr
          245          250          255
Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro
          260          265          270
Arg Lys Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
          275          280          285
Met Asn Pro Phe Ile Tyr Ser Pro Arg Asn Arg Asp Met Lys Ser Val
          290          295          300
Leu Arg Arg Pro His Gly Ser Thr Phe Xaa Ser Gln Tyr Leu Leu Ile
          305          310          315          320
Cys Ser Ile Pro Phe Ala Val Trp Val Glu Lys Gly Cys Met Met Lys
          325          330          335

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&lt;210&gt; 1462

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g379 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1462

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
  1          5          10          15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
          20          25          30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
          35          40          45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
          50          55          60
Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Cys | Thr | Cys | Leu | Asp | Thr | Phe | Thr | Lys | Ser | Tyr | Ile | Thr | Xaa | Ile | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Leu | Lys | Gly | Phe | Asn | His | Leu | Cys | Phe | Leu | Leu | His | Tyr | Cys | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Ala | Arg | Ala | Gln | Val | Ser | Xaa | Asn | Ala | Pro | Trp | Ser | Leu | Ala | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Cys | Gln | Pro | Asn | Met | Leu | Ile | Arg | Xaa | Leu | Phe | Cys | Leu | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Val | His | Asp | Arg | Leu | Xaa | His | Val | Leu | Ser | Leu | Leu |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

&lt;210&gt; 1463

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g380 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1463

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Asn | Gln | Thr | Ile | Leu | Lys | Glu | Phe | Ile | Leu | Val | Gly | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | Tyr | Pro | His | Val | Gln | Thr | Phe | Leu | Phe | Val | Val | Phe | Phe | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Tyr | Leu | Leu | Thr | Leu | Ala | Gly | Asn | Leu | Thr | Ile | Met | Gly | Leu | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Val | Asp | Arg | Ser | Leu | His | Thr | Pro | Met | Tyr | Leu | Phe | Leu | Ser | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Ser | Phe | Ser | Glu | Thr | Cys | Tyr | Thr | Leu | Thr | Ile | Val | Pro | Lys | Met |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Glu | Asp | Leu | Leu | Ala | Lys | Asp | Arg | Ser | Ile | Ser | Val | Thr | Gly | Cys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Leu | Gln | Met | Cys | Phe | Phe | Leu | Gly | Leu | Gly | Gly | Thr | Asn | Cys | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Leu | Thr | Leu | Met | Gly | Tyr | Asp | Arg | Phe | Leu | Ala | Ile | Cys | Asn | Pro |
|     |     | 115 |     |     | 120 |     |     |     |     |     |     | 125 |     |     |     |
| Leu | Arg | Tyr | Pro | Leu | Leu | Met | Thr | Asn | Ile | Val | Cys | Gly | Gln | Leu | Val |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ala | Ser | Ala | Cys | Thr | Ala | Gly | Phe | Phe | Ile | Ser | Leu | Thr | Glu | Thr | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Ile | Phe | Arg | Asp | Ser | Phe | Cys | Arg | Pro | Asn | Leu | Val | Lys | His | Phe |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Cys | His | Met | Leu | Ala | Val | Ile | Arg | Leu | Ser | Cys | Ile | Asp | Ser | Asn |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Thr | Glu | Phe | Ile | Ile | Thr | Leu | Ile | Ser | Val | Ser | Gly | Leu | Leu | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Leu | Leu | Leu | Ile | Ile | Leu | Thr | Asp | Val | Phe | Ile | Ile | Ser | Thr | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Arg | Ile | Pro | Ser | Ala | Glu | Gly | Lys | Gln | Lys | Ala | Phe | Thr | Thr | Cys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Ser | His | Leu | Thr | Val | Val | Ile | Ile | His | Phe | Gly | Phe | Ala | Ser | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Tyr | Leu | Lys | Pro | Glu | Ala | Ser | Gly | Asp | Asp | Thr | Leu | Ile | Ala | Val |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Tyr | Thr | Val | Ile | Thr | Pro | Phe | Leu | Ser | Pro | Ile | Ile | Phe | Ser | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |

Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr  
 290 295 300  
 Val Ala Leu Lys Lys Ile Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu  
 305 310 315 320  
 Gly Leu Asn Val Pro  
 325

<210> 1464

<211> 313

<212> PRT

<213> Unknown (H38g381 protein)

<220>

<223> Synthetic construct

<400> 1464

Met Gly Gln Thr Asn Val Thr Ser Trp Arg Asp Phe Val Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Ser Gly Glu Leu Gln Leu Leu Leu Phe Ala Leu Phe Leu  
 20 25 30  
 Ser Leu Tyr Leu Val Thr Leu Thr Ser Asn Val Phe Ile Ile Ile Ala  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Phe Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Gly Ile Ile Pro Arg  
 65 70 75 80  
 Met Leu Ser Gly Leu Ala Gly Gly Asp Gln Ala Ile Ser Tyr Val Gly  
 85 90 95  
 Cys Ala Ala Gln Met Phe Phe Ser Ala Ser Trp Ala Cys Thr Asn Cys  
 100 105 110  
 Phe Leu Leu Ala Ala Met Gly Phe Asp Arg Tyr Val Ala Ile Cys Ala  
 115 120 125  
 Pro Leu His Tyr Ala Ser His Met Asn Pro Thr Leu Cys Ala Gln Leu  
 130 135 140  
 Val Ile Thr Ser Phe Leu Thr Gly Tyr Leu Phe Gly Leu Gly Met Thr  
 145 150 155 160  
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His  
 165 170 175  
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr  
 180 185 190  
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu  
 195 200 205  
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser  
 245 250 255  
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln  
 260 265 270  
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile  
 275 280 285  
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala  
 290 295 300  
 Phe Arg Gly Arg Leu Leu Gly Lys Gly  
 305 310

<210> 1465

<211> 289

<212> PRT

<213> Unknown (H38g382 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(289)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1465

```

Leu Leu Phe Phe Ile Leu Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1           5           10           15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
          20           25           30
Ser Ser Leu Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Trp
          35           40           45
Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu
          50           55           60
Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Phe
65           70           75           80
Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met
          85           90           95
Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr
          100          105          110
Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly
          115          120          125
Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe
          130          135          140
Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile
145          150          155          160
Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val
          165          170          175
Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val
          180          185          190
Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser
          195          200          205
Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala
          210          215          220
Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe
225          230          235          240
Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe
          245          250          255
Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu
          260          265          270
Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr
          275          280          285
His

```

&lt;210&gt; 1466

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g383 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1466

```

Met Glu Ser Pro Asn Arg Thr Thr Ile Gln Glu Phe Ile Phe Ser Ala
 1           5           10           15
Phe Pro Tyr Ser Trp Val Lys Ser Val Val Cys Phe Val Pro Leu Leu
          20           25           30

```

Phe Ile Tyr Ala Phe Ile Val Val Gly Asn Leu Val Ile Ile Thr Val  
 35 40 45  
 Val Gln Leu Asn Thr His Leu His Thr Pro Met Tyr Thr Phe Ile Ser  
 50 55 60  
 Ala Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ser Ser Leu Leu Ser Glu Arg Ser Ile Ser Phe Asn Gly Cys  
 85 90 95  
 Leu Leu Gln Met Tyr Phe Phe His Ser Thr Gly Ile Cys Glu Val Cys  
 100 105 110  
 Leu Leu Thr Val Met Ala Phe Asp His Tyr Leu Ala Ile Cys Ser Pro  
 115 120 125  
 Leu His Tyr Pro Ser Ile Met Thr Pro Lys Leu Cys Thr Gln Leu Thr  
 130 135 140  
 Leu Ser Cys Trp Val Cys Gly Phe Ile Thr Pro Leu Pro Glu Ile Ala  
 145 150 155 160  
 Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn His Leu Glu His Ile  
 165 170 175  
 Phe Cys Asp Phe Leu Pro Val Leu Arg Leu Ala Cys Thr Asp Thr Arg  
 180 185 190  
 Ala Ile Val Met Ile Gln Val Val Asp Val Ile His Ala Val Glu Ile  
 195 200 205  
 Ile Thr Ala Val Met Leu Ile Phe Met Ser Tyr Asp Gly Ile Val Ala  
 210 215 220  
 Val Ile Leu Arg Ile His Ser Ala Gly Gly Arg Arg Thr Ala Phe Ser  
 225 230 235 240  
 Thr Cys Val Ser His Phe Ile Val Phe Ser Leu Phe Phe Gly Ser Val  
 245 250 255  
 Thr Leu Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Leu Phe Trp Asp  
 260 265 270  
 Ile Ala Ile Ala Leu Ala Phe Ala Val Leu Ser Pro Phe Phe Asn Pro  
 275 280 285  
 Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Ile Lys Lys  
 290 295 300  
 His Ile Gly Gln Ala Lys Ile Phe Phe Ser Val Arg Pro Gly  
 305 310 315

&lt;210&gt; 1467

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g384 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1467

Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn Glu Val Ile Ile  
 1 5 10 15  
 Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe Leu Cys Ile Leu  
 20 25 30  
 Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys Val Pro Ser Thr  
 35 40 45  
 Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val  
 50 55 60  
 Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr Phe Asn Pro Leu  
 65 70 75 80  
 Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr Val Leu Tyr Thr  
 85 90 95  
 Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg  
 100 105 110  
 Tyr Leu Lys Gly Ala Leu Lys Lys Val Val Gly Arg Val Val Phe Ser

Val 115 120 125

<210> 1468  
 <211> 162  
 <212> PRT  
 <213> Unknown (H38g385 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(162)  
 <223> Xaa = Any Amino Acid

<400> 1468  
 Leu Leu Ile Ile Pro Ala Ile Ala Thr Asp Thr Arg Leu Ser Val Leu  
 1 5 10 15  
 Val Arg Phe Phe Leu Ala Asn Leu Ala Phe Val Val Thr Cys Phe Thr  
 20 25 30  
 Ser Thr Thr Ile Pro Lys Met Leu Ala Cys Lys Glu Ile Pro Cys Val  
 35 40 45  
 Met Ser Gly Cys Lys Gly Ile Pro Tyr Ala Gly Cys Leu Thr Gln Met  
 50 55 60  
 Leu Phe Phe Ile Trp Leu Gly Ile His Ser Phe Leu Leu Thr Ala Met  
 65 70 75 80  
 Ala Asn Glu His Cys Val Ala Ile Cys His Ser Leu Asn Ser Ile Arg  
 85 90 95  
 Ser Val Thr Pro Xaa Leu Cys Gly Leu Leu Val Val Ala Ser Trp Thr  
 100 105 110  
 Phe Ala Phe Arg Asn Ala Leu Thr His Pro Val Leu Leu Thr Arg Leu  
 115 120 125  
 Ser Leu Cys Thr Tyr Glu Trp Val Ser His Val Phe Cys Asn Leu Ser  
 130 135 140  
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ala Thr Leu Asn Asn Val Thr  
 145 150 155 160  
 Val Gln

<210> 1469  
 <211> 327  
 <212> PRT  
 <213> Unknown (H38g386 protein)

<220>  
 <223> Synthetic construct

<400> 1469  
 Met Leu Thr Pro Asn Asn Ala Cys Ser Val Pro Thr Ser Phe Arg Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Ile Trp Leu Ser Ile Pro  
 20 25 30  
 Phe Gly Ser Met Tyr Leu Val Ala Val Leu Gly Asn Ile Thr Ile Leu  
 35 40 45  
 Ala Val Val Arg Met Glu Tyr Ser Leu His Gln Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Cys Met Leu Ala Val Ile Asp Leu Val Leu Ser Thr Ser Thr Met  
 65 70 75 80  
 Pro Lys Leu Leu Ala Ile Phe Trp Phe Gly Ala His Asn Ile Gly Val  
 85 90 95



```

Asn Ala Cys Leu Ala Gln Met Phe Phe Ile His Cys Phe Ala Thr Val
      100                      105                      110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp His Tyr Val Ala Ile
      115                      120                      125
Cys Asp Pro Leu His His Thr Leu Leu Leu Thr His Ala Val Val Gly
      130                      135                      140
Arg Leu Gly Leu Ala Ala Leu Leu Arg Gly Val Ile Tyr Ile Gly Pro
      145                      150                      155                      160
Leu Pro Leu Val Ile Cys Leu Arg Leu Pro Leu Tyr His Thr Gln Ile
      165                      170                      175
Ile Ala His Ser Tyr Cys Glu His Met Ala Val Val Thr Leu Ala Cys
      180                      185                      190
Gly Asp Asp Thr Arg Val Asn Asn Leu Tyr Gly Met Gly Ile Gly Phe
      195                      200                      205
Leu Val Leu Ile Leu Asp Ser Leu Ala Ile Thr Ala Ser Tyr Val Met
      210                      215                      220
Ile Phe Arg Ala Val Met Gly Leu Ala Thr Ser Glu Ala Arg Leu Lys
      225                      230                      235                      240
Thr Leu Gly Thr Cys Gly Ser His Ile Cys Ala Ile Leu Val Phe Tyr
      245                      250                      255
Ile Pro Ile Ala Val Ser Ser Leu Thr His Arg Phe Gly His Arg Val
      260                      265                      270
Pro Pro His Ile His Ile His Ile His Ile His Ile His Ile
      275                      280                      285
Leu Leu Ala Asn Ile Tyr Leu Leu Ile Pro Pro Ile Leu Asn Pro Ile
      290                      295                      300
Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu Ala Leu Leu His Ile
      305                      310                      315                      320
Lys Ala Arg Thr Gln Thr Arg
      325

```

&lt;210&gt; 1470

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g387 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1470

```

Val Ala Cys Tyr Leu Pro Glu Leu Ser Val Gly Cys Pro Gly Gly Lys
  1          5          10          15
Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser
  20          25          30
Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His
  35          40          45
Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser
  50          55          60
Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe
  65          70          75          80
Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn
  85          90          95
His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu
  100         105         110
Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu
  115         120         125
Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu

```

|   |     |     |
|---|-----|-----|
| 130   | 135 | 140 |
| Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val |     |     |
| 145   | 150 | 155 |
| Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile |     |     |
|   | 165 | 170 |
| Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr |     |     |
|   | 180 | 185 |
| Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn |     |     |
|   | 195 | 200 |
| Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala |     |     |
|   | 210 | 215 |
| Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ala Ile Leu Arg Ile |     |     |
| 225   | 230 | 235 |
| Pro Ser Pro Thr Arg Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His |     |     |
|   | 245 | 250 |
| Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile |     |     |
|   | 260 | 265 |
| Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met |     |     |
|   | 275 | 280 |
| Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met |     |     |
|   | 290 | 295 |
| Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser |     |     |
| 305   | 310 | 315 |
| His Ser Ser   |     | 320 |

&lt;210&gt; 1471

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g388 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(202)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1471

|   |     |
|---|-----|
| Leu His Phe Cys Gly Ile Asp Val Thr Ser Tyr Gln Ala Xaa Gln Ile |     |
| 1   | 5   |
| Leu Ala Xaa Gln Pro Tyr Asp Thr Thr Xaa Cys Gly Gln Arg Ile Val |     |
|   | 20  |
| Gly Ile Met Ala Val Ala Trp Gly Ile Gly Phe Leu His Ser Leu Ser |     |
|   | 35  |
| Gln Leu Ala Phe Ala Val His Leu Pro Phe Cys Gly Pro Asn Glu Phe |     |
|   | 50  |
| Asp Ser Phe Tyr Cys Asp Leu Pro Arg Val Ile Lys Leu Ala Cys Thr |     |
| 65  | 70  |
| Asp Thr Tyr Arg Leu Asp Ile Met Val Ile Ala Asn Ser Gly Val Leu |     |
|   | 85  |
| Thr Val Cys Ser Phe Val Leu Leu Ile Ile Ser Tyr Thr Ile Ile Leu |     |
|   | 100 |
| Met Thr Ile Gln His Arg Pro Leu Asp Lys Ser Ser Lys Ala Leu Ser |     |
|   | 115 |
| Thr Leu Thr Ala His Ile Thr Val Val Leu Leu Phe Phe Gly Pro Cys |     |
|   | 130 |
| Val Phe Ile Tyr Ala Trp Pro Phe Pro Ile Lys Ser Leu Asp Lys Phe |     |
| 145   | 150 |
| Leu Ala Val Phe Tyr Ser Val Ile Thr Pro Leu Leu Asn Pro Ile Ile |     |
|   | 165 |
|   | 170 |
|   | 175 |

Tyr Thr Leu Arg Asn Lys Asp Met Lys Thr Ala Ile Arg Gln Leu Arg  
 180 185 190  
 Lys Trp Asp Ala His Ser Ser Val Lys Phe  
 195 200

<210> 1472

<211> 311

<212> PRT

<213> Unknown (H38g389 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1472

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro  
 20 25 30  
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu  
 35 40 45  
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile  
 65 70 75 80  
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu  
 85 90 95  
 Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val  
 100 105 110  
 Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly  
 130 135 140  
 Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro  
 145 150 155 160  
 Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val  
 165 170 175  
 Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys  
 180 185 190  
 Gly Asp Ser Lys Val Asn Asn Val Tyr Gly Met Ser Ile Gly Phe Leu  
 195 200 205  
 Val Leu Ile Met Glu Ser Val Asp Ser Asp Ala Ser Xaa Val Arg Ser  
 210 215 220  
 Ile Arg Ala Val Met Gly Leu Ala Asn His Glu Asp Arg Ile Lys Thr  
 225 230 235 240  
 Met Gly Thr Gly Glu Tyr His Ile Cys Ala Ile Met Ile Phe Arg Ile  
 245 250 255  
 Pro Val Met Tyr Ile Pro Xaa Asp His Arg Asp Gly Gln Cys Val His  
 260 265 270  
 His Pro Val His Asn Met Met Ala Arg Ile Tyr Ile Ile Ser His Pro  
 275 280 285  
 Ser Ile Lys Pro Ser Val Xaa Asp Asp Arg Thr Lys Gln Ser Arg Glu  
 290 295 300  
 Ser Tyr Ile Gln Arg Ala Arg  
 305 310

<210> 1473

<211> 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g390 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1473

```

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
          20           25           30
Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
          35           40           45
Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
          65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
          145          150          155          160
Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
          165          170          175
His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
          180          185          190
Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala His Ile Leu Gly
          210          215          220
Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
          225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
          305          310          315

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&lt;210&gt; 1474

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g391 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1474

Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu  
 1 5 10 15  
 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val  
 20 25 30  
 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe  
 35 40 45  
 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro  
 65 70 75 80  
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val  
 85 90 95  
 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu  
 100 105 110  
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser  
 115 120 125  
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln  
 130 135 140  
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln  
 145 150 155 160  
 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp  
 165 170 175  
 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp  
 180 185 190  
 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu  
 195 200 205  
 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly  
 210 215 220  
 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala  
 245 250 255  
 Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp  
 260 265 270  
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys  
 290 295 300  
 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His Xaa Thr Pro Glu Ser  
 305 310 315 320  
 Gly Ala Cys Cys Ala Pro  
 325

&lt;210&gt; 1475

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g392 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1475

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly  
 1 5 10 15  
 Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala  
 20 25 30  
 Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu  
 35 40 45  
 Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys

```

65          70          75          80
Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly
      85          90          95
Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly
      100         105         110
Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln
      115         120         125
Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met
      130         135         140
Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr
145          150         155          160
Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His
      165         170         175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
      180         185         190
Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
      195         200         205
Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala
210          215         220
Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr
225          230         235          240
Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val
      245         250         255
Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn
      260         265         270
Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu
      275         280         285
Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val
290          295         300
Leu Ser Arg Ala Gly Leu Arg Gln Met Cys
305          310

```

&lt;210&gt; 1476

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g393 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1476

```

Asn Ile Lys Gly Ile Ala Val Pro Met Phe Ile Glu Val Leu Asp Leu
1          5          10          15
Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln
      20          25          30
Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser
      35          40          45
His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser
      50          55          60
Val Met His Arg Val Ala Arg Cys Ala Ala Pro His Val His Ile Leu
65          70          75          80
Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile
      85          90          95
Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val Leu Gly Val Phe
      100         105         110
Pro Arg Lys Asp Val
      115

```

&lt;210&gt; 1477

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g394 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1477

```

Met Pro Ser Gln Asn Tyr Ser Ile Ile Ser Glu Phe Asn Leu Phe Gly
 1           5           10           15
Phe Ser Ala Phe Pro Gln His Leu Leu Pro Ile Leu Phe Leu Leu Tyr
          20           25           30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
          35           40           45
Thr Ile Trp Ile Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu
          50           55           60
Cys Thr Leu Ser Val Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
65          70          75          80
Arg Met Leu Ala Asp Leu Leu Ser Thr His His Ser Ile Thr Phe Val
          85          90          95
Ala Cys Ala Asn Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
          100         105         110
Ser Phe Leu Leu Leu Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
          115         120         125
His Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Asp Cys Ala His
          130         135         140
Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
145         150         155         160
Thr Thr Ile Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
          165         170         175
His Phe Phe Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Glu Asn
          180         185         190
Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
          195         200         205
Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Tyr Val Phe Ile Val
          210         215         220
Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
225         230         235         240
Ser Thr Cys Val Ser His Leu Thr Val Val Val Thr His Tyr Ser Phe
          245         250         255
Ala Ser Phe Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
          260         265         270
Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
          275         280         285
Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
          290         295         300
Lys Asn Phe Tyr Arg Lys Phe Cys Pro Pro Ser Ser
305         310         315

```

&lt;210&gt; 1478

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g395 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1478

```

Met Cys Ser Phe Phe Leu Cys Gln Thr Gly Lys Gln Ala Lys Ile Ser
 1           5           10           15
Met Gly Glu Glu Asn Gln Thr Phe Val Ser Lys Phe Ile Phe Leu Gly
          20           25           30
Leu Ser Gln Asp Leu Gln Thr Gln Ile Leu Leu Phe Ile Leu Phe Leu

```

```

      35      40      45
Ile Ile Tyr Leu Leu Thr Val Leu Gly Asn Gln Leu Ile Ile Ile Leu
  50      55      60
Ile Phe Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg
  65      70      75      80
Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Thr Ser Ile Val Pro Gln
      85      90      95
Val Leu Val His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Tyr Gly
      100      105      110
Cys Met Thr Gln Ile Ile Val Phe Leu Leu Val Gly Cys Thr Glu Cys
      115      120      125
Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys
      130      135      140
Pro Leu Tyr Tyr Ser Thr Ile Met Thr Gln Arg Val Cys Leu Trp Leu
      145      150      155      160
Ser Phe Arg Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr
      165      170      175
Ser Phe Thr Phe His Leu Pro Tyr Trp Gly Gln Asn Ile Ile Asn His
      180      185      190
Tyr Phe Cys Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ile Asp Thr
      195      200      205
Tyr Ser Thr Glu Met Ala Ile Phe Ser Met Gly Val Val Ile Leu Leu
      210      215      220
Ala Pro Val Ser Leu Ile Leu Gly Ser Tyr Trp Asn Ile Ile Ser Thr
      225      230      235      240
Val Ile Gln Met Gln Ser Gly Glu Gly Arg Leu Lys Ala Phe Ser Thr
      245      250      255
Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Gly Ile
      260      265      270
Phe Thr Tyr Met Arg Pro Asn Ser Lys Thr Thr Lys Glu Leu Asp Lys
      275      280      285
Met Ile Ser Val Phe Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Ile
      290      295      300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Arg Lys Leu
      305      310      315      320
Val Gly Arg Lys Cys Phe Ser His Arg Gln
      325      330

```

&lt;210&gt; 1479

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g396 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(227)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1479

```

Gly Lys Glu Arg Glu Thr Arg Val Trp Arg Pro Arg Ala Gln Asp Arg
  1      5      10      15
Gly Val Ser Thr Arg His Ala Ala Arg Val Thr Ser Tyr Gln Glu Cys
      20      25      30
Gly Val Arg Gly Gly Gly Val Leu Cys Gly Ala Val Arg Pro Ser Pro
      35      40      45
Leu Asp Ala Gln Leu His Asn Val Ile Ala Tyr Arg Arg Thr Cys Phe
      50      55      60
Lys Asp Val Glu Ile Pro Asn Phe Val Trp Asp Pro Ser Gln Leu Pro
      65      70      75      80

```



Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe  
                             85                            90                            95  
 Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser  
                             100                            105                            110  
 Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly  
                             115                            120                            125  
 Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys  
                             130                            135                            140  
 Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser  
 145                            150                            155                            160  
 Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala  
                             165                            170                            175  
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile  
                             180                            185                            190  
 Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr  
                             195                            200                            205  
 Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser  
                             210                            215                            220  
 Lys Val Lys  
 225

&lt;210&gt; 1480

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g397 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1480

Met Lys Ile Phe Asn Thr Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe  
 1                            5                            10                            15  
 Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Val  
                             20                            25                            30  
 Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser  
                             35                            40                            45  
 Ile Asn Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr  
                             50                            55                            60  
 Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser  
 65                            70                            75                            80  
 Thr Val Pro Asn Val Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile  
                             85                            90                            95  
 Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly  
                             100                            105                            110  
 Ser Thr Glu Cys Phe Phe Leu Gly Ala Met Ala Phe Asp Leu Tyr Leu  
                             115                            120                            125  
 Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu  
                             130                            135                            140  
 Cys Asn Ile Leu Val Gly Ser Cys Trp Val Leu Gly Phe Leu Trp Phe  
 145                            150                            155                            160  
 Leu Ile Pro Ile Ser Val Ile Ser Gln Met Thr Cys Gly Ser Arg Ile  
                             165                            170                            175  
 Ile Asp His Phe Pro Cys Asp Pro Gly Pro Leu Leu Ala Leu Thr Cys  
                             180                            185                            190  
 Ala Arg Ala Pro Leu Leu Glu Leu Thr Ser Ser Thr Leu Ser Ser Leu  
                             195                            200                            205  
 Leu Leu Phe Ile Pro Phe Leu Phe Ile Val Gly Cys Tyr Ala Leu Val  
                             210                            215                            220  
 Leu Arg Ala Val Leu Arg Val Pro Ser Ala Ser Gly Arg Arg Lys Ala  
 225                            230                            235                            240  
 Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly

```

                245                250                255
Ser Met Met Ile Thr Tyr Val Ser Pro Thr Ser Gly His Glu Phe Gly
                260                265                270
Met Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu Ile
                275                280                285
Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys His Ala Met
                290                295                300
Arg Asn Tyr Thr Val Met Phe Tyr Leu Ser Arg Ile His Arg Ala Thr
305                310                315                320
Arg Asp Val Lys Asp Val Phe Tyr Leu Phe Asn Phe
                325                330

```

&lt;210&gt; 1481

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g398 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(269)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1481

```

Phe Ser Ser Ile Tyr Ala Trp Tyr Ile Ser Asp Leu Tyr Leu Asn Tyr
1          5          10          15
Leu Ser Asn His Leu Ser Ile Phe Lys Leu Val Asp Trp Ile Ile Asn
20          25          30
Cys Tyr Leu Tyr Tyr Phe Tyr Ser Leu Leu Thr Leu Phe Xaa Gln Phe
35          40          45
Ile Tyr Thr Cys Glu Met Asn Gln Phe Lys Xaa Xaa Gln Asn Arg Asn
50          55          60
Asn Leu Thr Thr Phe Xaa Gly Tyr Phe Tyr Ser Gly Ile Cys Gly Arg
65          70          75          80
Arg Asn Cys Thr Met Xaa Leu Ile Thr Ile Phe Ile Leu Lys Tyr Cys
85          90          95
Xaa His Gly Phe Ile Thr Ile His Ser Val Met Asp Ser Gly Gln His
100         105         110
Leu Ala Ile Cys His Pro Leu His Tyr Leu Ile Leu Met Thr Asp Glu
115         120         125
Asn Arg Asp Arg Met Phe Met Gly Pro Leu Thr Ala Phe Pro Tyr Thr
130         135         140
Asp Ala Thr Ser Gln Asn Met His Tyr Val Asn Phe Leu Ile Ile Ile
145         150         155         160
Leu Ser Ile Leu Tyr Ile Pro Gly Pro Tyr Thr Leu Ile Leu Arg Ala
165         170         175
Met Leu Gln Leu Leu Ser Ala Ala Ser His Gln Asn Ala Phe Ser Ile
180         185         190
Arg Gly Ser His Leu Ile Val Val Ser Leu Phe Cys Glu Thr Ile Met
195         200         205
Met Met Cys Val Asn Leu Ile Ser Asp His Leu Val Xaa Met Lys Met
210         215         220
Thr Asn His Asn Ile Ile Met Ile Ser Ser Ile Lys Thr Leu Val Leu
225         230         235         240
Asn Phe Val Asn Tyr Thr Leu Leu Asn Met Asn Leu Lys Leu Tyr Leu
245         250         255
Gln Phe Phe Phe Tyr Gly Met Ser Ile Ser Gln Ser Ser
260         265

```

&lt;210&gt; 1482

<211> 311  
 <212> PRT  
 <213> Unknown (H38g399 protein)

<220>  
 <223> Synthetic construct

<400> 1482  
 Met Lys Ile Phe Asn Ser Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe  
 1 5 10 15  
 Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Phe  
 20 25 30  
 Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser  
 35 40 45  
 Ile Ile Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr  
 50 55 60  
 Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser  
 65 70 75 80  
 Thr Val Pro Ser Met Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile  
 85 90 95  
 Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly  
 100 105 110  
 Ser Thr Glu Cys Phe Phe Leu Ala Val Met Ala Phe Asp Arg Tyr Leu  
 115 120 125  
 Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu  
 130 135 140  
 Cys Thr Asn Leu Val Val Asn Cys Trp Val Leu Gly Phe Ile Trp Phe  
 145 150 155 160  
 Leu Ile Pro Ile Val Asn Ile Ser Gln Met Ser Phe Cys Gly Ser Arg  
 165 170 175  
 Ile Ile Asp His Phe Leu Cys Asp Pro Ala Pro Leu Leu Thr Leu Thr  
 180 185 190  
 Cys Lys Lys Gly Pro Val Ile Glu Leu Val Phe Ser Val Leu Ser Pro  
 195 200 205  
 Leu Pro Val Phe Met Leu Phe Leu Phe Ile Val Gly Ser Tyr Ala Leu  
 210 215 220  
 Val Val Arg Ala Val Leu Arg Val Pro Ser Ala Ala Gly Arg Arg Lys  
 225 230 235 240  
 Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr  
 245 250 255  
 Gly Ser Val Leu Val Met Tyr Gly Ser Pro Pro Ser Lys Asn Glu Ala  
 260 265 270  
 Gly Lys Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu  
 275 280 285  
 Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Asp Met Arg Lys Ala  
 290 295 300  
 Leu Lys Lys Phe Trp Gly Thr  
 305 310

<210> 1483  
 <211> 326  
 <212> PRT  
 <213> Unknown (H38g400 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(326)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1483

```

Thr Ala Leu Glu Phe Thr Asn Asn Ser Glu Thr Ser Thr Met Thr Glu
1      5      10
Phe Val Leu Leu Gly Phe Pro Gly Cys Gln Glu Met Gln Ser Phe Leu
20      25      30
Phe Ser Leu Phe Phe Val Ile Tyr Val Phe Thr Ile Ile Gly Asn Gly
35      40      45
Thr Ile Val Cys Ala Val Arg Leu Asp Lys Arg Leu His Thr Pro Met
50      55      60
Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu Glu Ile Arg Xaa Val Thr
65      70      75      80
Ser Thr Val Pro Asn Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr
85      90      95
Ile Ser Phe Val Gly Cys Phe Leu Gln Phe Tyr Phe Phe Thr Ser Leu
100     105     110
Gly Thr Ile Glu Ala Tyr Phe Leu Cys Ile Met Ala Tyr Asp Arg Tyr
115     120     125
Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Ile Met Thr Pro Gln
130     135     140
Leu Cys Tyr Ile Leu Met Ser Phe Cys Trp Val Phe Gly Phe Leu Ser
145     150     155     160
Tyr Ser Val Ser Thr Val Gln Leu Ser Gln Leu Pro Phe Cys Gly Pro
165     170     175
Asn Ile Ile Asn His Phe Leu Cys Asp Met Asp Pro Leu Met Ala Leu
180     185     190
Ser Cys Ala Ser Ala Pro Ile Thr Glu Ile Ile Phe Tyr Ile Leu Ser
195     200     205
Ser Leu Ile Ile Ile Leu Thr Leu Leu Tyr Ile Cys Gly Ser Tyr Met
210     215     220
Leu Leu Leu Ile Ala Val Leu Lys Val Pro Ser Ala Ala Gly Gln Gln
225     230     235     240
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe
245     250     255
Phe Gly Ala Leu Leu Ala Met Tyr Val Ser Pro Thr Thr Asp Asn Pro
260     265     270
Ala Ala Ile Xaa Lys Ile Ile Thr Leu Phe Tyr Ser Val Val Thr Pro
275     280     285
Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Ala
290     295     300
Ala Leu Lys Lys Val Leu Arg Ile Glu Xaa Glu Xaa Ser His Leu His
305     310     315     320
Glu Thr Lys Gln Thr Ile
325

```

&lt;210&gt; 1484

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g401 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1484

```

Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly
1      5      10      15
Phe Pro Gln Leu Gln Asp Gly Ser Leu Leu Tyr Phe Phe Pro Leu Leu
20      25      30
Phe Ile Tyr Thr Phe Ile Ile Ile Asp Asn Leu Leu Ile Phe Ser Ala
35      40      45
Val Arg Leu Asp Thr His Leu His Asn Pro Met Tyr Asn Phe Ile Ser
50      55      60

```

Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ser Asn Leu Ile Ser Glu Lys Lys Ala Ile Ser Met Thr Gly  
 85 90 95  
 Cys Ile Leu Gln Met Tyr Phe Phe His Ser Leu Glu Asn Ser Glu Gly  
 100 105 110  
 Ile Leu Leu Thr Thr Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Gln Met Ile Met Thr Pro Arg Leu Cys Ala Gln Leu  
 130 135 140  
 Ser Ala Gly Ser Cys Leu Phe Gly Phe Leu Ile Leu Leu Pro Glu Ile  
 145 150 155 160  
 Val Met Ile Ser Thr Leu Pro Phe Cys Gly Pro Asn Gln Ile His Gln  
 165 170 175  
 Ile Phe Cys Asp Leu Val Pro Val Leu Ser Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Met Ile Leu Ile Glu Asp Val Ile His Ala Val Thr Ile Ile Ile  
 195 200 205  
 Thr Phe Leu Ile Ile Ala Leu Ser Tyr Val Arg Ile Val Thr Val Ile  
 210 215 220  
 Leu Arg Ile Pro Ser Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ala Gly His Leu Met Val Phe Leu Ile Phe Phe Gly Ser Val Ser Leu  
 245 250 255  
 Met Tyr Leu Arg Phe Ser Asp Thr Tyr Pro Pro Val Leu Asp Thr Ala  
 260 265 270  
 Ile Ala Leu Met Phe Thr Val Leu Ala Pro Phe Phe Asn Pro Ile Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met Asn Asn Ala Ile Lys Lys Leu Phe  
 290 295 300  
 Cys Leu Gln Lys Val Leu Asn Lys Pro Gly Gly  
 305 310 315

&lt;210&gt; 1485

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g402 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1485

Met His Phe Val Thr Glu Phe Val Leu Leu Gly Phe His Gly Gln Arg  
 1 5 10 15  
 Glu Met Gln Ser Cys Phe Phe Ser Phe Ile Leu Val Leu Tyr Leu Leu  
 20 25 30  
 Thr Leu Leu Gly Asn Gly Ala Ile Val Cys Ala Val Lys Leu Asp Arg  
 35 40 45  
 Arg Leu His Thr Pro Met Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu  
 50 55 60  
 Glu Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn Ile  
 65 70 75 80  
 Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe  
 85 90 95  
 Tyr Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser Val  
 100 105 110  
 Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro  
 115 120 125  
 Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys Trp  
 130 135 140  
 Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser Gln

```

145          150          155          160
Leu Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp Pro
          165          170          175
Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu Leu
          180          185          190
Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu Ser
          195          200          205
Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile Pro
          210          215          220
Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
225          230          235          240
Met Val Val Ser Leu Phe Tyr Gly Thr Leu Met Val Met Tyr Val Ser
          245          250          255
Pro Thr Ser Gly Asn Pro Ala Gly Met Gln Lys Ile Ile Thr Leu Val
          260          265          270
Tyr Thr Ala Met Thr Pro Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          275          280          285
Asn Lys Asp Met Lys Asp Ala Leu Lys Arg Val Leu Gly Leu Thr Val
          290          295          300
Ser Gln Asn
305

```

&lt;210&gt; 1486

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g403 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1486

```

Met Tyr Asn Phe Ile Ser Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr
 1          5          10          15
Thr Ala Thr Ile Pro Lys Met Leu Ser Ile Leu Ile Ser Arg Gln Arg
          20          25          30
Thr Ile Ser Met Val Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser
          35          40          45
Leu Gly Asn Ser Glu Gly Ile Leu Leu Thr Thr Met Ala Ile Asp Arg
          50          55          60
Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Thr Pro
65          70          75          80
Gly Leu Cys Val Gln Leu Ser Val Gly Ser Cys Ile Phe Gly Phe Leu
          85          90          95
Val Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly
          100          105          110
Pro Asn Gln Ile His Gln Ile Phe Cys Asp Phe Glu Pro Val Leu Arg
          115          120          125
Leu Ala Cys Thr Asp Thr Ser Met Ile Leu Ile Glu Asp Val Ile His
          130          135          140
Ala Val Ala Ile Val Phe Ser Val Leu Ile Ile Ala Leu Ser Tyr Ile
145          150          155          160
Arg Ile Ile Thr Val Ile Leu Arg Ile Pro Ser Val Glu Gly Arg Gln
          165          170          175
Lys Ala Phe Ser Thr Cys Ala Ala His Leu Ser Val Phe Leu Met Phe
          180          185          190
Tyr Gly Ser Val Ser Leu Met Tyr Leu Arg Phe Ser Ala Thr Phe Pro
          195          200          205
Pro Ile Leu Asp Thr Ala Val Ala Leu Met Phe Ala Val Leu Ala Pro
          210          215          220
Phe Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Ile
225          230          235          240

```

Ala Ile Lys Lys Leu Phe Cys Pro Gln Lys Met Val Asn Leu Ser Val  
 245 250 255

<210> 1487

<211> 320

<212> PRT

<213> Unknown (H38g404 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1487

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Gly | Ser | Met | Asn | Asn | Ser | Gln | Ile | Ser | Thr | Val | Thr | Gln | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Leu | Gly | Phe | Pro | Gly | Pro | Trp | Lys | Ile | Gln | Ile | Ile | Phe | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Met | Ile | Leu | Leu | Val | Tyr | Ile | Phe | Thr | Leu | Thr | Gly | Asn | Met | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ile | Cys | Ala | Val | Arg | Trp | Asp | His | Arg | Leu | His | Thr | Pro | Met | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Leu | Ala | Asn | Phe | Ser | Phe | Leu | Glu | Ile | Trp | Tyr | Val | Thr | Cys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Val | Pro | Asn | Met | Leu | Val | Asn | Phe | Phe | Ser | Lys | Thr | Lys | Thr | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Phe | Ser | Gly | Cys | Phe | Thr | Gln | Phe | His | Phe | Phe | Phe | Ser | Leu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Thr | Thr | Glu | Cys | Phe | Phe | Leu | Cys | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ile | Cys | His | Pro | Leu | His | Tyr | Pro | Ser | Ile | Met | Thr | Gly | Gln | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Gly | Ile | Leu | Val | Ser | Leu | Cys | Trp | Leu | Ile | Gly | Phe | Leu | Gly | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ile | Ser | Ile | Phe | Phe | Ile | Phe | Gln | Leu | Pro | Phe | Cys | Gly | Pro | Asn |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ile | Asp | His | Phe | Leu | Cys | Asp | Val | Asp | Pro | Leu | Met | Ala | Leu | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ala | Pro | Thr | His | Ile | Ile | Gly | His | Val | Phe | His | Ser | Val | Ser | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Phe | Ile | Asn | Leu | Thr | Met | Val | Tyr | Ile | Leu | Gly | Ser | Tyr | Thr | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Leu | Arg | Thr | Val | Leu | Xaa | Val | Pro | Ser | Ser | Ala | Gly | Trp | Gln | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Ile | Ser | Thr | Cys | Gly | Ser | His | Leu | Val | Val | Val | Ser | Leu | Phe | Tyr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Ala | Ile | Met | Leu | Met | Tyr | Val | Ser | Pro | Thr | Pro | Gly | Asn | Ser | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Met | His | Lys | Leu | Ile | Thr | Leu | Ile | Tyr | Ser | Val | Val | Thr | Pro | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Asn | Pro | Leu | Ile | Tyr | Ser | Leu | Arg | Asn | Lys | Asp | Met | Lys | Tyr | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | His | His | Val | Phe | Cys | Gly | Met | Arg | Ile | Ile | Gln | Arg | Ser | Xaa | Ile |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |

<210> 1488

<211> 319

<212> PRT

<213> Unknown (H38g405 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1488

```

Met Asp Pro Glu Asn Gln Thr Met Val Thr Glu Phe Tyr Phe Ser Asp
 1           5           10           15
Phe Pro Gln Ser Lys Asn Gly Ser Leu Leu Phe Phe Ile Pro Met Leu
          20           25           30
Phe Ile Tyr Ile Phe Ile Leu Val Gly Asn Phe Met Ile Phe Phe Ala
          35           40           45
Val Gln Pro Asp Pro His Leu His Asn Pro Met Tyr Ser Phe Ile Ser
          50           55           60
Val Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Val Thr Ile Pro Lys
65           70           75           80
Met Leu Ser Asn Leu Leu Ser Glu Gln Lys Thr Ile Ser Phe Ile Gly
          85           90           95
Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly Val Thr Glu Ala
          100          105          110
Leu Val Leu Thr Val Met Ala Ile Asp Arg Cys Val Ala Ile Cys Asn
          115          120          125
Pro Leu Arg Tyr Ala Ile Thr Met Ser Pro Xaa Leu Cys Ile Gln Leu
          130          135          140
Ser Thr Gly Ser Cys Ile Phe Gly Phe Leu Met Leu Leu Pro Glu Ile
145          150          155          160
Val Cys Ile Ser Thr Leu Pro Phe Cys Gly Ala Asn Gln Ile His Gln
          165          170          175
Leu Phe Cys Asp Phe Glu Pro Val Leu Gln Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Ile Ile Leu Val Glu Asp Val Ile Arg Ala Ile Ser Ile Leu Thr
          195          200          205
Ser Val Ser Val Ile Thr Leu Phe Tyr Leu Arg Ile Ile Thr Val Ile
          210          215          220
Leu Arg Ile Pro Ser Gly Glu Ser Arg Gln Lys Ala Phe Phe Thr Cys
225          230          235          240
Ala Ala His Ile Ala Ile Phe Leu Leu Phe Phe Gly Ser Val Ser Leu
          245          250          255
Met Tyr Leu Arg Phe Ser Val Thr Phe Pro Pro Leu Leu Asp Lys Ala
          260          265          270
Ile Ala Leu Met Phe Ala Val Leu Ala Leu Leu Phe Asn Pro Val Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Asn Ala Thr Lys Lys Ile Leu
          290          295          300
Cys Ser Gln Lys Met Phe Asn Ala Ser Gly Ser Xaa Trp Ser Ser
305          310          315

```

&lt;210&gt; 1489

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g406 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1489

```

Met Thr Gln Leu Thr Ala Ser Gly Asn Gln Thr Met Val Thr Glu Phe
 1           5           10           15

```



Leu Phe Ser Met Phe Pro His Ala His Arg Gly Gly Leu Leu Phe Phe  
 20 25 30  
 Ile Pro Leu Leu Leu Ile Tyr Gly Phe Ile Leu Thr Gly Asn Leu Ile  
 35 40 45  
 Met Phe Ile Val Ile Gln Val Gly Met Ala Leu His Thr Pro Leu Tyr  
 50 55 60  
 Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Cys Tyr Thr Thr Thr  
 65 70 75 80  
 Thr Ile Pro Lys Met Leu Ser Cys Leu Ile Ser Glu Gln Lys Ser Ile  
 85 90 95  
 Ser Val Ala Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly  
 100 105 110  
 Ile Thr Glu Ser Cys Val Leu Thr Ala Met Ala Ile Asp Arg Tyr Ile  
 115 120 125  
 Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Ile Pro Lys Leu  
 130 135 140  
 Cys Ile Gln Leu Thr Val Gly Ser Cys Phe Cys Gly Phe Leu Leu Val  
 145 150 155 160  
 Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn  
 165 170 175  
 Gln Ile His Gln Ile Phe Cys Asp Phe Thr Pro Val Leu Ser Leu Ala  
 180 185 190  
 Cys Thr Asp Thr Phe Leu Val Val Ile Val Asp Ala Ile His Ala Ala  
 195 200 205  
 Glu Ile Val Ala Ser Phe Leu Val Ile Ala Leu Ser Tyr Ile Arg Ile  
 210 215 220  
 Ile Ile Val Ile Leu Gly Met His Ser Ala Glu Gly His His Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Ala Ala His Leu Ala Val Phe Leu Leu Phe Phe Gly  
 245 250 255  
 Ser Val Ala Val Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Val Phe  
 260 265 270  
 Trp Asp Thr Ala Ile Ala Val Thr Phe Val Ile Leu Ala Pro Phe Phe  
 275 280 285  
 Asn Pro Ile Ile Tyr Ser Leu Lys Asn Lys Asp Met Lys Glu Ala Ile  
 290 295 300  
 Gly Arg Leu Phe His Tyr Gln Lys Arg Ala Gly Trp Ala  
 305 310 315

&lt;210&gt; 1490

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g407 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1490

Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu Asp  
 1 5 10 15  
 Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu  
 20 25 30  
 Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser Asp  
 35 40 45  
 Phe Leu Ser Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile Gln  
 50 55 60  
 Ser Phe Phe Phe Ser Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu Ala  
 65 70 75 80  
 Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro Leu His Tyr  
 85 90 95  
 Pro Ile Arg Met Ser Lys Arg Met Cys Val Leu Met Ile Thr Gly Ser

```

      100      105      110
Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val Tyr Val Leu
      115      120      125
His Ile Pro Tyr Cys Gln Ser Arg Ala Ile Asn His Phe Phe Cys Asp
      130      135      140
Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp Val Tyr Glu
      145      150      155      160
Gly Thr Val Phe Leu Ser Thr Thr Ile Phe Leu Val Phe Pro Phe Ile
      165      170      175
Ala Ile Ser Cys Ser Tyr Gly Arg Val Leu Leu Ala Val Tyr His Met
      180      185      190
Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys Ser Thr His
      195      200      205
Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr Thr Tyr Leu
      210      215      220
Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val Leu Ala Val
      225      230      235      240
Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu
      245      250      255
Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg Ile
      260      265      270
Cys Ser Val Lys Met
      275

```

&lt;210&gt; 1491

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g408 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(241)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1491

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
  1      5      10      15
Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
      20      25      30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
      35      40      45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
      50      55      60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
      65      70      75      80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
      85      90      95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
      100      105      110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
      115      120      125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
      130      135      140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
      145      150      155      160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
      165      170      175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
      180      185      190

```

Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu  
 195 200 205  
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser  
 210 215 220  
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val  
 225 230 235 240  
 Gly

&lt;210&gt; 1492

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g409 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1492

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly  
 1 5 10 15  
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu  
 20 25 30  
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val  
 35 40 45  
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser  
 50 55 60  
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys  
 100 105 110  
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile  
 130 135 140  
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile  
 145 150 155 160  
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His  
 165 170 175  
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu  
 195 200 205  
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr  
 210 215 220  
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu  
 245 250 255  
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln  
 260 265 270  
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln  
 290 295 300  
 Leu Lys Arg Ile Gly Ile Leu Ala  
 305 310

&lt;210&gt; 1493

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g410 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1493

```

Glu Phe Leu Phe Tyr Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu
 1           5           10           15
Leu Gly Leu Phe Pro Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu
          20           25           30
Ile Phe Leu Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile
      35           40           45
Leu Leu Ile Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu
      50           55           60
Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val
      65           70           75           80
Pro Lys Met Val Tyr Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe
          85           90           95
Thr Gly Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala
          100          105          110
Glu Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val
          130          135          140
Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala
          145          150          155          160
His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile
          165          170          175
Asn His Phe Phe Cys Glu Gly Ser Ser Glu Arg Tyr Leu Gly Cys Met
          180          185          190
Gln Ala Trp Arg Trp Ala Ala Val Glu Thr Ala Xaa Leu Val Lys Pro
          195          200          205
Trp Ala Gly Pro
          210

```

&lt;210&gt; 1494

&lt;211&gt; 263

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g411 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1494

```

Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Gln Glu Val Cys Arg Ile Leu Phe Ala Thr Phe Phe Leu
          20           25           30
Leu Tyr Ala Val Thr Val Met Gly Asn Val Val Ile Ile Thr Val
          35           40           45
Cys Val Asp Lys Cys Leu Gln Ser Pro Ile Tyr Phe Phe Leu Gly His
          50           55           60
Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Val Pro Phe Met
          65           70           75           80
Leu Trp Gly Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala
          85           90           95

```

Cys Ala Ala Gln Leu Tyr Leu Tyr Leu Ser Leu Gly Thr Leu Glu Leu  
 100 105 110  
 Ala Leu Met Gly Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Phe Ile Trp Val  
 130 135 140  
 Ile Ile Val Ser Trp Val Leu Gly Phe Leu Ser Glu Ile Trp Pro Val  
 145 150 155 160  
 Tyr Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Ser Val Leu Asp His  
 165 170 175  
 Phe Tyr Cys Asp Arg Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr  
 180 185 190  
 Leu Phe Arg Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile  
 195 200 205  
 Gly Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr  
 210 215 220  
 Asn Leu Lys Ile Pro Ser Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Phe Thr Tyr Val Val Ile Gly Tyr Gly Ser Cys Leu  
 245 250 255  
 Phe Leu Tyr Val Lys Pro Lys  
 260

&lt;210&gt; 1495

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g412 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1495

Met Asp Gln Tyr Asn His Ser Ser Leu Ala Glu Phe Val Phe Leu Gly  
 1 5 10 15  
 Phe Ala Ser Val Gly Tyr Val Arg Gly Trp Leu Phe Val Leu Leu Leu  
 20 25 30  
 Leu Ala Tyr Leu Phe Thr Ile Cys Gly Asn Met Leu Ile Phe Ser Val  
 35 40 45  
 Ile Arg Leu Asp Ala Ala Leu His Thr Pro Met Tyr His Phe Val Ser  
 50 55 60  
 Val Leu Ser Phe Leu Glu Leu Trp Tyr Thr Ala Thr Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ser Asn Ile Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly  
 85 90 95  
 Cys Leu Leu Gln Thr Tyr Phe Phe His Ser Leu Gly Ala Ser Glu Cys  
 100 105 110  
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Ile Ile Met Thr Thr Thr Leu Cys Ala Lys Met  
 130 135 140  
 Ala Ala Ala Cys Trp Thr Cys Gly Phe Leu Cys Pro Ile Ser Glu Val  
 145 150 155 160  
 Ile Leu Ala Ser Gln Leu Pro Phe Cys Ala Tyr Asn Glu Ile Gln His  
 165 170 175  
 Ile Phe Cys Asp Phe Pro Pro Leu Leu Ser Leu Ala Cys Lys Asp Thr  
 180 185 190  
 Ser Ala Asn Ile Leu Val Asp Phe Ala Ile Asn Ala Phe Ile Ile Leu  
 195 200 205  
 Ile Thr Phe Phe Phe Ile Met Ile Ser Tyr Ala Arg Ile Ile Gly Ala  
 210 215 220  
 Val Leu Lys Ile Lys Thr Ala Ser Gly Arg Lys Lys Ala Phe Ser Thr

225                      230                      235                      240  
 Cys Ala Ser His Leu Ala Val Val Leu Ile Phe Phe Gly Ser Ile Ile  
                                  245                      250                      255  
 Phe Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Thr Leu Asp Arg  
                                  260                      265                      270  
 Thr Leu Ala Ile Val Tyr Ser Val Leu Thr Pro Met Val Asn Pro Ile  
                                  275                      280                      285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Ile Ile Lys Ala Ile Lys Arg Thr  
                                  290                      295                      300  
 Ile Phe Gln Lys Gly Asp Lys Ala Ser Leu Ala His Leu  
 305                      310                      315

&lt;210&gt; 1496

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g413 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1496

Met Gln Gly Leu Asn His Thr Ser Val Ser Glu Phe Ile Leu Val Gly  
 1                      5                      10                      15  
 Phe Ser Ala Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu  
                                  20                      25                      30  
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr  
                                  35                      40                      45  
 Val Trp Ser Glu Arg Ser Leu His Met Pro Met Tyr Leu Phe Leu Cys  
                                  50                      55                      60  
 Ala Leu Ser Ile Thr Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg  
 65                      70                      75                      80  
 Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala  
                                  85                      90                      95  
 Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser  
                                  100                      105                      110  
 Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His  
                                  115                      120                      125  
 Pro Leu Arg Tyr Asn Val Leu Met Ser Leu Arg Gly Cys Thr Cys Arg  
                                  130                      135                      140  
 Val Gly Cys Ser Trp Ala Gly Gly Leu Val Met Gly Met Val Val Thr  
 145                      150                      155                      160  
 Ser Ala Ile Phe His Leu Ala Phe Cys Gly His Lys Glu Ile His His  
                                  165                      170                      175  
 Phe Phe Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asp Asp  
                                  180                      185                      190  
 Val Leu Val Val Ala Lys Gly Val Gly Leu Val Cys Ile Thr Ala Leu  
                                  195                      200                      205  
 Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala  
                                  210                      215                      220  
 Ala Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser  
 225                      230                      235                      240  
 Thr Cys Ala Ser His Leu Thr Val Val Val Val His Tyr Gly Phe Ala  
                                  245                      250                      255  
 Ser Val Ile Tyr Leu Lys Pro Lys Gly Pro Gln Ser Pro Glu Gly Asp  
                                  260                      265                      270  
 Thr Leu Met Gly Ile Thr Tyr Thr Val Leu Thr Pro Phe Leu Ser Pro  
                                  275                      280                      285  
 Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Lys  
                                  290                      295                      300  
 Thr Cys Phe Thr Lys Leu Phe Pro Gln Asn Cys  
 305                      310                      315

<210> 1497  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g414 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)  
 <223> Xaa = Any Amino Acid

<400> 1497  
 His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser  
 20 25 30  
 Pro Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Val Ile Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Pro Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
 65 70 75 80  
 Lys Met Thr Val Asp Met Gln Ser His Ile Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Ser Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu  
 100 105 110  
 Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe  
 130 135 140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Ser Xaa Ile Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser His  
 165 170 175  
 Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser  
 180 185 190  
 Val Ile Asn Ser Ile Phe Met Tyr Phe Asn Ser Thr Met Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser  
 210 215 220  
 Ile Leu Arg Ile Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg Asn Gly Val  
 260 265 270  
 Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu  
 290 295 300  
 Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser  
 305 310 315

<210> 1498  
 <211> 157  
 <212> PRT  
 <213> Unknown (H38g415 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1498

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Pro | Leu | Trp | Glu | Cys | Val | Ser | Xaa | Gln | Arg | Ser | Pro | His | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Cys | Ser | Gly | Asp | Ser | Val | Phe | Cys | Leu | Val | His | Ser | Val | Gly | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Thr | Leu | Leu | Leu | Ser | Gln | Ser | Leu | Arg | Leu | Leu | Ser | Val | Phe | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Ser | Cys | Ala | Ala | Ser | Trp | Lys | Lys | Val | His | Ser | Met | Asn | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Thr | Pro | Phe | Cys | Leu | Ser | Lys | Trp | Xaa | Asn | His | Val | Asn | Asn | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Phe | Asn | Leu | Pro | Ser | Trp | Lys | Lys | Ser | Lys | Ser | Val | Val | Thr | Met | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Xaa | Gly | Pro | Ala | Met | Ile | Thr | Tyr | Leu | Arg | Ser | Asp | Ser | Xaa | Tyr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Thr | Val | Gly | Lys | Gln | Leu | Val | Leu | Phe | Tyr | Ser | Ile | Val | Ser | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Ile | Lys | Pro | Ile | Ile | Ser | Ser | Leu | Arg | Asn | Lys | Asp | Val | Lys | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ser | Trp | Lys | Val | Leu | Arg | Val | Lys | Gly | Thr | Ala | Gln |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

<210> 1499

<211> 287

<212> PRT

<213> Unknown (H38g416 protein)

<220>

<223> Synthetic construct

<400> 1499

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Tyr | Asn | Gln | Thr | Ser | Thr | Asp | Phe | Ile | Leu | Leu | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Pro | Pro | Ser | Arg | Ile | Asp | Leu | Phe | Phe | Phe | Ile | Leu | Phe | Val | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Phe | Leu | Met | Ala | Leu | Ile | Gly | Asn | Leu | Ser | Met | Ile | Leu | Leu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Asp | Thr | His | Leu | His | Thr | Pro | Met | Tyr | Phe | Leu | Leu | Ser | Gln |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Ser | Leu | Ile | Asp | Leu | Asn | Tyr | Ile | Ser | Thr | Ile | Val | Pro | Lys | Met |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ser | Asp | Phe | Leu | Tyr | Gly | Asn | Lys | Ser | Ile | Ser | Phe | Ile | Gly | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ile | Gln | Ser | Phe | Phe | Phe | Met | Thr | Phe | Ala | Gly | Ala | Glu | Ala | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Thr | Ser | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | Phe | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | His | Tyr | Pro | Ile | Arg | Met | Ser | Lys | Arg | Met | Tyr | Val | Leu | Met | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Gly | Ser | Trp | Met | Ile | Gly | Ser | Ile | Asn | Ser | Cys | Ala | His | Thr | Val |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Tyr | Ala | Phe | Arg | Ile | Pro | Tyr | Cys | Lys | Ser | Arg | Ala | Ile | Asn | His | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Cys | Asp | Val | Pro | Ala | Met | Leu | Thr | Leu | Ala | Cys | Thr | Asp | Thr | Trp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |



Val Tyr Glu Tyr Thr Val Phe Leu Ser Ser Thr Ile Phe Leu Val Phe  
 195 200 205  
 Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Trp Val Leu Leu Ala Val  
 210 215 220  
 Tyr Arg Met His Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys  
 225 230 235 240  
 Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Leu Arg Tyr  
 245 250 255  
 Thr Tyr Leu Cys Pro Arg Ser Leu Phe Ile Ser Thr Glu Asp Lys Val  
 260 265 270  
 Gly Gly Gly Gly Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile  
 275 280 285

&lt;210&gt; 1500

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g417 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1500

Met Asp Lys Glu Asn Ser Ser Met Val Thr Glu Phe Ile Phe Met Gly  
 1 5 10 15  
 Ile Thr Gln Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu  
 20 25 30  
 Ile Val Tyr Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu  
 35 40 45  
 Ile Thr Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys  
 50 55 60  
 Asn Leu Ser Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg  
 65 70 75 80  
 Met Leu Ala Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser  
 85 90 95  
 Cys Ala Thr Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys  
 100 105 110  
 Tyr Val Leu Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu  
 130 135 140  
 Met Leu Gly Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr  
 145 150 155 160  
 Thr Leu Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Ile Ile Asn His  
 165 170 175  
 Phe Phe Cys Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr  
 180 185 190  
 Tyr Ile Ser Glu Ile Leu Leu Phe Ser Leu Cys Gly Phe Ile Glu Phe  
 195 200 205  
 Ser Thr Ile Leu Ile Ile Phe Ile Ser Tyr Thr Phe Ile Leu Val Ala  
 210 215 220  
 Ile Ile Arg Met Arg Ser Ala Glu Gly Arg Leu Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Gly Ile Thr Leu Phe Tyr Gly Thr Val Met  
 245 250 255  
 Phe Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Leu Asp Gln Asp Lys  
 260 265 270  
 Trp Ala Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Lys Lys Leu  
 290 295 300  
 Ile Gly Lys Lys Ser Gln

305

310

&lt;210&gt; 1501

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g418 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1501

```

Ser Thr Asp Pro Gln Asn Leu Ile Asp Val Ser Ile Phe Leu Leu Leu
 1      5      10      15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
      65      70      75      80
Lys Met Ile Val Asp Ile Arg Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Thr Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100     105     110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
      115     120     125
Cys His Pro Leu Tyr His Ser Ala Val Met Asn Pro Cys Phe Cys Gly
      130     135     140
Phe Leu Val Leu Leu Thr Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
      145     150     155     160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
      165     170     175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Pro Leu Pro His Leu Ala Cys
      180     185     190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
      195     200     205
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
      210     215     220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
      225     230     235     240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
      245     250     255
Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
      260     265     270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
      275     280     285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu
      290     295     300
Arg Trp Leu His Gly Ser Ser Val Xaa Ser Gln His Leu Leu Ile Cys
      305     310     315     320
Cys Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Arg Val Lys
      325     330     335

```

&lt;210&gt; 1502

&lt;211&gt; 303

&lt;212&gt; PRT

<213> Unknown (H38g419 protein)

<220>

<223> Synthetic construct

<400> 1502

```

Met Asp His Val Ser His Asn Trp Thr Gln Ser Phe Ile Leu Ala Gly
 1           5           10          15
Phe Thr Thr Thr Gly Thr Leu Gln Pro Leu Ala Phe Leu Gly Thr Leu
      20           25          30
Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Ile Leu Ile Ile Val Leu
      35           40          45
Val Gln Leu Asp Ser Gly Leu Phe Thr Pro Met Tyr Leu Phe Ile Ser
      50           55          60
Val Leu Ser Phe Val Glu Val Trp Tyr Val Ser Thr Thr Val Pro Met
      65           70          75          80
Leu Leu His Thr Leu Leu Gln Gly Cys Ser Pro Val Ser Ser Ala Val
      85           90          95
Cys Phe Ile Gln Thr Met Phe Phe His Ser Leu Gly Met Thr Glu Cys
      100          105         110
Tyr Leu Leu Gly Val Met Ala Leu Asp Ser Tyr Leu Ile Ile Cys His
      115          120         125
Pro Leu His Tyr His Ala Leu Met Ser Arg Gln Val Gln Leu Arg Leu
      130          135         140
Ala Gly Ala Ser Trp Val Ala Gly Phe Ser Ala Ala Leu Val Pro Ala
      145          150         155         160
Thr Leu Thr Ala Thr Leu Pro Phe Cys Leu Lys Glu Val Ala His Tyr
      165          170         175
Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala Cys Val Asp Thr Ser
      180          185         190
Trp His Ala Arg Ala His Gly Thr Val Ile Gly Val Ala Thr Gly Cys
      195          200         205
Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly Ile Leu Asn Ala Val
      210          215         220
Leu Lys Leu Pro Ser Ala Ala Ser Ser Ala Lys Ala Phe Ser Thr Cys
      225          230         235         240
Ser Ser His Val Thr Val Val Ala Leu Phe Tyr Ala Ser Ala Phe Thr
      245          250         255
Val Tyr Val Gly Ser Pro Gly Ser Arg Pro Glu Ser Thr Asp Lys Leu
      260          265         270
Val Ala Leu Val Tyr Ala Leu Ile Thr Pro Phe Leu Asn Pro Ile Ile
      275          280         285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Arg Arg Val
      290          295         300

```

<210> 1503

<211> 336

<212> PRT

<213> Unknown (H38g420 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1503

```

Pro Thr Lys Arg Glu Asn His Thr Val Ile Arg Glu Phe Val Phe Gln
 1           5           10          15
Gly Phe Ser Ser Phe His Glu His Lys Leu Thr Leu Phe Val Val Phe

```

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 1504 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met        | Ser | Ile | Thr | Lys | Ala | Trp | Asn | Ser | Ser | Ser | Val | Thr | Met | Phe | Ile |
| 1          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu        | Leu | Gly | Phe | Thr | Asp | His | Pro | Glu | Leu | Gln | Ala | Leu | Leu | Phe | Val |
|            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr        | Phe | Leu | Gly | Ile | Tyr | Leu | Thr | Leu | Ala | Trp | Asn | Leu | Ala | Leu |     |
|            |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ile        | Phe | Leu | Ile | Arg | Gly | Asp | Thr | His | Leu | His | Thr | Pro | Met | Tyr | Phe |
|            | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Phe        | Leu | Ser | Asn | Leu | Ser | Phe | Ile | Asp | Ile | Cys | Tyr | Ser | Ser | Ala | Val |
| 65         |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala        | Pro | Asn | Met | Leu | Thr | Asp | Phe | Phe | Trp | Glu | Gln | Lys | Thr | Ile | Ser |
|            |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Phe Val Gly Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu  
 100 105 110  
 Ser Glu Cys Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala  
 115 120 125  
 Ile Ser Ser Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys  
 130 135 140  
 Thr Arg Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu  
 145 150 155 160  
 Ile Gln Ala Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile  
 165 170 175  
 Ile Asn His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys  
 180 185 190  
 Ser Asp Thr Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr  
 195 200 205  
 Val Gly Gly Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile  
 210 215 220  
 Val Ser Ala Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala  
 225 230 235 240  
 Cys Asn Thr Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly  
 245 250 255  
 Thr Ala Leu Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly  
 260 265 270  
 Arg Asp Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu  
 275 280 285  
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu  
 290 295 300  
 Trp Lys Val Leu Glu Arg Lys Lys Val Phe Ser  
 305 310 315

&lt;210&gt; 1505

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g422 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1505

Met Pro Xaa Lys Met Glu Ser Ile Asn Thr Asn Phe Thr Val Thr Glu  
 1 5 10 15  
 Phe Val Phe Leu Gly Leu Ser Ser Glu Pro Lys Ile Gln Leu Ile Leu  
 20 25 30  
 Phe Ile Met Phe Leu Phe Tyr Leu Ser Thr Val Ala Gly Asn Val Ile  
 35 40 45  
 Ile Ile Thr Ile Ile Xaa Met Glu Pro Leu Leu Gln Thr Pro Met Tyr  
 50 55 60  
 Phe Phe Leu Thr Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Thr  
 65 70 75 80  
 Asn Val Pro Gln Met Leu Ser Asn Met Ala Gly Lys Lys Asn Thr Ile  
 85 90 95  
 Ser Phe Ser Ser Cys Ala Thr Gln Met Tyr Phe Ser Leu Ser Phe Gly  
 100 105 110  
 Ser Asp Cys Val Leu Leu Gly Val Met Ala Tyr Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn Thr Cys  
 130 135 140  
 Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Ser Ser Met

```

145          150          155          160
Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro Asn Ile
          165          170          175
Leu Asn His Phe Phe Cys Glu Val Leu Ser Val Leu Arg Leu Ala Cys
          180          185          190
Thr Asn Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser Ile Ile
          195          200          205
Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg Ile
          210          215          220
Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr Gln Ala
225          230          235          240
Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly
          245          250          255
Thr Ala Ile Phe Met Asp Met Arg Pro Gln Ser Arg Ser Ser Trp Ala
          260          265          270
Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Val Lys Gly Ala Arg
          290          295          300
Arg Arg Ala Ile Ala Lys Gln Arg Met Xaa Gln Leu Leu
305          310          315

```

&lt;210&gt; 1506

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g423 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(340)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1506

```

Met Pro Lys Leu Asn Ser Thr Phe Val Thr Glu Phe Leu Phe Glu Gly
1          5          10          15
Phe Ser Ser Phe Arg Arg Gln His Lys Leu Val Phe Phe Val Val Phe
          20          25          30
Leu Thr Leu Tyr Leu Leu Thr Leu Ser Gly Asn Val Ile Ile Met Thr
          35          40          45
Ile Ile Arg Leu Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Cys Met Leu Ser Ile Ser Glu Thr Cys Tyr Thr Val Ala Ile Ile Pro
65          70          75          80
His Met Leu Ser Gly Leu Leu Asn Pro His Gln Pro Ile Ala Thr Gln
          85          90          95
Ser Cys Ala Thr Gln Leu Phe Phe Tyr Leu Thr Phe Gly Ile Asn Asn
          100          105          110
Cys Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Asn Pro Leu Arg Tyr Ser Val Ile Met Gly Lys Arg Ala Cys Ile Gln
          130          135          140
Leu Ala Ser Gly Ser Leu Gly Ile Gly Leu Gly Met Ala Ile Val Gln
145          150          155          160
Val Thr Ser Val Phe Gly Leu Pro Phe Cys Asp Ala Phe Val Ile Ser
          165          170          175
His Phe Phe Cys Asp Val Arg His Leu Leu Lys Leu Ala Cys Thr Asp
          180          185          190
Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val Cys Val Leu
          195          200          205

```

Val Leu Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser  
 210 215 220  
 Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Gln Lys Lys Ala Phe Ala  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala  
 245 250 255  
 Ser Ile Ile Tyr Leu Lys Pro Lys Ser Gln Ser Ser Leu Gly Gln Asp  
 260 265 270  
 Arg Leu Ile Ser Val Thr Tyr Thr Ile Thr Pro Leu Leu Asn Pro Val  
 275 280 285  
 Val Tyr Ser Leu Lys Asn Lys Glu Val Lys Asp Ala Leu His Arg Ala  
 290 295 300  
 Val Gly Gln Lys Thr Leu Ser Pro Xaa Xaa Arg Glu Val Val Lys Ala  
 305 310 315 320  
 Phe Pro Phe Val Tyr Lys Tyr Val Leu Ile Phe Asn Ala Leu Ser Ile  
 325 330 335  
 Met Pro Leu Cys  
 340

&lt;210&gt; 1507

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g424 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1507

Met Asp Ile Gly Leu Ser Ile Ala Asn Ser Ser Gly Phe Gln Leu Ser  
 1 5 10 15  
 Glu Phe Ile Leu Ile Gly Phe Pro Gly Ile His Glu Trp Gln His Trp  
 20 25 30  
 Leu Ser Leu Pro Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile Ile Thr  
 35 40 45  
 Ile Gln His Glu Thr Met Leu His Glu Pro Met Tyr His Leu Leu Gly  
 50 55 60  
 Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met Pro Lys  
 65 70 75 80  
 Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu Pro Glu  
 85 90 95  
 Cys Phe Ala Gln Ile Tyr Ala Ile His Ser Phe Met Cys Met Glu Ser  
 100 105 110  
 Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Met Ala Ile Cys Tyr  
 115 120 125  
 Pro Leu Gln Tyr Thr Ser Ile Val Thr Glu Ala Phe Val Ile Lys Ala  
 130 135 140  
 Thr Leu Ser Val Val Leu Arg Asn Gly Leu Leu Thr Ile Pro Val Pro  
 145 150 155 160  
 Val Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile Asp Gln  
 165 170 175  
 Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp Thr  
 180 185 190  
 Thr Ile Asn Arg Phe Tyr Gln Leu Ala Leu Val Trp Val Val Val Gly  
 195 200 205  
 Ser Asp Met Gly Leu Val Phe Ala Ser Tyr Ser Leu Ile Ile His Ser  
 210 215 220  
 Val Leu Lys Leu Asn Ser Ala Lys Ala Thr Ser Lys Ala Leu Asn Thr

225                      230                      235                      240  
 Cys Ser Ser His Leu Ile Leu Ile Leu Phe Phe Tyr Thr Ala Ile Ile  
                                  245                      250                      255  
 Val Val Ser Val Thr Asn Leu Ala Gly Arg Arg Ala Pro Arg Ile Pro  
                                  260                      265                      270  
 Val Leu Leu Asn Val Leu His Ile Val Ile Pro Ser Ala Leu Asn Pro  
                                  275                      280                      285  
 Ile Val Tyr Ala Leu Arg Thr Xaa Glu Leu Arg Ala Gly Phe Gln Lys  
                                  290                      295                      300  
 Leu Leu Gly Leu Gly Glu Tyr Val Ser  
 305                      310

<210> 1508

<211> 315

<212> PRT

<213> Unknown (H38g425 protein)

<220>

<223> Synthetic construct

<400> 1508

Met Phe Ser Pro Asn His Thr Ile Val Thr Glu Phe Ile Leu Leu Gly  
 1                      5                      10                      15  
 Leu Thr Asp Asp Pro Val Leu Glu Lys Ile Leu Phe Gly Val Phe Leu  
                                  20                      25                      30  
 Ala Ile Tyr Leu Ile Thr Leu Ala Gly Asn Leu Cys Met Ile Leu Leu  
                                  35                      40                      45  
 Ile Arg Thr Asn Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly  
                                  50                      55                      60  
 His Leu Ser Phe Val Asp Ile Cys Tyr Ser Ser Asn Val Thr Pro Asn  
 65                      70                      75                      80  
 Met Leu His Asn Phe Leu Ser Glu Gln Lys Thr Ile Ser Tyr Ala Gly  
                                  85                      90                      95  
 Cys Phe Thr Gln Cys Leu Leu Phe Ile Ala Leu Val Ile Thr Glu Phe  
                                  100                      105                      110  
 Tyr Ile Leu Ala Ser Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Ser  
                                  115                      120                      125  
 Pro Leu His Tyr Ser Ser Arg Met Ser Lys Asn Ile Cys Val Cys Leu  
                                  130                      135                      140  
 Val Thr Ile Pro Tyr Met Tyr Gly Phe Leu Ser Gly Phe Ser Gln Ser  
 145                      150                      155                      160  
 Leu Leu Thr Phe His Leu Ser Phe Cys Gly Ser Leu Glu Ile Asn His  
                                  165                      170                      175  
 Phe Tyr Cys Ala Asp Pro Pro Leu Ile Met Leu Ala Cys Ser Asp Thr  
                                  180                      185                      190  
 Arg Val Lys Lys Met Ala Met Phe Val Val Ala Gly Phe Asn Leu Ser  
                                  195                      200                      205  
 Ser Ser Leu Phe Ile Ile Leu Leu Ser Tyr Leu Phe Ile Phe Ala Ala  
                                  210                      215                      220  
 Ile Phe Arg Ile Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr  
 225                      230                      235                      240  
 Cys Ala Ser His Leu Thr Ile Val Thr Leu Phe Tyr Gly Thr Leu Phe  
                                  245                      250                      255  
 Cys Met Tyr Val Arg Pro Pro Ser Glu Lys Ser Val Glu Glu Ser Lys  
                                  260                      265                      270  
 Ile Thr Ala Val Phe Tyr Thr Phe Leu Ser Pro Met Leu Asn Pro Leu  
                                  275                      280                      285  
 Ile Tyr Ser Leu Arg Asn Thr Asp Val Ile Leu Ala Met Gln Gln Met  
                                  290                      295                      300  
 Ile Arg Gly Lys Ser Phe His Lys Ile Ala Val  
 305                      310                      315



<210> 1509  
 <211> 257  
 <212> PRT  
 <213> Unknown (H38g426 protein)

<220>  
 <223> Synthetic construct

<400> 1509  
 Met Phe Leu Leu Leu Ala Ile Leu Ala Ala Thr Asp Leu Gly Leu Ala  
 1 5 10 15  
 Thr Ser Ile Ala Pro Gly Leu Leu Ala Val Leu Trp Leu Gly Pro Arg  
 20 25 30  
 Ser Val Pro Tyr Ala Val Cys Leu Val Gln Met Phe Phe Val His Ala  
 35 40 45  
 Leu Thr Ala Met Glu Ser Gly Val Leu Leu Ala Met Ala Cys Asp Arg  
 50 55 60  
 Ala Ala Ala Ile Gly Arg Pro Leu His Tyr Pro Val Leu Val Thr Lys  
 65 70 75 80  
 Ala Cys Val Gly Tyr Ala Ala Leu Ala Leu Ala Leu Lys Ala Val Ala  
 85 90 95  
 Ile Val Val Pro Phe Pro Leu Leu Val Ala Lys Phe Glu His Phe Gln  
 100 105 110  
 Ala Lys Thr Ile Gly His Thr Tyr Cys Ala His Met Ala Val Val Glu  
 115 120 125  
 Leu Val Val Gly Asn Thr Gln Ala Thr Asn Leu Tyr Gly Leu Ala Leu  
 130 135 140  
 Ser Leu Ala Ile Ser Gly Met Asp Ile Leu Gly Ile Thr Gly Ser Tyr  
 145 150 155 160  
 Gly Leu Ile Ala His Ala Val Leu Gln Leu Pro Thr Arg Glu Ala His  
 165 170 175  
 Ala Lys Ala Phe Gly Thr Cys Ser Ser His Ile Cys Val Ile Leu Ala  
 180 185 190  
 Phe Tyr Ile Pro Gly Leu Phe Ser Tyr Leu Ala His Arg Phe Gly His  
 195 200 205  
 His Thr Val Pro Lys Pro Val His Ile Leu Leu Ser Asn Ile Tyr Leu  
 210 215 220  
 Leu Leu Pro Pro Ala Leu Asn Pro Leu Ile Tyr Gly Ala Arg Thr Lys  
 225 230 235 240  
 Gln Ile Arg Asp Arg Leu Leu Glu Thr Phe Thr Phe Arg Lys Ser Pro  
 245 250 255  
 Leu

<210> 1510  
 <211> 358  
 <212> PRT  
 <213> Unknown (H38g427 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(358)  
 <223> Xaa = Any Amino Acid

<400> 1510  
 Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro  
 1 5 10 15  
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala

<400> 1511  
Met Phe Gly Ala Asn Leu Thr Thr Phe His Pro Thr Leu Phe Ile Leu  
1 5 10 15  
Leu Gly Ile Pro Gly Leu Glu Gln Tyr His Ile Trp Leu Ser Ile Pro  
20 25 30

Phe Tyr Leu Met Tyr Ile Thr Ala Val Leu Gly Asn Gly Ala Leu Ile  
 35 40 45  
 Leu Val Val Leu Ser Glu His Thr Leu His Val Phe Leu Ser Met Leu  
 50 55 60  
 Ala Gly Thr Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys Ala Leu  
 65 70 75 80  
 Ala Ile Phe Trp Val His Ala Gly Glu Ile Ala Phe Asp Ala Cys Ile  
 85 90 95  
 Thr Gln Met Phe Phe Ile His Val Ala Phe Val Ala Glu Ser Gly Ile  
 100 105 110  
 Leu Leu Ala Met Ala Phe Asp Ser Tyr Val Ala Ile Cys Thr Pro Leu  
 115 120 125  
 Arg Tyr Thr Thr Ile Leu Thr Ser Met Val Asn Gly Lys Met Thr Leu  
 130 135 140  
 Thr Ile Trp Gly Gln Ser Ile Gly Thr Ile Phe Pro Val Ile Phe Leu  
 145 150 155 160  
 Leu Lys Arg Leu Pro Tyr Cys Gln Thr Asn Ile Ile Pro His Ser Tyr  
 165 170 175  
 Cys Glu His Ile Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Thr Val  
 180 185 190  
 Asn Ile Trp Tyr Gly Phe Ser Val Pro Met Ala Ser Val Leu Val Asp  
 195 200 205  
 Val Ala Phe Ile Gly Phe Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe  
 210 215 220  
 Arg Leu Pro Ser Gln Glu Ser Gln His Lys Ala Leu Asn Thr Cys Gly  
 225 230 235 240  
 Ser His Ile Gly Val Val Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr  
 245 250 255  
 Phe Leu Thr His Arg Phe Gly Lys Asn Ile Pro His His Val His Ile  
 260 265 270  
 Leu Leu Ala Asn Leu Tyr Leu Leu Val Pro Pro Met Leu Asn Pro Ile  
 275 280 285  
 Ile Tyr Gly Glu Lys Thr Lys Gln Ile Arg Asp Ser Met Ala His Met  
 290 295 300  
 Leu Ser Val Val Gly Lys Ser Xaa Asp  
 305 310

&lt;210&gt; 1512

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g429 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1512

Met Lys Met Lys Ile Asp Pro Lys Cys Asn Gly Thr Glu Val Thr Glu  
 1 5 10 15  
 Phe Ile Leu Leu Gly Leu Thr Ser Gln Pro Glu Leu Gln Pro Met Leu  
 20 25 30  
 Phe Val Val Phe Leu Leu Ile Tyr Leu Ile Thr Leu Thr Gly Lys Phe  
 35 40 45  
 Gly Met Ile Phe Leu Ile Arg Phe Thr Pro Gln Leu Gln Thr His Met  
 50 55 60  
 Tyr Phe Phe Leu Thr His Leu Ala Cys Val Asp Ile Phe Tyr Ser Thr  
 65 70 75 80  
 Asn Val Ser Pro Gln Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr  
 85 90 95  
 Ile Ser Tyr Ala Gly Cys Leu Ala Gln Cys Phe Val Phe Val Thr Leu  
 100 105 110  
 Leu Leu Thr Glu Tyr Tyr Met Leu Gly Ala Met Ala Tyr Asp Cys Tyr

```

      115      120      125
Met  Ala  Ile  Cys  Asn  Pro  Leu  His  Tyr  Ser  Ser  Lys  Met  Ser  Arg  Ala
   130      135      140
Val  Cys  Ile  Cys  Leu  Val  Thr  Phe  Pro  Tyr  Phe  Trp  Gly  Ser  Met  Val
   145      150      155      160
Gly  Thr  Met  Gln  Val  Ile  Leu  Thr  Ser  Arg  Leu  Ser  Phe  Phe  Gly  Pro
      165      170      175
Asn  Thr  Ile  Asn  His  Phe  Tyr  Cys  Thr  Asp  Pro  Pro  Leu  Leu  Met  Leu
      180      185      190
Thr  Ser  Ser  Asp  Thr  Tyr  Ile  Lys  Gln  Thr  Ala  Leu  Phe  Val  Ser  Ala
      195      200      205
Gly  Ile  Asn  Leu  Thr  Val  Ser  Leu  Leu  Ile  Ile  Leu  Ile  Ser  Tyr  Ile
   210      215      220
Phe  Ile  Phe  Ile  Thr  Ile  Met  Arg  Ile  Arg  Ser  Ser  Glu  Gly  Gln  Leu
   225      230      235      240
Lys  Ala  Phe  Ser  Thr  Cys  Gly  Ser  His  Leu  Thr  Ala  Val  Thr  Met  Phe
      245      250      255
Tyr  Gly  Ser  Leu  Phe  Cys  Met  Tyr  Leu  Arg  Pro  Thr  Asn  Glu  Leu  Ser
      260      265      270
Val  Glu  Gln  Gly  Lys  Met  Gly  Val  Val  Phe  Cys  Ile  Phe  Val  Ser  Pro
      275      280      285
Met  Leu  Asn  Pro  Phe  Ile  Tyr  Arg  Leu  Arg  Asn  Lys  Asp  Val  Lys  Gln
   290      295      300
Ala  Leu  Lys  Arg  Val  Phe  Met  Arg  Asn  Leu
   305      310

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&lt;210&gt; 1513

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g430 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1513

```

Met  Ser  Leu  Leu  Phe  Xaa  Asp  Xaa  Asp  Met  Arg  Asn  Phe  Thr  Pro  Leu
   1      5      10      15
Ser  Gly  Phe  Ile  Ile  Leu  Gly  Phe  Thr  Asp  His  Pro  Glu  Leu  Gln  Cys
      20      25      30
Leu  Leu  Phe  Val  Leu  Phe  Leu  Leu  Ile  Tyr  Met  Phe  Thr  Val  Val  Gly
   35      40      45
Asn  Leu  Gly  Met  Ile  Leu  Leu  Ile  Lys  Ile  Asp  Ser  His  Leu  His  Thr
   50      55      60
Pro  Met  Tyr  Phe  Phe  Leu  Ser  Asn  Leu  Cys  Leu  Val  Asp  Phe  Cys  Tyr
   65      70      75      80
Ser  Ser  Val  Ile  Ala  Pro  Asn  Met  Leu  Ile  Asn  Phe  Trp  Val  Glu  Asn
      85      90      95
Pro  Val  Ile  Ser  Phe  Asn  Glu  Cys  Ala  Thr  Gln  Phe  Phe  Phe  Gly
      100      105      110
Ser  Phe  Ala  Gly  Ile  Glu  Gly  Phe  Leu  Leu  Ala  Val  Met  Ala  Tyr  Asp
      115      120      125
Cys  Tyr  Val  Ala  Ile  Cys  Lys  Pro  Leu  Leu  Tyr  Thr  Val  Leu  Met  Ser
      130      135      140
Pro  His  Leu  Ser  Ala  Leu  Val  Leu  Ala  Thr  Tyr  Leu  Leu  Gly  Phe
   145      150      155      160
Val  Asn  Ala  Ala  Ile  His  Thr  Gly  Phe  Thr  Phe  Gln  Leu  Ser  Phe  Cys
      165      170      175

```

His Ser Asn Ile Ile Asn Tyr Phe Phe Cys Asp Ile Pro Pro Leu Leu  
 180 185 190  
 Lys Leu Cys Ser Asp Thr His Ile Asn Glu Val Val Ile Phe Ala Phe  
 195 200 205  
 Ala Ser Phe Asn Glu Leu Ser Cys Leu Leu Leu Ile Leu Val Ser Cys  
 210 215 220  
 Leu Tyr Ile Leu Ala Ala Ile Leu Lys Ile His Ser Ala Glu Gly Arg  
 225 230 235 240  
 His Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Ile  
 245 250 255  
 Phe Phe Gly Thr Ile Leu Phe Met Tyr Leu Leu Arg Pro Ser Ser Ser  
 260 265 270  
 Tyr Ser Met Asp Gln Asp Lys Val Val Ser Val Phe Tyr Thr Val Val  
 275 280 285  
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val  
 290 295 300  
 Lys Ala Ser Leu Ser Lys Met Phe Lys Thr Val Ser Tyr Ile Ser Thr  
 305 310 315 320

&lt;210&gt; 1514

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g431 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1514

Met Gly Leu Pro Gly Ile His Glu Trp Gln His Trp Leu Ser Leu Pro  
 1 5 10 15  
 Leu Thr Leu Leu Tyr Leu Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile  
 20 25 30  
 Ile Thr Ile Gln His Glu Thr Val Leu His Glu Pro Met Tyr His Leu  
 35 40 45  
 Leu Gly Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met  
 50 55 60  
 Pro Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu  
 65 70 75 80  
 Pro Met Cys Phe Ala Gln Ile Tyr Ala Ile His Cys Phe Phe Cys Ile  
 85 90 95  
 Glu Ser Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Ile Ala Ile  
 100 105 110  
 Cys Arg Pro Leu Gln Tyr Pro Ser Ile Val Thr Lys Ala Phe Val Phe  
 115 120 125  
 Lys Ala Thr Gly Phe Ile Met Leu Arg Asn Gly Leu Leu Thr Ile Pro  
 130 135 140  
 Val Pro Ile Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile  
 145 150 155 160  
 Glu His Cys Leu Cys Ser Asn Leu Gly Val Ile Ser Leu Ala Cys Asp  
 165 170 175  
 Asp Ile Thr Val Asn Lys Phe Tyr Gln Leu Met Leu Ala Trp Val Leu  
 180 185 190  
 Val Gly Ser Asp Met Ala Leu Val Phe Ser Ser Tyr Ala Val Ile Leu  
 195 200 205  
 His Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Met Ser Lys Ala Leu  
 210 215 220  
 Ser Thr Cys Ser Ser His Leu Ile Leu Ile Leu Phe His Thr Gly Ile  
 225 230 235 240  
 Ile Val Leu Ser Val Thr His Leu Ala Glu Lys Lys Ile Pro Leu Ile  
 245 250 255  
 Pro Val Phe Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu Asn

260 265 270  
 Pro Leu Ala Cys Ala Leu Arg Met His Lys Leu Arg Leu Gly Phe Gln  
 275 280 285  
 Arg Leu Leu Gly Leu Gly Gln Asp Val Ser Lys  
 290 295

<210> 1515  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g432 protein)

<220>  
 <223> Synthetic construct

<400> 1515  
 Met Met Arg Leu Met Lys Glu Val Arg Gly Arg Asn Gln Thr Glu Val  
 1 5 10 15  
 Thr Glu Phe Leu Leu Gly Leu Ser Asp Asn Pro Asp Leu Gln Gly  
 20 25 30  
 Val Leu Phe Ala Leu Phe Leu Leu Ile Tyr Met Ala Asn Met Val Gly  
 35 40 45  
 Asn Leu Gly Met Ile Val Leu Ile Lys Ile Asp Leu Cys Leu His Thr  
 50 55 60  
 Pro Met Tyr Phe Phe Leu Ser Ser Leu Ser Phe Val Asp Ala Ser Tyr  
 65 70 75 80  
 Ser Ser Ser Val Thr Pro Lys Met Leu Val Asn Leu Met Ala Glu Asn  
 85 90 95  
 Lys Ala Ile Ser Phe His Gly Cys Ala Ala Gln Phe Tyr Phe Phe Gly  
 100 105 110  
 Ser Phe Leu Gly Thr Glu Cys Phe Leu Leu Ala Met Met Ala Tyr Asp  
 115 120 125  
 Arg Tyr Ala Ala Ile Trp Asn Pro Leu Leu Tyr Pro Val Leu Val Ser  
 130 135 140  
 Gly Arg Ile Cys Phe Leu Leu Ile Ala Thr Ser Phe Leu Ala Gly Cys  
 145 150 155 160  
 Gly Asn Ala Ala Ile His Thr Gly Met Thr Phe Arg Leu Ser Phe Cys  
 165 170 175  
 Gly Ser Asn Arg Ile Asn His Phe Tyr Cys Asp Thr Pro Pro Leu Leu  
 180 185 190  
 Lys Leu Ser Cys Ser Asp Thr His Phe Asn Gly Ile Val Ile Met Ala  
 195 200 205  
 Phe Ser Ser Phe Ile Val Ile Ser Cys Val Met Ile Val Leu Ile Ser  
 210 215 220  
 Tyr Leu Cys Ile Phe Ile Ala Val Leu Lys Met Pro Ser Leu Glu Gly  
 225 230 235 240  
 Arg His Lys Ala Phe Ser Thr Cys Ala Ser Tyr Leu Met Ala Val Thr  
 245 250 255  
 Ile Phe Phe Gly Thr Ile Leu Phe Met Tyr Leu Arg Pro Thr Ser Ser  
 260 265 270  
 Tyr Ser Met Glu Gln Asp Lys Val Val Ser Val Phe Tyr Thr Val Ile  
 275 280 285  
 Ile Pro Val Leu Asn Pro Leu Ile Tyr Ser Leu Lys Asn Lys Asp Val  
 290 295 300  
 Lys Lys Ala Leu Lys Lys Ile Leu Trp Lys His Ile Leu  
 305 310 315

<210> 1516  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g433 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1516

```

Met Ser His Thr Asn Val Thr Ile Phe His Pro Ala Val Phe Val Leu
 1           5           10           15
Pro Gly Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro
          20           25           30
Leu Cys Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile
          35           40           45
Val Val Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe
          50           55           60
Leu Ser Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val
65           70           75           80
Pro Lys Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe
          85           90           95
Asp Ala Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly
          100          105          110
Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Cys Ala Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly
          130          135          140
Arg Ile Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro
145           150           155           160
Val Ile Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val
          165          170          175
Pro His Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala
          180          185          190
Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met
          195          200          205
Val Ile Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu
          210          215          220
Arg Ala Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu
225           230           235           240
Ser Thr Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro
          245          250          255
Ser Phe Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln
          260          265          270
His Val His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met
          275          280          285
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gly
          290          295          300
Val Ala His Arg Phe Phe Asp Ile Lys Thr Trp Cys Cys
305           310           315

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&lt;210&gt; 1517

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g434 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1517

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
          20           25           30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
          35           40           45
Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Ala Gly Asn

```

|                     |                     |                         |
|---------------------|---------------------|-------------------------|
| 50                  | 55                  | 60                      |
| Leu Ser Phe Leu Asp | Leu Trp Tyr Ser Ser | Val Tyr Thr Pro Lys Ile |
| 65                  | 70                  | 75                      |
| Leu Val Thr Cys Ile | Ser Glu Asp Lys Ser | Ile Ser Phe Ala Gly Cys |
| 85                  | 90                  | 95                      |
| Leu Cys Gln Phe Phe | Phe Ser Ala Gly Leu | Ala Tyr Ser Glu Cys Tyr |
| 100                 | 105                 | 110                     |
| Leu Leu Ala Ala Val | Ala Tyr Asp Arg Tyr | Val Ala Ile Ser Lys Pro |
| 115                 | 120                 | 125                     |
| Leu Leu Tyr Ala Gln | Ala Met Ser Ile Lys | Leu Cys Ala Leu Leu Val |
| 130                 | 135                 | 140                     |
| Ala Val Ser Tyr Cys | Gly Gly Phe Ile Asn | Ser Ser Ile Ile Thr Lys |
| 145                 | 150                 | 155                     |
| Lys Thr Phe Ser Phe | Asn Phe Cys Arg Glu | Asn Ile Ile Asp Asp Phe |
| 165                 | 170                 | 175                     |
| Phe Cys Asp Leu Leu | Pro Leu Val Glu Leu | Ala Cys Gly Glu Lys Gly |
| 180                 | 185                 | 190                     |
| Gly Tyr Lys Ile Met | Met Tyr Phe Leu Leu | Ala Ser Asn Val Ile Cys |
| 195                 | 200                 | 205                     |
| Pro Ala Val Leu Ile | Leu Ala Ser Tyr Leu | Phe Ile Ile Thr Ser Val |
| 210                 | 215                 | 220                     |
| Leu Arg Ile Ser Ser | Ser Lys Gly Tyr Leu | Lys Ala Phe Ser Thr Cys |
| 225                 | 230                 | 235                     |
| Ser Ser His Leu Thr | Ser Val Thr Leu Tyr | Gly Ser Ile Leu Tyr     |
| 245                 | 250                 | 255                     |
| Ile Tyr Ala Leu Pro | Arg Ser Ser Tyr Ser | Phe Asp Met Asp Lys Ile |
| 260                 | 265                 | 270                     |
| Val Ser Thr Phe Tyr | Thr Val Val Phe Pro | Met Leu Asn Leu Met Ile |
| 275                 | 280                 | 285                     |
| Tyr Ser Leu Arg Asn | Lys Asp Val Lys Glu | Ala Leu Lys Lys Leu Leu |
| 290                 | 295                 | 300                     |
| Pro                 |                     |                         |
| 305                 |                     |                         |

&lt;210&gt; 1518

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g435 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1518

|                     |                     |                         |
|---------------------|---------------------|-------------------------|
| Met Leu Pro Ser Asn | Ile Thr Ser Thr His | Pro Ala Val Phe Leu Leu |
| 1                   | 5                   | 10                      |
| Val Gly Ile Pro Gly | Leu Glu His Leu His | Ala Trp Ile Ser Ile Pro |
| 20                  | 25                  | 30                      |
| Phe Cys Phe Ala Tyr | Thr Leu Ala Leu Leu | Gly Asn Cys Thr Leu Leu |
| 35                  | 40                  | 45                      |
| Phe Ile Ile Arg Ala | Asp Ala Ala Leu His | Glu Pro Met Tyr Leu Phe |
| 50                  | 55                  | 60                      |
| Leu Ala Met Leu Ala | Thr Ile Asp Leu Val | Leu Ser Ser Thr Thr Leu |
| 65                  | 70                  | 75                      |
| Pro Lys Met Leu Ala | Ile Phe Trp Phe Arg | Asp Gln Glu Ile Asn Phe |
| 85                  | 90                  | 95                      |
| Phe Ala Cys Leu Val | Gln Met Phe Phe Leu | His Ser Phe Ser Ile Met |
| 100                 | 105                 | 110                     |
| Glu Ser Ala Val Leu | Leu Ala Met Ala Phe | Asp Arg Tyr Val Ala Ile |
| 115                 | 120                 | 125                     |
| Cys Lys Pro Leu His | Tyr Thr Val Leu Thr | Gly Ser Leu Ile Thr     |
| 130                 | 135                 | 140                     |



Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile  
 165 170 175  
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly  
 180 185 190  
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ser  
 195 200 205  
 Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu  
 210 215 220  
 Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe  
 225 230 235 240  
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro  
 245 250 255  
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro  
 260 265 270  
 Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met  
 275 280 285  
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Tyr  
 290 295 300  
 Val Leu Ser Leu Phe Gln Arg Lys Asn Met  
 305 310

&lt;210&gt; 1519

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g436 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1519

Met Leu Lys Lys Asn His Thr Ala Val Thr Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Arg Ala Glu Leu Gln Ser Leu Leu Phe Val Val Phe Leu  
 20 25 30  
 Val Ile Tyr Leu Ile Thr Val Ile Gly Asn Val Ser Met Ile Leu Leu  
 35 40 45  
 Ile Arg Ser Asp Ser Thr Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 His Leu Ser Phe Val Asp Leu Cys Tyr Thr Thr Asn Val Thr Pro Gln  
 65 70 75 80  
 Met Leu Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Ser Phe Ile Gly  
 85 90 95  
 Cys Phe Ile Gln Phe His Phe Phe Ile Ala Leu Val Ile Thr Asp Tyr  
 100 105 110  
 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Met Ala Ile Cys Lys  
 115 120 125  
 Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys Val Cys Leu Cys Leu  
 130 135 140  
 Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn Gly Leu Ser Gln Thr  
 145 150 155 160  
 Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro Asn Asp Ile Asn His  
 165 170 175  
 Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala Gly Ser Asn Leu Ile  
 195 200 205  
 Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Thr Ala  
 210 215 220  
 Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg Lys Ala Phe Ser Thr

```

225          230          235          240
Cys Gly Ser His Val Thr Ala Val Thr Val Phe Tyr Gly Thr Leu Phe
          245          250          255
Cys Met Tyr Leu Arg Pro Pro Ser Glu Thr Ser Ile Gln Gln Gly Lys
          260          265          270
Ile Val Ala Val Phe Tyr Ile Phe Val Ser Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Arg Ser Ile Arg Lys Val
          290          295          300
Ile Gln Lys Lys Leu Phe Ala Lys
305          310

```

&lt;210&gt; 1520

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g437 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1520

```

Met Ser Ala Ser Asn Ile Thr Leu Thr His Pro Thr Ala Phe Leu Leu
1          5          10          15
Val Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
          20          25          30
Phe Cys Leu Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu
          35          40          45
Leu Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe
          50          55          60
Leu Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu
65          70          75          80
Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe
          85          90          95
Phe Ala Cys Leu Ala Gln Met Phe Phe Leu His Ser Phe Ser Ile Met
          100          105          110
Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Lys Pro Leu His Tyr Thr Lys Val Leu Thr Gly Ser Leu Ile Thr
          130          135          140
Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro
145          150          155          160
Leu Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile
          165          170          175
Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
          180          185          190
Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile
          195          200          205
Val Val Leu Asp Leu Leu Leu Val Ile Leu Ser Tyr Ile Phe Ile Leu
          210          215          220
Gln Ala Val Leu Leu Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
225          230          235          240
Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Thr
          245          250          255
Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
          260          265          270
His Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met
          275          280          285
Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser
          290          295          300
Ile Leu Gly Val Phe Pro Arg Lys Asp Met
305          310

```

<210> 1521  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g438 protein)

<220>  
 <223> Synthetic construct

<400> 1521  
 Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu  
 1 5 10 15  
 Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu  
 35 40 45  
 Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Ile Tyr Leu Phe Leu  
 50 55 60  
 Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu Pro  
 65 70 75 80  
 Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe Phe  
 85 90 95  
 Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met Glu  
 100 105 110  
 Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr Lys  
 130 135 140  
 Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro Leu  
 145 150 155 160  
 Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile Ala  
 165 170 175  
 Arg Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly Asn  
 180 185 190  
 Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile Gly  
 195 200 205  
 Val Leu Asp Leu Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln  
 210 215 220  
 Ala Val Leu Gln Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly  
 225 230 235 240  
 Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser  
 245 250 255  
 Val Ile Ser Ser Val Met His Arg Val Ala Arg Cys Ala Ala Pro His  
 260 265 270  
 Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val  
 275 280 285  
 Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val  
 290 295 300  
 Leu Gly Val Phe Pro Arg Lys Asp Val  
 305 310

<210> 1522  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g439 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)... (318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1522

```

Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
 1          5          10          15
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
 20          25          30
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
 35          40          45
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
 50          55          60
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
 65          70          75          80
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
 85          90          95
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
 100          105          110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115          120          125
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
 130          135          140
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro
 145          150          155          160
Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu
 165          170          175
Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala
 180          185          190
Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr
 195          200          205
Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Xaa Ser Phe Ile Leu
 210          215          220
Tyr Thr Gly Phe His Leu Pro Ser Pro Gly Ala Arg Gln Lys Ala Leu
 225          230          235          240
Gly Thr Cys Gly Ser His Leu Arg Val Ile Ser Met Phe Tyr Leu Pro
 245          250          255
Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro Leu
 260          265          270
His Thr His Ile Leu Leu Gly Asn Val Trp Val Leu Ala Pro Pro Met
 275          280          285
Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu Cys
 290          295          300
Val Leu Ser Leu Leu Ser Ser Gln Arg Lys Xaa Cys Xaa Ile
 305          310          315

```

&lt;210&gt; 1523

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g440 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1523

```

Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
 20          25          30
Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35          40          45
Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50          55          60

```

```

Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
65          70          75          80
Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
          85          90          95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
          100          105          110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
          115          120          125
Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
          130          135          140
Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
145          150          155          160
Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
          165          170          175
Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
          180          185          190
Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
          195          200          205
Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
          210          215          220
Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225          230          235          240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
          245          250          255
Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
          260          265          270
Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
          290          295          300
Val Ala Arg Val Phe Leu Ile Lys Lys
305          310

```

&lt;210&gt; 1524

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g441 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1524

```

Met Glu Lys Ser Asn Val Ser Ser Val Tyr Gly Phe Ile Leu Val Gly
1          5          10          15
Phe Ser Asp Arg Pro Lys Leu Glu Met Val Leu Phe Thr Val Asn Phe
          20          25          30
Ile Leu Tyr Ser Val Ala Val Leu Gly Asn Ser Thr Ile Ile Leu Val
          35          40          45
Cys Ile Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Ser Thr Ser Cys Ile Pro Gln
65          70          75          80
Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Cys Ala Gly
          85          90          95
Cys Val Val Gln Leu Phe Ser Phe Leu Ser Val Arg Gly Ile Glu Cys
          100          105          110
Ile Leu Leu Ala Val Met Ala Tyr Asp Ser Tyr Ala Ala Val Cys Lys

```

```

      115      120      125
Pro Leu Arg Tyr Leu Val Ile Met His Leu Gln Leu Cys Leu Gly Leu
  130      135      140
Met Ala Ala Ala Trp Gly Ser Gly Leu Val Asn Ala Val Val Met Ser
  145      150      155      160
Pro Leu Thr Met Thr Leu Ser Arg Ser Gly Arg Arg Arg Val Asn His
      165      170      175
Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Met Ala Cys Leu Asp Val
      180      185      190
Arg Ala Val Glu Met Leu Ala Phe Ala Val Leu Ile Val Leu
      195      200      205
Leu Pro Leu Thr Leu Ile Leu Val Ser Tyr Gly Tyr Ile Ala Ala Ala
      210      215      220
Val Leu Ser Ile Lys Ser Ala Ala Arg Gln Trp Lys Ala Phe His Thr
  225      230      235      240
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ser Ile Ile
      245      250      255
Tyr Met Tyr Met Gln Pro Gly Asn Ser Ser Ser Gln Asp Gln Gly Lys
      260      265      270
Phe Leu Thr Leu Phe Tyr Asn Leu Val Thr Pro Met Leu Asn Leu Leu
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Lys Val
      290      295      300
Leu Gly Arg Gln Xaa Xaa Thr Gly Glu Ile Xaa Xaa Val Val Lys Ser
  305      310      315      320
Xaa Ala Lys Tyr Leu Phe Gln Tyr Thr Phe Ile Leu Cys
      325      330

```

&lt;210&gt; 1525

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g442 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1525

```

Gln Val Val His Thr Gly Phe Ser Pro Xaa Leu Tyr Val Phe Thr Leu
  1      5      10      15
Leu Gly Asn Gly Ser Ile Leu Gly Leu Ile Trp Leu Asp Ser Arg Leu
      20      25      30
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Ile Ile Asp Ile
      35      40      45
Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr Asn Leu Gly Leu
      50      55      60
Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr Met Gln Thr Phe
      65      70      75      80
Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile Leu Val Met Met
      85      90      95
Ser Tyr Asp Arg Tyr Met Ala Val Cys His Pro Leu Gln Tyr Ser Val
      100      105      110
Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val Thr Ser Trp Ala
      115      120      125
Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu Ile Leu Arg Leu
      130      135      140
Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe Cys Glu Ile Leu
  145      150      155      160

```

Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val  
 165 170 175  
 Ile Phe Ala Ser Ser Val Phe Ile Leu Val Gly Ala Leu Cys Leu Val  
 180 185 190  
 Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu Arg Asn Gln Ser  
 195 200 205  
 Gly Glu Gly Arg Arg Lys Gly Phe Ser Thr Cys Tyr Ser His Leu Cys  
 210 215 220  
 Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met Ala Pro  
 225 230 235 240  
 Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu Phe Tyr  
 245 250 255  
 Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn  
 260 265 270  
 Ala Glu Val Lys Gly Ala Leu Arg Ser Ala Leu Arg Lys Glu Arg Leu  
 275 280 285  
 Thr Xaa Asp Ile Ser Lys Gly Thr Met Gly Arg Glu Pro Cys Ser Leu  
 290 295 300  
 Gln Asn Ile Glu Val Gly Phe Phe Phe Cys Leu Leu Leu  
 305 310 315

&lt;210&gt; 1526

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g443 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(239)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1526

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val  
 1 5 10 15  
 Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr  
 20 25 30  
 Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr  
 35 40 45  
 Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Met Thr  
 50 55 60  
 Trp Ser Asp Asn Ser Phe Ile Phe Val Ile Met Tyr Thr Leu Ile Leu  
 65 70 75 80  
 Lys Phe Pro Ser Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His  
 85 90 95  
 Val Leu Leu Ala Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu  
 100 105 110  
 Glu Met Ser Val Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu  
 115 120 125  
 Ile Ser Asn Phe Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met  
 130 135 140  
 Asn Thr Ser Asn Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His  
 145 150 155 160  
 His His His Arg Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile  
 165 170 175  
 Ile Val Xaa Met Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln  
 180 185 190  
 Glu Arg Phe Phe Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys  
 195 200 205  
 Leu Leu Val Tyr Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg

210 215 220  
 Arg Ile Leu Arg Phe Gly Arg Glu Ser Ser Lys Met Lys Gly Asn  
 225 230 235

<210> 1527  
 <211> 255  
 <212> PRT  
 <213> Unknown (H38g444 protein)

<220>  
 <223> Synthetic construct

<400> 1527  
 Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile  
 1 5 10 15  
 Ser Thr Ile Val Pro Lys Met Ala Ser Asp Phe Leu His Gly Asn Lys  
 20 25 30  
 Ser Ile Ser Phe Thr Gly Cys Gly Ile His Ser Phe Phe Phe Thr Thr  
 35 40 45  
 Leu Ala Val Val Glu Ala Leu Leu Leu Ile Ser Met Ala Tyr Val Arg  
 50 55 60  
 Cys Ile Ala Ile Cys Phe Pro Leu His Tyr Leu Met Arg Met Ser Lys  
 65 70 75 80  
 Arg Val Cys Val Leu Met Ile Thr Gly Ser Trp Ile Ile Gly Ser Ile  
 85 90 95  
 Asn Ala Cys Ala His Thr Val Tyr Ile Leu His Ile Pro Tyr Cys Pro  
 100 105 110  
 Ser Arg Val Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Val Thr  
 115 120 125  
 Leu Ala Cys Met Asp Thr Trp Val Tyr Glu Gly Thr Val Leu Leu Ser  
 130 135 140  
 Ala Thr Ile Phe Leu Val Phe Pro Phe Ile Ala Ile Ser Cys Ser Tyr  
 145 150 155 160  
 Gly Arg Val Leu Leu Ala Val Tyr His Met Lys Ser Ala Glu Gly Lys  
 165 170 175  
 Lys Lys Ala Tyr Leu Thr Cys Ser Thr His Leu Thr Val Val Thr Phe  
 180 185 190  
 Tyr Tyr Ala Pro Phe Ala Tyr Thr Tyr Leu Arg Pro Arg Ser Leu Arg  
 195 200 205  
 Ser Pro Thr Glu Asp Lys Val Leu Ala Val Phe Tyr Thr Ile Leu Thr  
 210 215 220  
 Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Met  
 225 230 235 240  
 Gly Ala Leu Thr Arg Val Ile Gln Lys Ile Phe Ser Val Lys Ile  
 245 250 255

<210> 1528  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g445 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(320)  
 <223> Xaa = Any Amino Acid

<400> 1528  
 Leu Ser Xaa Pro Thr Arg Ala Ala Gln Lys Gln Phe Ile Leu Leu Gly  
 1 5 10 15



Phe Ser Gly Arg Pro Arg Leu Glu His Val Leu Phe Val Phe Val Leu  
 20 25 30  
 Ile Phe Tyr Leu Val Thr Leu Val Gly Asn Ile Ile Ile Ile Leu Ile  
 35 40 45  
 Ser His Leu Asp Pro Cys Leu His Met Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ser Ile Pro Gln  
 65 70 75 80  
 Leu Leu Phe Asn Leu Gly Ser Pro Gly Lys Thr Ile Ser His Thr Gly  
 85 90 95  
 Cys Ala Ile Gln Leu Phe Met Phe Leu Gly Leu Gly Gly Thr Glu Cys  
 100 105 110  
 Ile Leu Leu Ala Ala Val Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Ser Val Ile Met His Pro Gln Leu Cys Trp Lys Leu  
 130 135 140  
 Val Ser Val Ala Arg Gly Cys Trp Thr Pro Gln Phe Ser Ser Tyr Val  
 145 150 155 160  
 Ser Trp Thr Met Lys Leu Pro Arg Cys Gly Arg Cys Lys Leu Lys His  
 165 170 175  
 Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Ile Thr Cys Val Asp Thr  
 180 185 190  
 Val Ala Met Glu Ser Thr Val Phe Thr Leu Ser Val Val Ile Val Leu  
 195 200 205  
 Met Pro Leu Cys Leu Ile Leu Ile Ser Tyr Ser Tyr Ile Ala Leu Ala  
 210 215 220  
 Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Arg Lys Ala Phe Asn Met  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile  
 245 250 255  
 Tyr Met Tyr Met Gln Pro Xaa Asn Asn Ser Ser Gln Asp Gln Gly Lys  
 260 265 270  
 Phe Leu Thr Leu Phe Tyr Asn Leu Met Thr Pro Met Leu Asn Pro Val  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Arg Leu  
 290 295 300  
 Val Ser Arg Lys His Ser Asp Ser Asp Cys Ser Xaa Asp Cys Phe Phe  
 305 310 315 320

&lt;210&gt; 1529

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g446 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1529

Met Glu Asn Tyr Asn Gln Thr Ser Thr Ala Phe Ile Leu Leu Gly Leu  
 1 5 10 15  
 Ser Pro Pro Pro Lys Ile Gly His Phe Ile Phe Ile Leu Ile Asn Phe  
 20 25 30  
 Val Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile  
 35 40 45  
 Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln  
 50 55 60  
 Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met  
 65 70 75 80  
 Val Tyr Asp Phe Ser Cys His Gly Asn Lys Ser Ile Ser Phe Thr Gly  
 85 90 95  
 Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |
| Leu | Leu | Leu | Thr | Ser | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |

<210> 1530  
 <211> 326  
 <212> PRT  
 <213> Unknown (H38g447 protein)

<220>  
 <223> Synthetic construct

<400> 1530

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Ala | Asn | Asp | Ser | Thr | Phe | Ser | Gly | Phe | Ile | Leu | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Asn | Arg | Pro | Gln | Leu | Glu | Thr | Ala | Leu | Phe | Val | Val | Ile | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Ile | Tyr | Phe | Leu | Ser | Phe | Leu | Gly | Asn | Gly | Thr | Ile | Ile | Leu | Leu |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ile | Val | Asp | Pro | Arg | Leu | His | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Leu | Ser | Phe | Met | Asp | Leu | Cys | Leu | Thr | Thr | Cys | Thr | Val | Pro | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Leu | Val | Asn | Phe | Lys | Gly | Lys | Asp | Lys | Thr | Ile | Thr | Tyr | Gly | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Val | Thr | Gln | Leu | Phe | Ile | Ala | Leu | Gly | Leu | Gly | Gly | Ser | Glu | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Leu | Leu | Ser | Ala | Met | Ala | Tyr | Asp | Arg | Tyr | Ala | Ala | Val | Cys | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | His | Tyr | Met | Val | Ser | Met | His | Pro | Gln | Leu | Cys | Leu | Gln | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Val | Thr | Thr | Trp | Leu | Thr | Gly | Phe | Gly | Asn | Ser | Val | Ile | Gln | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Leu | Thr | Met | Thr | Leu | Pro | Leu | Cys | Asp | Lys | Asn | Gln | Val | Asp | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Phe | Cys | Glu | Val | Pro | Val | Met | Leu | Lys | Leu | Ser | Cys | Thr | Asn | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ile | Asn | Glu | Ala | Glu | Ile | Phe | Ala | Val | Ser | Val | Phe | Phe | Leu | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Pro | Leu | Ser | Leu | Ile | Leu | Ala | Ser | Tyr | Gly | His | Ile | Thr | His | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Leu | Lys | Ile | Lys | Ser | Ala | Gln | Gly | Arg | Gln | Lys | Ala | Phe | Gly | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Gly | Ser | His | Leu | Leu | Val | Val | Ile | Ile | Phe | Phe | Gly | Thr | Leu | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Met | Tyr | Leu | Gln | Pro | Pro | Ser | Ser | Tyr | Ser | Gln | Asp | Val | Asn | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ile | Ala | Leu | Phe | Tyr | Thr | Leu | Val | Thr | Pro | Leu | Leu | Asn | Pro | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Tyr | Thr | Leu | Arg | Asn | Lys | Glu | Val | Lys | Gly | Ala | Thr | Lys | Lys | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Gly | Glu | Asp | His | Arg | Cys | Met | Arg | Lys | Leu | Thr | Gln | Gly | Leu | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Gln | Thr | Phe | Val | His |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

<210> 1531  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g448 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1531

```

Met Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly Leu
 1           5           10           15
Phe Pro Pro Ser Ile Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe
      20           25           30
Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
      35           40           45
Phe Leu Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
      50           55           60
Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
65           70           75           80
Ala Ser Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys
      85           90           95
Gly Ile Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu
      100          105          110
Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro
      115          120          125
Leu His Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu Met Ile
      130          135          140
Thr Gly Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val
145          150          155          160
Tyr Val Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe
      165          170          175
Phe Cys Asp Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp
      180          185          190
Val Tyr Glu Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu Val Phe
      195          200          205
Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe Ala Val
      210          215          220
Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys
225          230          235          240
Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr
      245          250          255
Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val
      260          265          270
Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser
      290          295          300
Gln Arg Ile Cys Ser Val Lys Met
305          310

```

&lt;210&gt; 1532

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g449 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1532

```

Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser
 1           5           10           15
Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu
      20           25           30
Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Val Thr Thr
      35           40           45
Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu

```

```

      50      55      60
Ser Ile Leu Asp Ala Cys Tyr Ile Ser Val Thr Val Pro Thr Ser Cys
65      70      75      80
Val Asn Ser Leu Leu Asp Ser Thr Thr Ile Ser Lys Ala Gly Cys Val
      85      90      95
Ala Gln Val Phe Leu Val Val Phe Phe Val Tyr Val Glu Leu Leu Phe
      100      105      110
Leu Thr Ile Met Ala His Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
      115      120      125
His Tyr Pro Val Ile Val Asn Ser Arg Ile Cys Ile Gln Met Thr Leu
      130      135      140
Ala Ser Leu Leu Ser Gly Leu Val Tyr Ala Gly Met His Thr Gly Ser
145      150      155      160
Thr Phe Gln Leu Pro Phe Cys Arg Ser Asn Val Ile His Gln Phe Phe
      165      170      175
Cys Asp Ile Pro Ser Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ser
      180      185      190
Asn Glu Val Met Ile Val Val Ser Ala Leu Gly Val Gly Gly Cys
      195      200      205
Phe Ile Phe Ile Ile Arg Ser Tyr Ile His Ile Phe Ser Thr Val Leu
      210      215      220
Gly Phe Pro Arg Gly Ala Asp Arg Thr Lys Ala Phe Ser Thr Cys Ile
225      230      235      240
Pro His Ile Leu Val Ser Val Phe Leu Ser Ser Cys Ser Ser Val
      245      250      255
Tyr Leu Arg Pro Pro Ala Ile Pro Ala Ala Thr Gln Asp Leu Ile Leu
      260      265      270
Ser Gly Phe Tyr Ser Ile Met Pro Pro Leu Phe Asn Pro Ile Ile Tyr
      275      280      285
Ser Leu Arg Asn Lys Gln Ile Lys Val Ala Ile Lys Lys Ile Met Lys
      290      295      300
Arg Ile Phe Tyr Ser Glu Asn Val
305      310

```

&lt;210&gt; 1533

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g450 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1533

```

Arg Asn Ala Pro Leu Glu Lys Tyr Asn Gln Thr Ser Thr Asp Phe Ile
1      5      10      15
Leu Leu Gly Ile Phe Pro Pro Ser Arg Ile Gly Phe Leu Leu Phe Ile
      20      25      30
Leu Leu Val Leu Ile Leu Leu Leu Ala Leu Ile Gly Asn Gln Ser Val
      35      40      45
Ile Leu Leu Ile Phe Leu Asp Thr His Leu His Thr Pro Ile Tyr Phe
      50      55      60
Leu Leu Ser Arg Leu Tyr Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile
65      70      75      80
Val Pro Lys Met Phe Ser Asp Phe Leu Phe Gly Asn Lys Ser Ile Ser
      85      90      95
Phe Ile Gly Cys Gly Ile Gln Ser Phe Phe Phe Val Thr Leu Ala Gly
      100      105      110
Ala Glu Met Leu Pro Leu Thr Ser Met Ala Cys Asp His Tyr Val Ala
      115      120      125
Val Cys Phe Pro Leu His Tyr Pro Ile His Met Ser Lys Ile Val Cys
130      135      140

```

```

Leu Met Ile Ile Gly Ser Trp Ile Met Gly Ser Ile Asp Thr Cys Ala
145                      150                      155                      160
His Ile Ser Tyr Met Pro His Ile Pro Val Cys Ser Ala Arg Ala Cys
                      165                      170                      175
Asp Val Pro Ala Met Val Thr Leu Ala Phe Val Asp Thr Trp Val Tyr
                      180                      185                      190
Glu Cys Thr Val Phe Leu Ser Thr Thr Leu Phe Leu Met Phe Thr Phe
                      195                      200                      205
Ile Gly Ile Ala Cys Ser Tyr Gly Glu Val Leu Leu Thr Val Tyr His
210                      215                      220
Ile Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr
225                      230                      235                      240
His Leu Thr Val Val Ile Ile Tyr Tyr Ala Met Phe Ala Tyr Thr Tyr
                      245                      250                      255
Leu Tyr Pro Arg Tyr Leu Gln Ser Pro Thr Glu Asp Lys Val Leu Ala
                      260                      265                      270
Val Phe Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser
                      275                      280                      285
Leu Arg Asn Arg Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg
290                      295                      300
Ile Phe Pro Val Lys Met Lys
305                      310

```

&lt;210&gt; 1534

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g451 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(192)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1534

```

Arg His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu
1      5      10      15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu
20     25     30
Ser Leu Ser Leu Ser Leu Ser Leu Tyr Leu Val Met Val Leu Arg Asn
35     40     45
Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro
50     55     60
Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr
65     70     75     80
Ser Ala Thr Val Pro Lys Val Thr Val Asp Met Gln Ser His Ser Arg
85     90     95
Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu
100    105    110
Phe Ala Cys Ile Glu Cys Met Leu Leu Thr Val Met Ala Tyr Asp Gly
115    120    125
Phe Val Ala Ile Cys Leu Pro Leu His Tyr Pro Val Ile Met Asn Pro
130    135    140
His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu
145    150    155    160
Asp Ser Gln Leu His Gly Trp Ile Val Xaa Gln Phe Thr Ile Met Lys
165    170    175
Asn Val Glu Ile Ser His Phe Val Ser Asp Pro Ser Gln Leu Leu Asn
180    185    190

```

<210> 1535  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g452 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(317)  
 <223> Xaa = Any Amino Acid

<400> 1535

```

Met Asp Arg Arg Asn Gln Thr Cys Ile Tyr Glu Phe Leu Leu Met Gly
 1          5          10          15
Phe Ser Glu His Gln Glu Gln Ala Leu Leu Phe Gly Leu Phe Leu
          20          25          30
Val Met Tyr Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu Ala
          35          40          45
Ile Gly Ser Asp Leu His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Leu Asp Ile Gly Phe Ile Ser Thr Ile Ile Pro Lys
          65          70          75          80
Met Leu Asp His Ile Ser Ser Gly Ile Lys Leu Ile Ser Tyr Gly Glu
          85          90          95
Cys Leu Thr Gln Leu Tyr Phe Ser Gly Leu Phe Ala Asp Leu Asp Asn
          100          105          110
Asn Phe Leu Leu Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser
          115          120          125
His Pro Leu His Tyr Ala Leu Thr Met Asn Ser Gln Arg Cys Val Leu
          130          135          140
Leu Val Ala Val Ser Trp Val Ile Thr Ile Leu His Ala Leu Val His
          145          150          155          160
Thr Leu Leu Val Thr Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Pro
          165          170          175
His Phe Phe Cys Asp Leu Val Pro Leu Leu Lys Leu Ala Cys Ser Ser
          180          185          190
Thr Cys Val Asn Asp Leu Val Leu Ile Leu Val Ala Gly Thr Leu Leu
          195          200          205
Ile Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Phe Tyr Ile Ala Leu
          210          215          220
Ala Ile Leu Arg Ile Asp Ser Pro Arg Gly Lys Gln Arg Ala Phe Ser
          225          230          235          240
Ser Cys Thr Ser His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Ala
          245          250          255
Ile Gly Val Tyr Leu Cys Pro Pro Ser Ser His Ser Asp Gly Lys Asp
          260          265          270
Arg Val Phe Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
          275          280          285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Gly Lys
          290          295          300
Leu Leu Gly Ile Lys Thr Ser Xaa His Pro Tyr Ser Arg
          305          310          315

```

<210> 1536  
 <211> 252  
 <212> PRT  
 <213> Unknown (H38g453 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(252)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1536

```

His Leu Xaa Trp Cys Val Phe Arg Tyr Leu Gly Ile Val Val Glu Ile
 1           5           10           15
His Ile Val Phe Xaa Thr Phe Arg Cys Arg Ser Leu Val Ala Gly Tyr
 20           25           30
Val Leu Xaa Thr Phe Val Ala Ile His Leu Arg Arg Asn Ala Ala Phe
 35           40           45
Ser Ile Glu Phe Leu Cys Tyr Lys Xaa Arg Met Gln Asp Ile Asn Xaa
 50           55           60
Thr Lys Xaa Gly Lys Ile Leu Tyr Ser Leu Arg Glu Phe Lys Arg Leu
 65           70           75           80
Leu Ala Thr Ser Leu Tyr Ser Ala Xaa Val Asn Arg Phe Leu Leu Asn
 85           90           95
Lys Leu Leu Pro Gly Leu Val Ser Lys Gln Ile Glu Thr Tyr Phe Arg
 100          105          110
Lys Glu Ile Tyr Ile Leu Ile Ser Thr Ile Arg Phe Ser Tyr Val Glu
 115          120          125
Thr Leu Glu Gly Glu Xaa Gly Val Asn Val Ser Ser Ile Ile Phe Leu
 130          135          140
Leu Ile Pro Phe Ser Met Ile Ser Ala Ser Ser Val Gln Ile Leu Xaa
 145          150          155          160
Gly Val Leu Xaa Met Lys Leu Ser Gln Ala Trp Lys Arg Ser Phe Ser
 165          170          175
Thr Trp Ser Ile Leu Met Ile Ala Val Thr Tyr Trp Asp Ser Phe
 180          185          190
Ile Phe Thr Tyr Val Tyr Glu Thr Xaa Ile Ile His Ile Ser Gly Gln
 195          200          205
Val Lys Phe Leu Glu Ile Phe Tyr Ala Phe Leu Ala Leu Thr Leu Asn
 210          215          220
Pro Val Val Tyr Ser Val Gly Thr Asp Ser Val Leu Val Ala Met Lys
 225          230          235          240
Asn Met Leu Xaa Ser Asn Ile Leu His Lys Lys Lys
 245          250

```

&lt;210&gt; 1537

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g454 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1537

```

Met Asp Gln Ile Asn His Thr Asn Val Lys Glu Phe Phe Phe Leu Glu
 1           5           10           15
Leu Thr Arg Ser Arg Glu Leu Glu Phe Leu Phe Val Val Phe Phe
 20           25           30
Ala Val Tyr Val Ala Thr Val Leu Gly Asn Ala Leu Ile Val Val Thr
 35           40           45
Ile Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50           55           60
Asn Lys Ser Val Leu Asp Ile Val Phe Ser Ser Ile Thr Val Pro Lys
 65           70           75           80
Phe Leu Val Asp Leu Leu Ser Asp Arg Lys Thr Ile Ser Tyr Asn Asp
 85           90           95
Cys Met Ala Gln Ile Phe Phe Phe His Phe Ala Gly Gly Ala Asp Ile

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Ile | Asn | His | Thr | Ser | Ser | Val | Ser | Glu | Phe | Ile | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Ser | Ser | Arg | Pro | Glu | Asp | Gln | Lys | Thr | Leu | Phe | Val | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Val | Tyr | Leu | Val | Thr | Ile | Thr | Gly | Asn | Leu | Leu | Ile | Ile | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ile | Arg | Phe | Asn | Pro | His | Leu | Gln | Thr | Pro | Met | Tyr | Phe | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Phe | Leu | Ser | Leu | Thr | Asp | Ile | Cys | Phe | Thr | Thr | Ser | Val | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Met | Leu | Met | Asn | Phe | Leu | Ser | Glu | Lys | Lys | Thr | Ile | Ser | Tyr | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Cys | Leu | Thr | Gln | Met | Tyr | Phe | Leu | Tyr | Ala | Leu | Gly | Asn | Ser | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Cys | Leu | Ala | Val | Met | Ala | Phe | Asp | Arg | Tyr | Val | Ala | Val | Cys |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asp | Pro | Phe | His | Tyr | Val | Thr | Thr | Met | Ser | His | His | His | Cys | Val | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Val | Ala | Phe | Ser | Cys | Ser | Phe | Pro | His | Leu | His | Ser | Leu | Leu | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Leu | Leu | Leu | Asn | Arg | Leu | Thr | Phe | Cys | Asp | Ser | Asn | Val | Ile | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Phe | Leu | Cys | Asp | Leu | Ser | Pro | Val | Leu | Lys | Leu | Ser | Cys | Ser | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |



Ile Phe Val Asn Glu Ile Val Gln Met Thr Glu Ala Pro Ile Val Leu  
 195 200 205  
 Val Thr Arg Phe Leu Cys Ile Ala Phe Ser Tyr Ile Arg Ile Leu Thr  
 210 215 220  
 Thr Val Leu Lys Ile Pro Ser Thr Ser Gly Lys Arg Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Phe Tyr Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile  
 245 250 255  
 Phe Cys Val Tyr Leu Gln Pro Pro Ser Thr Tyr Ala Val Lys Asp His  
 260 265 270  
 Val Ala Thr Ile Val Tyr Thr Val Leu Ser Ser Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Leu Lys Gln Gly Leu Arg Lys Leu  
 290 295 300  
 Met Ser Lys Arg Ser  
 305

<210> 1539

<211> 313

<212> PRT

<213> Unknown (H38g456 protein)

<220>

<223> Synthetic construct

<400> 1539

Met Ala Asn Val Thr Leu Val Thr Gly Phe Leu Leu Met Gly Phe Ser  
 1 5 10 15  
 Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile  
 20 25 30  
 Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr  
 35 40 45  
 Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu  
 50 55 60  
 Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile  
 65 70 75 80  
 Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala  
 85 90 95  
 Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile  
 100 105 110  
 Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu  
 115 120 125  
 Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser  
 130 135 140  
 Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly  
 145 150 155 160  
 Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe  
 165 170 175  
 Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met  
 180 185 190  
 Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys  
 195 200 205  
 Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu  
 210 215 220  
 Lys Ile Pro Thr Thr Lys Gly Gln Ser Lys Ala Phe Ser Thr Cys Phe  
 225 230 235 240  
 Pro His Leu Thr Val Phe Thr Val Phe Ile Ile Thr Ala Tyr Phe Val  
 245 250 255  
 Tyr Leu Lys Pro Pro Ser Asn Ser Pro Ser Val Ile Asp Arg Leu Leu  
 260 265 270  
 Ser Val Ile Tyr Thr Val Met Pro Pro Val Phe Asn Pro Val Thr Tyr

275                      280                      285  
 Ser Leu Arg Asn Asn Asp Met Lys Cys Ala Leu Ile Arg Leu Leu Gln  
     290                      295                      300  
 Lys Thr Tyr Gly Gln Glu Ala Tyr Phe  
 305                      310

&lt;210&gt; 1540

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g457 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1540

Met Ala Val Gly Arg Asn Asn Thr Ile Val Thr Lys Phe Ile Leu Leu  
 1                      5                      10                      15  
 Gly Leu Ser Asp His Pro Gln Met Lys Ile Phe Leu Phe Met Leu Phe  
     20                      25                      30  
 Leu Gly Leu Tyr Leu Leu Thr Leu Ala Trp Asn Leu Ser Leu Ile Ala  
     35                      40                      45  
 Leu Ile Lys Met Asp Ser His Leu His Met Pro Met Tyr Phe Phe Leu  
     50                      55                      60  
 Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Val Ser Ser Thr Ala Pro  
     65                      70                      75                      80  
 Lys Met Leu Ser Asp Ile Ile Thr Glu Gln Lys Thr Ile Ser Phe Val  
     85                      90                      95  
 Gly Cys Ala Thr Gln Tyr Phe Val Phe Cys Gly Met Gly Leu Thr Glu  
     100                      105                      110  
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys  
     115                      120                      125  
 Asn Pro Leu Leu Tyr Thr Val Leu Ile Ser His Thr Leu Cys Leu Lys  
     130                      135                      140  
 Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Phe Ile Glu  
     145                      150                      155                      160  
 Thr Tyr Ser Val Tyr Gln His Asp Phe Cys Gly Pro Tyr Met Ile Asn  
     165                      170                      175  
 His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp  
     180                      185                      190  
 Thr Phe Thr Ser Glu Val Val Thr Phe Ile Val Ser Val Val Val Gly  
     195                      200                      205  
 Ile Val Ser Val Leu Val Val Leu Ile Ser Tyr Gly Tyr Ile Val Ala  
     210                      215                      220  
 Ala Val Val Lys Ile Ser Ser Ala Thr Gly Arg Thr Lys Ala Phe Ser  
     225                      230                      235                      240  
 Thr Cys Ala Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ser Gly  
     245                      250                      255  
 Phe Phe Met Tyr Met Arg Pro Ser Ser Ser Tyr Ser Leu Asn Arg Asp  
     260                      265                      270  
 Lys Val Val Ser Ile Phe Tyr Ala Leu Val Ile Pro Val Val Asn Pro  
     275                      280                      285  
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Asn Ala Met Arg Lys  
     290                      295                      300  
 Ala Met Glu Arg Asp Pro Gly Ile Ser His Gly Gly Pro Phe Ile Phe  
     305                      310                      315                      320  
 Met Thr Leu Gly

&lt;210&gt; 1541

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g458 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1541

```

Met Thr Asn Gln Thr Gln Met Met Glu Phe Leu Leu Val Arg Phe Thr
1      5      10      15
Glu Asn Trp Val Leu Leu Arg Leu His Ala Leu Leu Phe Ser Leu Ile
20      25      30
Tyr Leu Thr Ala Val Leu Met Asn Leu Val Ile Ile Leu Leu Met Ile
35      40      45
Leu Asp His Arg Leu His Met Ala Met Tyr Phe Phe Leu Arg His Leu
50      55      60
Ser Phe Leu Asp Leu Cys Leu Ile Ser Ala Thr Val Pro Lys Ser Ile
65      70      75      80
Leu Asn Ser Val Ala Ser Thr Asp Ser Ile Ser Phe Leu Gly Cys Val
85      90      95
Leu Gln Leu Phe Leu Val Val Leu Leu Ala Gly Ser Glu Ile Gly Ile
100     105     110
Leu Thr Ala Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Cys Pro Leu
115     120     125
His Cys Glu Ala Val Met Ser Arg Gly Leu Cys Val Gln Leu Met Ala
130     135     140
Leu Ser Trp Leu Asn Arg Gly Ala Leu Gly Leu Leu Tyr Thr Ala Gly
145     150     155     160
Thr Phe Ser Leu Asn Phe Tyr Gly Ser Asp Glu Leu His Gln Phe Phe
165     170     175
Cys Asp Val Pro Ala Leu Leu Lys Leu Thr Cys Ser Lys Glu His Ala
180     185     190
Ile Ile Ser Val Ser Val Ala Ile Gly Val Cys Tyr Ala Phe Ser Cys
195     200     205
Leu Val Cys Ile Val Val Ser Tyr Val Tyr Ile Phe Ser Ala Val Leu
210     215     220
Arg Ile Ser Gln Arg Gln Arg Gln Ser Lys Ala Phe Ser Asn Cys Val
225     230     235     240
Pro His Leu Ile Val Val Thr Val Phe Leu Val Thr Gly Ala Val Ala
245     250     255
Tyr Leu Lys Pro Gly Ser Asp Ala Pro Ser Ile Leu Asp Leu Leu Val
260     265     270
Ser Val Phe Tyr Ser Val Ala Pro Pro Thr Leu Asn Pro Val Ile Tyr
275     280     285
Cys Leu Lys Asn Lys Asp Ile Lys Ser Ala Leu Ser Lys Val Leu Trp
290     295     300
Asn Val Arg Ser Ser Gly Val Met Lys Arg
305     310

```

&lt;210&gt; 1542

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g459 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1542

```

Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys
1      5      10      15
Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr
20      25      30
Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr

```

```

      35      40      45
Asn Asn Thr Leu His Thr Pro Met Tyr Val Phe Leu Leu Thr Leu Ala
 50      55      60
Val Val Asp Ile Ile Cys Thr Thr Ser Ile Ile Pro Lys Met Leu Gly
65      70      75      80
Thr Met Leu Thr Ser Glu Asn Thr Ile Ser Tyr Ala Gly Cys Met Ser
      85      90      95
Gln Leu Phe Leu Phe Thr Trp Ser Leu Gly Ala Glu Met Val Leu Phe
      100      105      110
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      115      120      125
Tyr Ser Thr Val Met Asn His His Met Cys Val Ala Leu Leu Ser Met
      130      135      140
Val Met Ala Ile Ala Val Thr Asn Ser Trp Val His Thr Ala Leu Ile
145      150      155      160
Met Arg Leu Thr Phe Cys Gly Pro Asn Thr Ile Asp His Phe Phe Cys
      165      170      175
Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Pro Val Arg Ile Asn
      180      185      190
Glu Val Met Val Tyr Val Ala Asp Ile Thr Leu Ala Ile Gly Asp Phe
      195      200      205
Ile Leu Thr Cys Ile Ser Tyr Gly Phe Ile Ile Val Ala Ile Leu Arg
      210      215      220
Ile Arg Thr Val Glu Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
225      230      235      240
His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val Ile Tyr Thr Tyr
      245      250      255
Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp Lys Val Val Ala
      260      265      270
Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Met Val Tyr Ser
      275      280      285
Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys Val Phe Ala Phe
290      295      300
Leu Lys His
305

```

&lt;210&gt; 1543

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g460 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1543

```

Met Glu Val Ser Gly Asn His Thr Ser Val Ala Met Phe Val Leu Leu
 1      5      10      15
Gly Leu Ser Asp Glu Lys Glu Leu Gln Leu Ile Leu Phe Pro Val Phe
      20      25      30
Leu Val Ile Tyr Leu Val Thr Leu Ile Trp Asn Met Gly Leu Ile Ile
      35      40      45
Leu Ile Arg Ile Asp Ser His Leu Asn Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Phe Leu Ser Phe Thr Asp Ile Cys Tyr Ser Ser Thr Ile Ser Pro
65      70      75      80
Arg Met Leu Ser Asp Phe Leu Lys Asp Lys Lys Thr Ile Ser Phe Leu
      85      90      95
Ala Cys Ala Thr Gln Tyr Phe Leu Gly Ala Trp Met Ser Leu Ala Glu
      100      105      110
Cys Cys Leu Leu Val Ile Met Ala Cys Asp Arg Tyr Val Ala Ile Gly
      115      120      125

```

```

Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys
 130          135          140
Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His
145          150          155          160
Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pro Asn Ile Ile Gln
          165          170          175
His Phe Phe Cys Asn Thr Leu Gln Ile Ile Ser Leu Ser Cys Ser Asn
          180          185          190
Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly
          195          200          205
Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala
          210          215          220
Ser Ile Leu Lys Ile Ser Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn
225          230          235          240
Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala
          245          250          255
Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys
          260          265          270

```

&lt;210&gt; 1544

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g461 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1544

```

Tyr Ser Lys Glu Ile Ile Glu Xaa Cys Thr Ser Asn Asp Ile Ile Lys
 1          5          10          15
Cys Gly Xaa His Asn Lys Ile Thr Phe Phe Leu Phe Ile Leu Leu Glu
          20          25          30
Phe Thr Glu Asp Leu Gly Leu Gln Val Leu Phe Phe Ile Phe Leu
          35          40          45
Ile Ile Tyr Val Ile Ser Leu Ser Gly Asn Ile Ile Leu Asn Ser Leu
          50          55          60
Ile Cys Ala Asp Ser Trp Pro Tyr Thr Pro Met Tyr Phe Phe Thr Gly
65          70          75          80
Asn Arg Phe Leu Leu Asp Leu Trp Tyr Ser Ser Val His Ile Pro Asp
          85          90          95
Ile Leu Leu Thr Cys Ile Ser Asp Asp Lys Thr Ile Ser Phe Pro Gly
          100          105          110
Cys Leu Ala Gln Phe Phe Ser Ala Val Leu Ala Xaa Asn Glu Cys Tyr
          115          120          125
Met Met Ala Ser Met Ala Tyr Asp Arg Tyr Met Ala Ile Ser Lys Pro
130          135          140
Leu Leu Tyr Ser Arg Ala Thr Phe Pro Glu Leu Cys Ala Ser Leu Val
145          150          155          160
Glu Ala Ser His Leu Gly Gly Phe Val Asn Ser Thr Ile Ile Thr Ser
          165          170          175
Glu Thr Pro Thr Leu Ser Phe Cys Gly Ser Asn Ile Ile Asp Asp Phe
          180          185          190
Phe Cys Asp Leu Pro Pro Leu Val Lys Leu Val Cys Asp Val Lys Glu
          195          200          205
Arg Tyr Gln Ala Val Leu His Phe Met Leu Ala Ser Asn Ile Thr Pro
210          215          220
Thr Ala Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Ala Ala Ile Ser

```

```

225          230          235          240
Lys Ile Arg Ser Ile Lys Gly Arg Leu Gln Val Phe Ser Thr Cys Gly
          245          250          255
Ser Pro Leu Thr Ala Leu Thr Leu Tyr Tyr Gly Ala Ile Phe Phe Ile
          260          265          270
Tyr Ser Gln Pro Arg Thr Ser Tyr Ala Leu Lys Met Asp Lys Leu Gly
          275          280          285
Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
          290          295          300
Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Leu Lys Lys Met Leu Asp
305          310          315          320
Arg Leu Gln Phe Leu Lys Glu Lys Tyr
          325

```

&lt;210&gt; 1545

&lt;211&gt; 349

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g462 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(349)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1545

```

Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly
1          5          10          15
Leu Phe Ser Lys Pro Val Ser Pro Gly Phe Phe Ala Leu Ile Leu Leu
          20          25          30
Val Phe Val Thr Ser Ile Ala Ser Asn Val Val Lys Ile Ile Leu Ile
          35          40          45
His Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
          50          55          60
Leu Ser Leu Arg Asp Ile Leu Tyr Ile Ser Thr Ile Val Pro Lys Met
65          70          75          80
Leu Val Asp Gln Val Met Ser Gln Arg Ala Ile Ser Phe Ala Gly Cys
          85          90          95
Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Ala Gly Ala Glu Phe Phe
          100          105          110
Leu Leu Gly Leu Met Ser Cys Asp Arg Tyr Val Ala Ile Cys Asn Pro
          115          120          125
Leu His Tyr Pro Asp Leu Met Ser Arg Lys Ile Cys Trp Leu Ile Val
          130          135          140
Ala Ala Ala Trp Leu Gly Gly Ser Ile Asn Gly Phe Leu Leu Thr Pro
145          150          155          160
Val Thr Thr Gln Phe Pro Phe Cys Ala Ser Arg Glu Ile Asn His Phe
          165          170          175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser
          180          185          190
Ala Tyr Glu Thr Ala Met Tyr Val Cys Cys Ile Met Met Leu Leu Ile
          195          200          205
Pro Phe Ser Val Ile Ser Gly Ser Tyr Thr Arg Ile Leu Ile Thr Val
          210          215          220
Tyr Arg Met Ser Glu Ala Glu Gly Arg Arg Lys Ala Val Ala Thr Cys
225          230          235          240
Ser Ser His Met Val Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr
          245          250          255
Thr Tyr Val Leu Pro His Ser Tyr His Thr Pro Glu Gln Asp Lys Ala
          260          265          270

```

Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Gln Lys Val Val  
 290 295 300  
 Gly Arg Cys Val Ser Ser Gly Lys Val Thr Thr Phe Lys Gln Ile Ala  
 305 310 315 320  
 Tyr Ala Ala Arg Asp Leu Lys Xaa Arg Ile Gln Asp Phe Ile Ile Ala  
 325 330 335  
 Leu Glu Phe Lys Tyr Ser Leu Pro Gly Asn Lys Xaa Pro  
 340 345

&lt;210&gt; 1546

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g463 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1546

Met Gly Val His Asn Leu Phe Thr Val Thr Gln Phe Ile Leu Ile Gly  
 1 5 10 15  
 Leu Ser Tyr Phe Ser Asn Glu His Tyr Leu Leu Phe Val Ala Leu Ala  
 20 25 30  
 Ile Ile Cys Gln Val Phe Leu Val Arg Ser Gly Asp Ile Leu Leu Ala  
 35 40 45  
 Ile Gly Thr Val Ile Lys Leu His Thr Thr Met Tyr Tyr Phe Leu Ala  
 50 55 60  
 Asn Val Ser Ile Leu Asp Ile Leu Cys Ser Ser Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Pro Lys Ile Leu Xaa Thr Glu Asp His Ser Ile Ser Phe Val Arg  
 85 90 95  
 Xaa Ala Leu Gln Pro Tyr Phe Leu Val Ala Trp Ala Gly Lys Lys Cys  
 100 105 110  
 Phe Leu Thr Val Thr Ala Tyr Asp Trp Cys Val Val Thr Cys Phe Ser  
 115 120 125  
 Leu Cys Tyr Ile Leu Ile Met Asn Lys Leu Val Ser Val Gln Leu Val  
 130 135 140  
 Tyr Gly Thr Xaa Ala Ala Gly Phe Leu Asn Phe Leu Leu Leu His Val  
 145 150 155 160  
 Val Ser Thr Leu Cys Leu Ser Phe Cys Lys Pro Asp Arg Val Asn Gln  
 165 170 175  
 Tyr Tyr Cys Asp Ile Ser Pro Met Gly Ala Leu Leu Cys Gln Ser Met  
 180 185 190  
 His Leu Ala Asn Met Leu Val Leu Val Glu Ser Val Ile Leu Gly Ile  
 195 200 205  
 Ser Ala Phe Leu Ala Ala Phe Asn Phe Tyr Ile Tyr Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Gln Cys Val Glu Trp Ser Ala Lys Cys Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Leu Thr Val Cys Leu Phe Tyr Gly Ile Leu Thr  
 245 250 255  
 Phe Thr Tyr Ile Tyr Ser Phe Ser Ser His Thr His Met Ser Lys Ala  
 260 265 270  
 Ser Pro Asp Leu Ala Thr Asp Arg Leu Ile Ser Met Leu Tyr Arg Val  
 275 280 285  
 Ile Thr Leu Met Phe Asn Phe Ile Thr Asp Asn Leu Arg Asn Thr Glu

|   |  |     |  |     |
|---|--|-----|--|-----|
| 290   |  | 295 |  | 300 |
| Val Lys Gly Ala Ser Glu Arg Phe Tyr Val Ile Glu His Val Tyr |  |     |  |     |
| 305   |  | 310 |  | 315 |

<210> 1547  
 <211> 280  
 <212> PRT  
 <213> Unknown (H38g464 protein)

<220>  
 <223> Synthetic construct

<400> 1547

|   |     |     |     |  |
|---|-----|-----|-----|--|
| Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu Ile |     |     |     |  |
| 1   | 5   | 10  | 15  |  |
| Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser His |     |     |     |  |
|   | 20  | 25  | 30  |  |
| Leu Ala Leu Thr Tyr Phe Ser Phe Ser Ser Val Thr Val Pro Lys Met |     |     |     |  |
|   | 35  | 40  | 45  |  |
| Leu Met Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys |     |     |     |  |
|   | 50  | 55  | 60  |  |
| Ile Ser Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe |     |     |     |  |
| 65  | 70  | 75  | 80  |  |
| Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro |     |     |     |  |
|   | 85  | 90  | 95  |  |
| Leu His Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu Val |     |     |     |  |
|   | 100 | 105 | 110 |  |
| Ala Val Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr Leu |     |     |     |  |
|   | 115 | 120 | 125 |  |
| Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val |     |     |     |  |
|   | 130 | 135 | 140 |  |
| Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe |     |     |     |  |
| 145   | 150 | 155 | 160 |  |
| Leu Asn Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu |     |     |     |  |
|   | 165 | 170 | 175 |  |
| Pro Phe Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile |     |     |     |  |
|   | 180 | 185 | 190 |  |
| Leu Arg Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys |     |     |     |  |
|   | 195 | 200 | 205 |  |
| Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly |     |     |     |  |
|   | 210 | 215 | 220 |  |
| Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile |     |     |     |  |
| 225   | 230 | 235 | 240 |  |
| Val Ala Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile |     |     |     |  |
|   | 245 | 250 | 255 |  |
| Tyr Ser Ile Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe |     |     |     |  |
|   | 260 | 265 | 270 |  |
| Ser Arg Ala Thr Phe Phe Ser Trp                                 |     |     |     |  |
|   | 275 | 280 |     |  |

<210> 1548  
 <211> 303  
 <212> PRT  
 <213> Unknown (H38g465 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(303)  
 <223> Xaa = Any Amino Acid



&lt;400&gt; 1548

```

Met Asn Ser Ser Ser Asp Xaa Arg Gln Pro Val Met Asp Gly Val Asn
 1           5           10           15
Asp Ser Ser Leu Gln Gly Phe Val Leu Met Gly Ile Ser Asp His Pro
 20           25           30
Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu Phe Ser Tyr Leu Leu
 35           40           45
Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu Ser Arg Leu Glu Ala
 50           55           60
Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Ser Leu
 65           70           75           80
Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln Met Leu Ile Asn Leu
 85           90           95
Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly Cys Ile Thr Gln Leu
100          105          110
Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys Ile Leu Leu Val Val
115          120          125
Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg Pro Leu Arg Tyr Thr
130          135          140
Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu Ala Val Ile Ala Cys
145          150          155          160
Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser Thr Phe Thr Leu Gln
165          170          175
Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly Phe Leu Cys Glu Val
180          185          190
Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr Ser Leu Asn Gln Ala
195          200          205
Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala Val Pro Leu Ser Ile
210          215          220
Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala Val Leu Lys Ile Arg
225          230          235          240
Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Leu Ser His Leu
245          250          255
Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser Tyr Gly Tyr Leu Leu
260          265          270
Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys Phe Ile Ser Leu Phe
275          280          285
Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu Ile Tyr Thr Leu
290          295          300

```

&lt;210&gt; 1549

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g466 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(309)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1549

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20           25           30
Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile
 35           40           45
Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn

```

```

      50              55              60
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
65              70              75              80
Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
      85              90              95
Leu Cys Gln Phe Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu
      100              105              110
Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu
      115              120              125
Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu
      130              135              140
Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn
145              150              155              160
Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe
      165              170              175
Cys Asp Val Pro Leu Val Lys Leu Ala Cys Ser Arg Glu Ser Tyr
      180              185              190
Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro Thr
      195              200              205
Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu Arg
      210              215              220
Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser Ser
225              230              235              240
His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn Tyr
      245              250              255
Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val Ser
      260              265              270
Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr Ser
      275              280              285
Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys Ser
      290              295              300
Ala Xaa Ser Lys Val
305

```

&lt;210&gt; 1550

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g467 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1550

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
      20      25      30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
      35      40      45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
65      70      75      80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
      85      90      95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100      105      110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115      120      125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
      130      135      140

```

Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser  
 145 150 155 160  
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly  
 165 170 175  
 Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr  
 180 185 190  
 Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala  
 195 200 205  
 Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala  
 210 215 220  
 Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr  
 225 230 235 240  
 Cys Leu Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser  
 245 250 255  
 Tyr Gly Tyr Leu Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys  
 260 265 270  
 Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu  
 290 295 300  
 Leu Gly Lys Gly Arg Glu Val Gly  
 305 310

&lt;210&gt; 1551

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g468 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(82)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1551

Gly Glu Arg Leu Lys Thr Leu Asn Thr Cys Val Ser His Ile Tyr Ala  
 1 5 10 15  
 Val Leu Ile Phe Tyr Val Pro Met Val Ser Val Ser Met Val His Arg  
 20 25 30  
 Phe Gly Arg His Ala Pro Glu Tyr Val His Lys Phe Met Ser Phe Val  
 35 40 45  
 Pro Pro Met Leu Tyr Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile  
 50 55 60  
 Arg Arg Arg Leu His Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Arg  
 65 70 75 80  
 Lys Thr

&lt;210&gt; 1552

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g469 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1552

Met Glu Val Gly Asn Cys Thr Ile Leu Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Ala Asp Ser Gln Trp Gln Pro Ile Leu Phe Gly Val Phe Leu

[illegible]

**<210> 1553**

<211> 318

<212> PRT

<213> Unknown (H38g470 protein)

<220>

<223> Synthetic construct

<400> 1553

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Thr | Val | Asn | His | Ser | Gly | Thr | Ser | His | Thr | Val | Phe | His | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gly | Ile | Pro | Gly | Leu | Gln | Asp | Gln | His | Met | Trp | Ile | Ser | Ile | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Phe | Ile | Ser | Tyr | Val | Thr | Ala | Leu | Leu | Gly | Asn | Ser | Leu | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ile | Ile | Leu | Thr | Lys | Arg | Ser | Leu | His | Glu | Pro | Met | Tyr | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Cys | Met | Leu | Ala | Gly | Ala | Asp | Ile | Val | Leu | Ser | Thr | Cys | Thr | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Gln | Ala | Leu | Ala | Ile | Phe | Trp | Phe | Arg | Ala | Gly | Asp | Ile | Ser | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Asp | Arg | Cys | Ile | Thr | Gln | Leu | Phe | Phe | Ile | His | Ser | Thr | Phe | Ile | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys  
 130 135 140  
 Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro  
 145 150 155 160  
 Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile  
 165 170 175  
 Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn  
 180 185 190  
 Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr  
 195 200 205  
 Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu  
 210 215 220  
 His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu  
 225 230 235 240  
 Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser  
 245 250 255  
 Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro  
 260 265 270  
 Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met  
 275 280 285  
 Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln  
 290 295 300  
 Val Val Gln Phe Leu Phe Ile Lys Gln Lys Ile Thr Leu Val  
 305 310 315

&lt;210&gt; 1554

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g471 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1554

Met Glu Ala Ala Asn Glu Ser Ser Glu Gly Ile Ser Phe Val Leu Leu  
 1 5 10 15  
 Gly Leu Thr Thr Ser Pro Gly Gln Gln Arg Pro Leu Phe Val Leu Phe  
 20 25 30  
 Leu Leu Leu Tyr Val Ala Ser Leu Leu Gly Asn Gly Leu Ile Val Ala  
 35 40 45  
 Ala Ile Gln Ala Ser Pro Ala Leu His Ala Pro Met Tyr Phe Leu Leu  
 50 55 60  
 Ala His Leu Ser Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro  
 65 70 75 80  
 Lys Met Leu Ala Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Tyr Phe Phe Ala Leu Gly Val Thr Asp  
 100 105 110  
 Ser Cys Leu Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Arg  
 115 120 125  
 His Pro Leu Pro Tyr Ala Thr Arg Met Ser Arg Ala Met Cys Ala Ala  
 130 135 140  
 Leu Val Gly Met Ala Trp Leu Val Ser His Val His Ser Leu Leu Tyr  
 145 150 155 160  
 Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro  
 165 170 175  
 His Phe Phe Cys Asp His Gln Pro Leu Leu Arg Leu Ser Cys Ser Asp  
 180 185 190  
 Thr His His Ile Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val

|   |     |     |
|---|-----|-----|
| 195   | 200 | 205 |
| Val Thr Pro Phe Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala |     |     |
| 210   | 215 | 220 |
| Ala Val Leu Gln Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser |     |     |
| 225   | 230 | 235 |
| Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val |     |     |
| 245   | 250 | 255 |
| Ile Ala Val Tyr Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly |     |     |
| 260   | 265 | 270 |
| Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro |     |     |
| 275   | 280 | 285 |
| Ile Ile Tyr Ser Leu Trp Asn Arg Asp Val Gln Gly Ala Leu Arg Ala |     |     |
| 290   | 295 | 300 |
| Leu Leu Ile Gly Arg Arg Ile Ser Ala Ser                         |     |     |
| 305   | 310 |     |

&lt;210&gt; 1555

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g472 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1555

|   |     |     |
|---|-----|-----|
| Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe |     |     |
| 1   | 5   | 10  |
| Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser |     |     |
| 20  | 25  | 30  |
| Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile |     |     |
| 35  | 40  | 45  |
| Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr |     |     |
| 50  | 55  | 60  |
| Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser |     |     |
| 65  | 70  | 75  |
| Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu |     |     |
| 85  | 90  | 95  |
| Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr |     |     |
| 100   | 105 | 110 |
| Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile |     |     |
| 115   | 120 | 125 |
| Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val |     |     |
| 130   | 135 | 140 |
| Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn |     |     |
| 145   | 150 | 155 |
| Leu Pro Gly Pro Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser |     |     |
| 165   | 170 | 175 |
| Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala |     |     |
| 180   | 185 | 190 |
| Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu |     |     |
| 195   | 200 | 205 |
| Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu |     |     |
| 210   | 215 | 220 |
| Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys |     |     |
| 225   | 230 | 235 |
| Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr |     |     |
| 245   | 250 | 255 |

Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp  
                   260                  265                  270  
 Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro  
                   275                  280                  285  
 Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg  
                   290                  295                  300  
 Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile  
 305                  310                  315

&lt;210&gt; 1556

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g473 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1556

His Thr Glu Pro Trp Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1                  5                  10                  15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser  
                   20                  25                  30  
 Arg Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ile Ile Leu  
                   35                  40                  45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
                   50                  55                  60  
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro  
 65                  70                  75                  80  
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
                   85                  90                  95  
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu  
                   100                  105                  110  
 Asp Met Leu Leu Thr Ala Met Ala Tyr Asp Cys Phe Val Ala Ile Cys  
                   115                  120                  125  
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Ser Val Phe  
                   130                  135                  140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145                  150                  155                  160  
 Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser  
                   165                  170                  175  
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp  
                   180                  185                  190  
 Ser Val Ile Asn Ser Ile Phe Leu Tyr Phe Asp Ser Thr Met Phe Gly  
                   195                  200                  205  
 Phe Leu Pro Ile Ser Arg Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro  
 210                  215                  220  
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser  
 225                  230                  235                  240  
 Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly  
                   245                  250                  255  
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Ser Gly  
                   260                  265                  270  
 Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro  
                   275                  280                  285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg  
                   290                  295                  300  
 Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser

305

310

315

320

&lt;210&gt; 1557

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g474 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1557

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Met Lys Leu Ile Asn His Thr Asp Gln Asn Pro Thr Ser Phe Leu Leu
 1           5           10           15
Met Gly Ile Pro Gly Pro Glu Ala Ser His Phe Trp Ile Ala Phe Pro
          20          25          30
Phe Cys Ser Met Tyr Ala Leu Ala Val Leu Gly Asn Met Val Val Leu
          35          40          45
Leu Val Val His Ser Glu Pro Val Leu His Gln Pro Met Tyr Leu Phe
          50          55          60
Leu Cys Met Leu Ser Thr Ile Asp Leu Val Leu Cys Thr Ser Thr Val
65          70          75          80
Pro Lys Leu Leu Ala Leu Phe Trp Ala Lys Asp Ala Glu Ile Asn Phe
          85          90          95
Gly Ala Cys Ala Ala Gln Met Phe Phe Ile His Gly Phe Ser Ala Val
          100         105         110
Glu Ser Gly Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Leu Ala Ile
          115         120         125
Cys Trp Pro Leu His Tyr Gly Ser Leu Leu Ser Pro Glu Ser Val Gly
          130         135         140
Lys Leu Gly Ala Ala Ala Val Leu Arg Gly Leu Gly Leu Met Thr Pro
145          150         155         160
Leu Thr Cys Leu Leu Ala Arg Leu Ser Tyr Cys Ser Arg Val Val Ala
          165         170         175
His Ser Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Gly
          180         185         190
Thr Gln Pro Asn Asn Ile Tyr Gly Ile Thr Ala Ala Thr Leu Val Val
          195         200         205
Gly Thr Asp Ser Ile Cys Ile Ala Val Ser Tyr Ala Leu Ile Leu Arg
          210         215         220
Ala Val Leu Gly Leu Ser Ser Lys Glu Ala Arg Ala Lys Thr Phe Gly
225          230         235         240
Thr Cys Gly Ser His Leu Gly Val Ile Leu Leu Phe Tyr Thr Pro Gly
          245         250         255
Leu Phe Ser Phe Tyr Thr Gln Arg Phe Gly Gln His Val Pro Arg His
          260         265         270
Ile His Ile Leu Leu Ala Asp Leu Tyr Leu Val Val Pro Pro Met Leu
          275         280         285
Asn Pro Ile Ile Tyr Gly Met Lys Thr Lys Gln Ile Trp Asp Gly Ala
          290         295         300
Leu Arg Leu Leu Lys Trp Gly Pro Ala Gln Ser Xaa Ser Leu Gln Pro
305          310         315         320
His Pro Glu Thr Phe Ile Phe Phe Ala
          325

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&lt;210&gt; 1558

&lt;211&gt; 330

&lt;212&gt; PRT